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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and
uses thereof.



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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, circulating soluble factors, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

5 The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-5497. The polypeptides sequences are designated SEQ
10 ID NO: 5498-10994. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that
15 hybridize to the complement of SEQ ID NO: 1-5497 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-5497. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ
20 ID NO: 1-5497 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-5497. The sequence information can be a segment of any one of SEQ ID NO: 1-5497 that uniquely identifies or represents the sequence
25 information of SEQ ID NO: 1-5497.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed
30 to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their
35 reverse or direct complements) according to the invention have numerous applications in a variety

of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

5 In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-5497 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-5497 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath
10 et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-5497; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-5497;
15 and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-5497. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-5497; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing
20 (*e.g.*, SEQ ID NO: 5498-10994); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (*e.g.* orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

25 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-5497; or (b) polynucleotides that hybridize to the complement of the
30 polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably

produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the
5 polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of
10 interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex
15 and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and
20 monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds
25 that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a
30 polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the
35 administration of the polynucleotides or polypeptides of the invention to individuals exhibiting

symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in the sequence listing). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100

nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-5497.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-5497. The sequence information can be a segment of any one of SEQ ID NO: 1-5497 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-5497. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an

eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

5 The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic
10 elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

15 The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino
20 acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that
25 have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

30 The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue
35 may be removed from the protein during processing in the cell. The peptide may be produced

synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural

or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*,

washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for
5 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse
10 functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided
by the total number of residues in the substantially equivalent sequence is about 0.35 or less).

Such a sequence is said to have 65% sequence identity to the listed sequence. In one
15 embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this
20 embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably
25 at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence
30 identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation
35 of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be

disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

5 The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction
10 of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the
15 suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the
20 context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the
25 nucleotide sequences of SEQ ID NO: 1-5497; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 5498-10994; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 5498-10994. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of
30 the nucleotides sequences of SEQ ID NO: 1-5497; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 5498-10994.
35 Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in

receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-5497 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-5497 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-5497 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-5497, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most

preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-5497, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-5497 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-5497 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the

polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-5497, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-5497 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-5497 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example.

Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia).

- 5 Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many
10 suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed
15 (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine
20 kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the
30 periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination
35 signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-5497, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO: 5498-10994 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-5497 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-5497), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxycarboxymethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of
10 an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified
15 such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the
20 control of a strong pol II or pol III promoter are preferred.

 In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The
25 antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

30 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit
35 translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-5497). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-5497 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and
5 Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical
10 structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or
15 solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral
20 backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For
25 example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or
30 primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug
35 delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the
5 gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than
10 the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or
15 more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the
20 Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No.
25 PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

30 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 5498-10994 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-5497 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a
35 polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-5497 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 5498-10994 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 5498-10994 or the corresponding full length or mature protein; and "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity.

10 Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 5498-10994.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

30 The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 5498-10994.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequence can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing
5 an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present
10 invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification
15 of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form that will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His-tag. Kits for expression and purification of such fusion proteins are commercially available
20 from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other
30 aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*.

The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked
5 in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal
10 activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example,
15 Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or
20 artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease
25 states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be
30 inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*,
5 by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and
10 PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard
15 selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to
20 replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or
25 protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene
30 under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally
35 occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or

5 polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or

10 indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation

15 or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

20 protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic

25 disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as

30 an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of

35 the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its
5 receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

10 Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch
15 and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional
20 sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the
25 polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

30 A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one
35 or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6—Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11—Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9—Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce
5 autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and
10 identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be
15 used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In
20 addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated
25 cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al.,
30 Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention
35 exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions that may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5 A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the
10 growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.
15 WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A
25 protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More
30 specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be
5 sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

10 The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et
15 al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune
20 diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production
25 of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine
30 experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means
35 of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

5 Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected
10 cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

 A polypeptide of the present invention may provide the necessary stimulation signal to T
15 cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain
20 protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as
25 the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

 The activity of a protein of the invention may, among other means, be measured by the
30 following methods:

 Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;
35 Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA

78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bowman et al., *J. Virology* 61:1992-1998; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. *Immunol.* 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1
10 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3,
15 In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in:
20 Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation*
25 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research*
30 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

5 A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention,
10 alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as
15 a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

20 The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci.
25 USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils,
30 T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (*e.g.* proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other
35 trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margules, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates
15 and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

20 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events
25 in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

35 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention
5 may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation,
10 inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma,
15 acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including
20 bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma,
25 tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically
30 effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, *e.g.* reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a
35 portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D,

5 Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate
10 (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

15 In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (*e.g.* exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

20 *In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30
25 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available,
30 *e.g.* from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the
35 invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen
5 recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

10 The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28,
15 Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a
20 ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the
25 present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent
30 molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the
35 novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the

art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The responses of the two cell populations to the addition of ligand(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then

be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

5 Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
10 of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or
15 chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid
20 arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia,
30 acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- 10 (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord
15 infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- 20 (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the
25 nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to
30 diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or
35 injured by a demyelinating disease including but not limited to multiple sclerosis, human

immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye

color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or
5 elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other
10 than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or
15 entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis
20 and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes
25 possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the
30 polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately
35 adjacent to the position of the polymorphism is extended with one or more labeled nucleotides).

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified
5 nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*,
10 by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model
15 system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, *Science*, 219:56, or by B. Waksman et al., 1963, *Int. Arch. Allergy Appl. Immunol.*, 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed *Mycobacterium tuberculosis* in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant
20 mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed *Mycobacterium tuberculosis* in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and
25 24 days after injection of *Mycobacterium* CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

30 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents

include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

5 The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine,
10 lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or
15 complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that
20 therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the
25 relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or
30 simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in
35 combination with other therapies such as treatments employing cytokines, lymphokines or other

hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use

in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systemically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally

capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the

5 compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential
10 matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and
15 biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

20 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,
25 poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the
30 protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and
35 insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue
5 regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution
10 and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

15 Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of
20 proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include
25 compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in
30 the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of

the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred.

The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' , and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of any of the full length proteins of the invention, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region on the surface of the protein of the invention, *e.g.*, a hydrophilic

region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of

adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (*The Scientist*, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the

culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or

myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from

the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)2} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated

by reducing the disulfide bridges of an $F_{(ab)}2$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

5 Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the
10 recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct
15 bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion
20 preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable
25 host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the
30 CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for
35 increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

5.13.8 Immunoconjugates

5 The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

35 4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-5497 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-5497 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited

to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

5 In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see
10 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA
15 molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

20 The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise
25 contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed
30 polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a
35 polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

- 5 Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard,
10 T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the
15 present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a
20 sample which is compatible with the system utilized.

- In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present
25 invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

- In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to
30 another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which
35 contain the reagents used to detect the bound antibody or probe. Types of detection reagents

include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-5497, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester,

ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see
5 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into
10 polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the
15 present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid
20 hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-5497. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-5497 can be used as an indicator of the presence of RNA of cell type of such a tissue
25 in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The
30 probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes
35 *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-Melm₇), is then added to a final concentration of 10 mM 1-Melm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-Melm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, *e.g.*, Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be

employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) *Science* 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) *Nucleic Acids Res.* 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) *Anal. Biochem.* 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) *PNAS USA* 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schrieffer *et al.* (1990) *Nucleic Acids Res.* 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of

these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviJI*, described by Fitzgerald *et al.* (1992) Nucleic Acids Res.

5 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the

subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

- 5 Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic
10 strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader
15 aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon
20 consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

25 5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The
30 inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Rapid
5 Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from
10 a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-5497 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases
15 (*i.e.*, Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score
20 greater than 300 and percent identity greater than 95%.

The novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-5497) of the present invention are incorporated in the attached Sequence Listing. A subset of the predicted polypeptide sequences contain an unknown amino acid; a stop codon; a possible nucleotide deletion; or a possible nucleotide insertion. These sequences have also been
25 shown in their entirety in Table 2. Table 2 also shows the corresponding start and stop nucleotide locations to each of SEQ ID NO: 1-5497. Table 2 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to
30 a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers

to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-5497 were obtained by a BLASTX version 2.0a1 19MP-WashU search against Genpept release 122 and Geneseq release 200105 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-5497. The nearest neighbor results for SEQ ID NO: 1-5497 are incorporated in the attached Sequence Listing.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. The attached Sequence Listing provides the results obtained by eMatrix analysis for each polypeptide as follows: the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. The attached Sequence Listing provides the results obtained by pFam analysis for each polypeptide, namely: the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

Tables 1 and 2 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-5497. Table 2 shows the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 2 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO: in USSN 09/770,160.

Table 1

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
|---------------|------------|--------------|---|
| adult brain | GIBCO | AB3001 | 81-82 126 136 154-156 175-177 213-215 278-283 346-349 445-446 459 491-492 543 561-562 652-653 709-711 755-757 794-795 822-823 899 924 971-988 995 997-998 1017- 1021 1026-1027 1036-1037 1048 1085 1128 1143 1154 1173 1202-1204 1269-1270 1290- 1291 1300-1301 1320-1321 1353-1355 1357- 1359 1363-1371 1388 1394-1396 1410 1415- 1417 1422-1424 1426 1455-1456 1465-1470 1508-1510 1533-1535 1541-1546 1550 1580- 1581 1585 1588-1589 1592 1603-1608 1648 1655 1663 1674-1682 1685 1709 1719-1721 1723 1727-1734 1746 1753 1755-1756 1773- 1774 1805-1806 1827-1829 1839-1847 1876- 1877 1915-1918 1951 2005 2021-2024 2027- 2034 2042-2043 2054 2057 2072-2074 2092 2096-2097 2118 2144-2145 2177 2188-2190 2193-2195 2208-2210 2214-2215 2251-2252 2281-2283 2288-2291 2294-2299 2331 2344 2382 2417-2420 2422 2430 2437 2439-2441 2446 2456 2483 2496 2499 2510-2513 2552 2656 2686 2741-2743 2746-2747 2774-2778 2783 2786 2842-2843 2857-2860 2865 2873- 2874 2879-2881 2883-2884 2960-2962 2976- 2977 3009 3136-3137 3139-3148 3167-3168 3170-3171 3174 3198 3207 3213-3214 3220- 3222 3230 3240 3257-3259 3276-3277 3280- 3282 3289-3290 3304-3307 3323-3324 3345- 3346 3394-3395 3456 3477-3478 3536-3543 3558-3562 3587 3689 3694-3696 3729-3730 3737-3738 3772 3822-3825 3831-3833 3864- 3865 3891 3963-3965 4001 4055-4056 4060- 4061 4093 4098 4112-4113 4123 4125 4136- 4141 4230-4231 4273-4274 4291-4295 4520 4546-4548 4569-4571 4575-4576 4691-4692 4740-4741 4796-4797 4804-4805 4864-4865 4900 4907-4909 5148-5149 5276-5277 5295- 5296 5298-5302 5464-5466 |
| adult brain | GIBCO | ABD003 | 1-11 52 64 81-82 123 154-156 175-177 233 248 258-260 278-283 313-315 335 339 354 357-361 365 379-380 388-390 394 459 491- 492 557 561-562 574-577 582 597-598 607 652-653 670-671 677-678 682-684 719-722 743-744 794-795 799-800 814-816 818 822- 823 840-844 863-869 873-875 878 882-886 889-897 909-914 916-920 924 927 930-936 944-960 964-966 969 971-988 993-995 997- 999 1008-1009 1017-1021 1023-1027 1036- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
|---------------|------------|--------------|--|
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| adult brain | Clontech | ABR001 | 3-11 70 137 175-177 478 491-492 597-598 755-757 796 852-854 910-914 964-966 1026-1027 1049 1158-1159 1173 1198-1201 1271 1274 1281-1282 1297 1351 1363-1371 1389 1479 1671-1673 1685 1719-1721 1784-1790 1870-1875 1900-1902 1919-1922 1926-1927 2035 2072-2074 2224-2228 2298-2299 2305-2306 2404 2419-2420 2436 2528-2531 2644 2713-2714 2751 2762 2774-2776 2786 2978 3113 3151-3152 3181-3183 3213-3214 3424-3427 3554-3556 3577-3582 3587 3595-3596 3638-3640 3663 3742-3744 3853 3911-3919 3931 3941-3942 3962 4036-4039 4077-4079 4125 4220-4223 4320 4545 4549 4570-4571 4672-4674 4738-4739 4764-4766 4781 4815 4910 5001-5003 5435-5437 5464-5466 |
| adult brain | Clontech | ABR006 | 47 126 130 154-156 278-283 395 561-562 583-590 661-662 709-711 855-856 889-897 903-905 909 945 961-962 1063-1067 1069 1088 1095 1154-1155 1235-1236 1281-1282 1349-1350 1360-1362 1394 1418-1420 1580-1584 1626 1634-1637 1671-1673 1688-1689 1694-1698 1715-1716 1728-1734 1763-1764 1770-1771 1773-1774 1839-1844 1903-1911 1913-1914 2027-2030 2035 2054-2056 2076-2077 2121-2124 2145 2163-2168 2188 2197-2199 2214-2215 2445 2591-2592 2598 2650 2686 2737-2738 2745 2774-2778 2857-2860 3323-3324 3328-3330 3342-3344 3354 3396-3398 3498-3501 3536-3543 3658-3660 3856-3857 4300-4308 4379-4380 4410-4412 4451-4452 4481-4489 4549 4624-4626 4660 4824-4826 4832-4834 4967-4970 5050-5052 5278-5279 |
| adult | Clontech | ABR008 | 30-31 39-40 45-46 62 74-77 81-82 116-119 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| brain | | | 129-130 136-137 143-148 154-156 175-177 187-190 195-196 216-218 227-230 254 258- 260 294-295 301-303 313-315 340 388-390 395-398 400-404 407-410 413-414 435 449 465 493-495 499 509 520-521 531-532 545 557-560 579-581 592-594 602-603 607 611 629-630 647-649 652-653 659-660 675-676 685 697-698 709-711 747-750 758-759 796 804-808 817-818 829-831 836-837 840-844 885-886 903-905 909-914 916-918 924 944 946-949 957-960 971-974 993-994 997-1002 1017-1021 1028 1038-1040 1042-1049 1053- 1054 1070-1072 1076 1095 1117-1119 1128- 1136 1139-1143 1151-1154 1160-1164 1175 1182-1184 1192 1202-1204 1222-1223 1228 1230-1232 1235-1236 1271 1278-1282 1285 1294-1296 1320-1321 1323-1327 1349-1350 1353-1354 1357-1359 1380 1383-1384 1386- 1387 1389 1398-1401 1403-1404 1407 1411 1421-1423 1426-1432 1446-1449 1451-1456 1463-1464 1479-1480 1485 1488 1491-1494 1508-1510 1527-1538 1547-1548 1557 1580- 1584 1605-1608 1629-1632 1634-1638 1640- 1645 1648 1667-1670 1685 1691-1692 1694- 1698 1701-1704 1706-1709 1715-1716 1724 1727 1737-1739 1742-1746 1754 1765-1769 1773-1774 1780-1783 1796-1817 1827-1829 1839-1844 1848-1851 1870-1875 1879-1885 1896-1897 1900-1911 1915-1922 1926-1927 1950 1952-1962 1966-1974 1978-1979 1981- 1983 1990-1991 2005-2007 2010-2013 2017- 2020 2025-2030 2040-2041 2044 2048 2052- 2053 2055-2056 2058-2059 2062-2064 2068- 2074 2076-2079 2095 2118 2134-2136 2138- 2142 2144-2147 2161-2162 2174-2177 2186- 2188 2191-2199 2204-2215 2223-2233 2254- 2257 2281-2282 2286-2291 2347-2356 2362 2380-2381 2419-2420 2437 2456 2464 2496 2511-2513 2534-2536 2548 2554-2556 2592 2596 2603-2604 2626 2629-2631 2633-2637 2645-2647 2650-2655 2657-2658 2665 2669- 2671 2675-2680 2696-2697 2702-2705 2709- 2711 2728-2729 2749-2750 2762 2777-2778 2784 2828-2829 2843 2846-2850 2857-2862 2865 2869-2870 2885-2888 2904 2925-2929 2931-2939 2945-2946 2955 2969-2973 3084- 3085 3118 3136-3137 3172-3173 3196 3208- 3209 3213-3216 3219 3229-3230 3234 3240 3243 3304-3307 3312 3331-3332 3342-3346 3371 3403-3404 3406-3407 3424-3427 3444- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| adult brain | Clontech | ABR011 | 154-156 388-390 1076 1128 1182-1184 1193 1202-1204 1422-1424 2072-2074 2144 2251- 2252 2549-2550 4062-4064 5298-5302 |
| adult brain | BioChain | ABR012 | 440-441 602-603 889-897 997-998 1582- 1584 1719-1721 1780-1783 2072-2074 2186- 2187 2223 2377-2379 3394-3395 4291-4295 4581-4582 5123-5124 |
| adult brain | Invitrogen | ABR013 | 341-344 491-492 1205-1207 1580-1581 1599-1602 1857-1859 1925 2072-2074 2186- 2187 2208-2210 2377-2379 2469 3250-3252 3304-3307 4267-4270 4796-4797 |
| adult brain | Invitrogen | ABT004 | 12-13 38 52 70 92-95 126 175-177 255-257 291 341-344 346-349 354 478 557 583-590 612-620 675 789-793 796 840-844 871-872 879-884 909 919-920 964-966 997-998 1017- 1021 1026-1027 1042-1043 1051 1070-1071 1076 1088 1108 1151-1153 1160-1164 1193 1217-1218 1228-1229 1269-1270 1281-1282 1320-1321 1349-1350 1385 1427-1431 1467- 1469 1485 1532 1575-1576 1626 1629-1632 1640-1645 1708 1715-1716 1727 1742-1746 1773-1774 1799-1804 1807-1813 1852 1860 1865-1875 1900-1911 1948-1949 1954-1962 1964-1965 1981-1983 1990-1991 2010-2013 2036-2037 2054 2072-2074 2078-2082 2086- 2087 2143-2147 2174-2176 2186-2187 2224- 2228 2231-2232 2255-2257 2264 2284 2310- 2312 2369-2375 2397-2399 2419-2420 2436 2526-2527 2592 2604 2624 2626 2629-2631 2696-2697 2734 2751 2785 2813 2857-2860 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| cultured preadipocytes | Stratagene | ADP001 | 74-77 134 154-156 175-177 201-205 213-215 278-283 313-315 489-492 520-521 652-653 670-671 680-684 736-740 743-744 784-786 796 814-816 822-823 857-859 885-886 944 950 964-966 994 1028 1042-1043 1052 1069- 1071 1089-1091 1129-1130 1143 1154 1156 1172 1198-1204 1249-1255 1278-1280 1317- 1318 1320-1321 1351 1359 1380 1410 1455- 1456 1473 1507 1532-1535 1547-1548 1553- 1556 1559-1560 1588-1589 1611 1617-1619 1640-1645 1648 1663 1666 1723-1724 1727 1746 1755-1756 1765-1769 1773-1774 1780- 1783 1839-1844 1870-1877 1925 1990-1991 2060-2061 2118 2193-2195 2197-2199 2223 2234-2242 2298-2299 2310 2331 2380-2381 2443 2452-2454 2524-2525 2572-2573 2591- 2592 2594-2595 2604 2672-2674 2709-2711 2734 2739 2819 2843-2847 2861-2862 2899- 2900 2913 2925-2929 2979 2985 3013-3014 3159-3162 3181-3183 3189-3191 3220-3222 3253-3255 3285 3310-3311 3462 3486-3487 3587 3638-3640 3673-3677 3754 3804-3806 3815-3816 3871-3872 3969-3971 4014-4015 4036-4039 4068-4069 4140-4141 4241-4242 4254 4341 4534 4554-4555 4570-4571 4581- 4582 4622-4623 4740-4741 4864-4865 4910 5001-5003 5038-5039 5095-5097 5137-5140 |
| adrenal gland | Clontech | ADR002 | 1-2 12-13 35 52 62 100-106 121-122 140-142 153-156 191-192 213-215 221 232 301-303 306 313-315 341-344 366-367 394 459 491- 492 513 551-553 583-590 592-595 652-653 670-671 719-722 728-733 743-744 747-750 755-757 772 784-786 814-816 847 849-851 889-897 909-914 916-920 944 946-949 961- 962 993-995 997-999 1049 1070-1071 1078 1089-1091 1117-1119 1128 1151-1153 1160- 1164 1175 1182-1184 1193 1220-1221 1269- 1270 1272-1273 1287 1307 1352 1355 1357- 1359 1407 1415-1417 1422-1423 1480 1485 1498-1499 1505 1507-1510 1526 1541-1546 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| adult. heart | GIBCO | AHR001 | 45-46 52 56 100-106 133-134 140-142 154- 156 173 175-177 192 195-196 201-205 212- 218 227-230 235 278-283 286-287 301-303 313-315 323 332-333 341-344 346-352 366- 367 379-380 395 400-404 413-414 436 469 478 491-492 511 520-521 531-532 551-553 557 574-577 583-590 599-601 604 607 612- 620 652-653 675 677-678 680-685 697 707 743-744 784-786 789-796 799-800 814-816 822-823 847 885-886 889-897 915-920 924- 929 931-936 944-945 950 957-960 964-966 969 971-979 992 994-1002 1017-1027 1044- 1050 1052-1054 1056-1057 1063-1067 1070- 1071 1075 1110-1113 1117-1119 1127-1136 1139-1143 1154 1156 1159 1172-1173 1182- 1185 1192-1193 1202-1207 1220-1221 1228 |

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| adult kidney | GIBCO | AKD001 | 32-34 36-37 39-40 42 45-47 74-78 87 100- 106 116-119 136 165 175-177 213-218 220 223-231 235 244 252-253 258-260 278-283 298-300 313-320 324-325 332-333 341-344 346-349 364 366-367 379-380 394 396-398 419 436 440-441 445-446 452 474 491-492 498 519 548-553 557 574-577 583-590 602- 603 607 629-630 652-653 677-678 682-684 707 709-711 719-722 728-733 736-740 778- 786 789-793 799-800 806-808 814-816 822- 823 836-838 840-844 852-854 857-859 871- 875 879-886 889-897 899-905 909-915 919- 920 924-926 931-936 944-962 964-966 969- 974 980-988 994-995 997-998 1000-1009 1017-1021 1026-1027 1036-1040 1042-1043 1049-1050 1052 1063-1071 1075-1076 1078- 1079 1081-1082 1085 1088-1091 1110-1113 1116-1121 1127-1130 1137-1142 1151-1155 1159 1172-1173 1182-1184 1189-1193 1198- 1207 1217-1218 1220-1221 1230-1232 1235- 1236 1249-1260 1269-1271 1278-1280 1287 1294-1297 1300-1301 1307 1315-1321 1328 1334-1335 1349-1350 1352-1354 1357-1362 1374 1385-1389 1397-1399 1403-1407 1410 1414-1420 1422-1423 1425-1426 1435-1436 1438 1440-1441 1444 1451-1462 1465-1466 1470-1472 1475-1477 1479 1481-1485 1488- 1489 1498-1499 1504-1505 1507-1510 1515- 1517 1524 1527-1532 1536-1538 1540-1548 1551-1557 1561-1563 1569-1576 1579-1589 1591 1597 1603-1608 1611-1619 1625-1626 1634-1648 1653-1654 1656 1663-1665 1667- 1682 1685 1688-1692 1694-1698 1701-1704 1707-1708 1710-1716 1719-1721 1723-1724 1727-1739 1743-1746 1753 1755-1758 1763- 1771 1773-1783 1796-1798 1805-1806 1814- 1817 1830-1847 1857-1860 1865-1877 1882- 1885 1903-1911 1913-1922 1925-1927 1948- 1953 1964-1974 1978-1979 1981-1983 1993- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| adult kidney | Invitrogen | AKT002 | 1-2 70 278-283 313-315 379-380 457 491- 492 574-577 582 604 652-653 699-701 707 709-711 719-722 764-771 794-795 814-816 822-823 840-844 906-909 924 944 950 963 975-988 993 995 1017-1021 1042-1043 1063- 1067 1070-1071 1076 1079 1110-1113 1117- 1119 1128 1137-1143 1172 1182-1184 1193 1208-1212 1220-1221 1235-1242 1278-1280 1287 1297 1315-1318 1323-1328 1355 1357- 1358 1360-1371 1374 1397 1405-1406 1414 1418-1420 1425 1457-1462 1488 1507 1515 1536-1538 1547-1548 1551-1552 1559-1560 1579 1626 1656 1664 1674-1682 1685-1689 1691-1693 1706 1708 1710-1716 1719-1721 1728-1734 1737-1739 1753 1773-1774 1845- 1851 1870-1875 1897 1903-1911 1913-1914 1925 1948-1949 1951-1953 1978-1979 1981- 1983 1990-1991 2004-2005 2017-2020 2027- 2030 2038 2048 2054 2062-2064 2072-2074 2076-2077 2116 2118 2125-2133 2156-2160 2174-2176 2179-2181 2186-2188 2208-2210 2214-2215 2224-2228 2275 2277 2296-2297 2321 2377-2379 2391 2397-2399 2421 2428 2452-2454 2473-2474 2492-2494 2499 2528- 2531 2536 2560 2579-2584 2592 2594-2595 2608-2616 2706 2734 2781 2785 2818 2843- 2845 2854 2861-2862 2886-2887 2974-2975 2979 2984 2996-2998 3008 3100 3139-3147 3149 3151-3152 3156-3157 3184 3195 3218 3250-3252 3260-3267 3269 3313 3325-3327 3336-3338 3341-3344 3424-3427 3550-3552 3554-3556 3590 3624-3625 3628 3658-3660 3663 3693 3791 3822-3824 3943-3948 4004 4040-4042 4055-4056 4076 4093 4109-4111 4232-4235 4241-4242 4275-4277 4534 4549 4622-4623 4633-4634 4740-4741 4764-4766 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| adult lung | GIBCO | ALG001 | 78 136 138-139 175-177 313-315 324-325 341-344 413-414 440-441 456 491-492 511 557 652-653 677-678 728-733 784-786 794- 795 822-823 849-851 855-856 885-886 919- 920 954-960 975-988 992-993 997-999 1003- 1006 1017-1021 1026-1027 1042-1043 1053- 1054 1075 1088 1129-1130 1143 1182-1184 1189-1191 1198-1201 1208-1212 1271 1297 1300-1301 1317-1318 1352-1355 1374 1407 1422-1423 1455-1462 1481-1484 1488-1489 1497 1507-1512 1516-1517 1532-1535 1541- 1548 1551-1556 1582-1584 1588-1589 1591 1603-1604 1611 1617-1619 1663 1723 1727- 1734 1742-1746 1753 1780-1783 1814-1817 1831-1834 1852 1870-1875 1919-1922 1925 1951 2005-2007 2038 2058-2061 2072-2074 2086-2087 2116 2118 2121-2136 2144 2153- 2155 2163-2168 2179-2181 2186-2187 2214- 2215 2223-2228 2230 2234-2242 2277 2283 2296-2299 2331 2380-2382 2389-2390 2467- 2469 2473-2474 2499 2536 2553 2564-2571 2574-2575 2604 2672-2674 2677-2680 2749- 2750 2759 2761 2774-2776 2843 2855-2856 2913 2957 2960 2969-2973 3081 3084-3085 3098-3099 3156-3157 3167-3168 3213-3214 3220-3222 3226-3228 3238 3256 3280-3282 3289-3290 3319-3322 3333-3335 3409-3410 3442 3466-3468 3558-3560 3588 3621-3625 3628 3689 3776-3777 3815-3816 3893 3908 4040-4042 4068-4069 4114-4116 4136 4232- 4235 4291-4295 4335-4337 4404-4407 4439 4545 4672-4674 4756-4757 4796-4797 4804- 4805 4886 4907-4909 5001-5003 5046-5047 5095-5097 5142-5143 5387-5388 5464-5466 |
| lymph node | Clontech | ALN001 | 39-40 143-148 154-156 269 278-283 313-315 445-446 728-733 736-742 764-771 814-816 822-823 931-936 950 961-962 994 1000-1002 1017-1021 1129-1130 1139-1142 1151-1153 1182-1184 1198-1204 1244-1246 1256 1319 1359 1398-1399 1425 1438 1455-1462 1478 1504 1507 1511-1512 1532 1539 1547-1549 1553-1556 1575-1576 1617-1619 1648 1659- 1660 1663 1719-1721 1735-1736 1753 1755- 1756 1839-1844 1857-1859 1919-1922 1925 1951 1993-1998 2004 2038 2042-2043 2048 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| young liver | GIBCO | ALV001 | 48-50 78 100-110 210-211 255-257 261-266 278-283 286-287 313-320 332-333 381-383 395 419 435-436 491-492 548-553 574-577 652-653 677-678 709-711 755-757 784-786 789-793 799-803 806-808 822-823 840-844 852-854 910-914 916-918 924 944 969 995 997-998 1056-1057 1063-1068 1085 1089-1091 1116 1120-1121 1128-1130 1139-1142 1151-1155 1172 1177-1179 1182-1184 1189-1191 1198-1201 1205-1207 1217-1218 1220-1221 1230-1232 1249-1256 1269-1273 1290-1291 1300-1301 1310-1314 1323-1328 1357-1358 1360-1362 1374 1410 1418-1420 1479-1484 1497 1507 1516-1517 1527-1531 1541-1546 1551-1552 1557 1579-1581 1585 1590 1592 1613-1619 1626 1656 1664 1685 1691-1692 1694-1698 1701-1702 1708-1709 1723 1725-1726 1735-1739 1753 1759-1762 1765-1771 1773-1774 1780-1790 1796-1798 1827-1829 1835-1838 1848-1852 1865-1875 1882-1885 1903-1911 1913-1914 1919-1922 1925 1951 1964-1965 1978-1979 2005 2031-2034 2060-2061 2075 2086-2091 2096-2097 2118 2144 2153-2160 2174-2176 2188 2200-2201 2223-2228 2234-2242 2244-2245 2281-2282 2288-2291 2321 2358 2380-2382 2414-2415 2423-2424 2427 2447 2451 2469 2477-2479 2484-2485 2503-2504 2510 2533 2543-2544 2560 2564-2571 2579-2584 2587 2648 2761 2836-2839 2843 2865 2873-2874 2879-2881 2945-2946 2951-2952 2957 2974-2975 3013-3014 3076-3078 3139-3147 3151-3152 3156-3157 3181-3183 3195 3226-3228 3242 3250-3252 3280-3282 3299 3310-3311 3328-3330 3345-3346 3403-3404 3456 3462 3561-3562 3599-3601 3619-3625 3628 3654-3657 3815- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| | | | 3816 3828 3969-3971 4023 4062-4064 4090-4092 4121-4122 4228 4373-4375 4403 4451-4452 4563 4622-4623 4635-4637 4738-4739 4768-4771 4796-4797 4815 4899 4907-4909 4915-4916 4998-4999 5001-5003 5045 5075-5077 5082-5083 5130-5131 5166-5167 5226 5335-5343 5399-5403 5414-5415 5452-5453 5456-5457 5464-5466 |
| adult liver | Invitrogen | ALV002 | 35-37 62 70 107-110 131-132 175-177 192 233 255-257 261-266 278-283 313-315 337 354 365 374-375 445-446 450-451 478 491-492 652-653 801-803 840-844 848 852-854 903-905 944 954-956 995 997-998 1003-1006 1026-1027 1032-1034 1042-1047 1049 1056-1060 1063-1071 1078 1089-1091 1117-1119 1139-1143 1151-1154 1158-1159 1177-1181 1188-1191 1193 1205-1207 1217-1218 1230-1232 1278-1282 1307 1310-1314 1323-1327 1337-1345 1351 1360-1371 1380 1451-1454 1485 1533-1535 1547-1548 1569-1574 1592 1626 1640-1647 1656 1663 1691-1692 1708-1709 1723 1725-1726 1735-1739 1759-1762 1770-1771 1773-1774 1827-1829 1835-1844 1913-1914 1919-1922 1925 1948-1949 1954-1962 1981-1983 2010-2013 2025-2026 2054 2060-2061 2118 2171 2174-2176 2186-2190 2193-2195 2208-2210 2223 2254 2267-2270 2276-2277 2296-2297 2308 2322 2338-2340 2380-2381 2499 2533 2536 2543-2544 2560 2579-2584 2629-2631 2648 2659-2662 2665 2741-2743 2800-2801 2828 2843 2865 2879-2882 2905 2914-2917 2925-2929 2957 2960-2962 2974-2975 3013-3014 3054 3089 3156-3157 3181-3183 3199 3220-3222 3229 3310-3311 3328-3330 3371-3373 3462 3466-3469 3472-3473 3536-3543 3577-3580 3667 3749-3752 3793 3997-3998 4014-4015 4036-4039 4082-4084 4096-4097 4282 4330-4331 4376-4377 4381 4451-4452 4616-4621 4633-4634 4636-4637 4649 4687-4689 4738-4739 4754-4755 4768-4771 4796-4797 5050-5052 5057-5065 5082-5083 5130-5131 5145 5148-5149 5164-5167 5229-5231 5335-5343 5367-5368 5387-5391 5414-5415 5451-5453 |
| adult liver | Clontech | ALV003 | 341-344 370-371 849-851 946-949 1177-1179 1202-1204 1626 1759-1762 1770-1771 1913-1914 2484-2485 3328-3330 4403 4998-4999 5130-5131 |
| adult ovary | Invitrogen | AOV001 | 12-13 32-34 39-40 42 44 47-50 52 63-64 70 74-78 87 100-110 116-119 133 135-139 153 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| | | | 173 175-177 185 201-205 212-215 220 222 227-230 233 245 267-268 277-283 286-287 291 301-303 313-315 321 341-344 357-361 364 372 376-377 379-380 394 396-398 436 445-446 459 462 474 478 491-495 509 511 520-524 538 543 545 551-553 561-562 574- 577 583-594 604-607 611-620 629-630 641 652-653 677-678 682-684 697 699-703 707- 711 719-722 728-733 743-744 747-750 755- 757 764-771 784-786 789-795 801-803 806- 808 814-816 822-825 836-837 840-844 855- 856 863-869 871-875 879-886 889-897 899- 908 910-914 916-920 924 927 930-936 944 950-962 964-966 969 971-988 990-995 997- 1006 1008-1009 1017-1027 1032-1040 1042- 1047 1049 1052-1054 1068 1070-1071 1075- 1076 1078-1079 1081-1082 1089-1091 1095 1108 1117-1121 1128-1142 1151-1156 1158- 1164 1171-1173 1175 1180-1185 1189-1193 1198-1207 1217-1218 1220-1221 1228-1232 1235-1242 1244-1246 1249-1256 1269-1271 1278-1280 1287 1290-1293 1297-1301 1307 1315-1328 1332-1335 1348-1359 1363-1371 1374 1380 1383-1384 1386-1389 1395-1396 1398-1399 1403-1410 1413-1417 1421-1423 1426 1432 1435-1436 1438-1444 1446-1449 1451-1464 1467-1473 1475-1480 1485 1488 1491-1494 1498-1499 1504-1505 1507-1512 1515-1517 1520 1527-1538 1541-1548 1550- 1557 1569-1576 1580-1589 1591 1603-1608 1611-1612 1617-1619 1621-1623 1625 1629- 1632 1638-1645 1648-1654 1656-1658 1663- 1664 1666-1670 1674-1682 1685-1686 1688- 1692 1694-1698 1701-1702 1707-1709 1717 1719-1721 1723 1727-1739 1743-1746 1753 1755-1756 1758 1763-1769 1780-1783 1792- 1817 1827-1830 1835-1838 1848-1853 1860 1865-1877 1879-1885 1900-1911 1915-1922 1925-1936 1948-1953 1964-1965 1978-1979 1981-1983 1990-1991 1993-1998 2000-2002 2004-2005 2017-2024 2027-2037 2042-2043 2045-2048 2052-2061 2066-2067 2076-2077 2080-2082 2086-2091 2093-2094 2096-2100 2111-2115 2118 2125-2133 2138-2147 2151- 2160 2174-2177 2179-2181 2186-2187 2189- 2195 2197-2201 2204-2215 2223 2229 2231- 2232 2234-2242 2251-2252 2254-2262 2264- 2265 2267-2271 2273 2275 2277 2281-2284 2286-2291 2296-2300 2321 2331 2380-2381 2386-2392 2395 2397-2399 2403 2414-2415 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| adult placenta | Clontech | APL001 | 313-315 491-492 605-606 719-722 736-740 834-835 950 971-979 1017-1022 1151-1153 1182-1184 1215-1216 1410 1418-1420 1532 1539-1540 1564-1566 1639 1719-1721 1747-1751 1870-1875 1925 1966-1974 1984 2101-2102 2230 2424 2510 2524-2525 2574-2575 2645-2647 2668 2818 2873-2874 3323-3324 3462 3483 4040-4042 4101-4102 4581-4582 4793-4795 5188-5189 5376 |
| placenta | Invitrogen | APL002 | 12-13 192 364 491-492 520-521 709-711 755-757 789-793 840-844 885-886 975-979 1026-1027 1042-1043 1050 1070-1071 1076 1117-1119 1160-1164 1202-1207 1215-1216 1272-1273 1320-1321 1351 1360-1362 1380 1400-1401 1442-1443 1473 1553-1556 1564-1566 1603-1608 1621-1623 1694-1698 1724 1737-1739 1743-1745 1747-1751 1780-1783 1860 1948-1949 2062-2064 2072-2074 2101-2102 2111-2114 2146-2147 2186-2187 2204-2207 2310 2434-2435 2470-2472 2488 2511-2513 2594-2595 2645-2647 2677-2680 2696-2697 2737-2738 2831-2832 2836-2839 2899-2900 2925-2929 2954 3065-3067 3195 3199 3220-3222 3288 3313 3336-3338 3391 3403-3404 3466-3468 3536-3543 3624-3625 3638-3640 3932-3933 4082-4084 4273-4274 4291-4295 4410-4412 4701-4709 4740-4741 5431-5433 5435-5437 |
| adult spleen | GIBCO | ASP001 | 78 137 154-156 175-177 213-215 274 278-283 313-315 324-325 332-333 341-344 346-349 420 456 479-480 491-492 511 530 557 612-620 652-653 659-660 677-678 699-701 728-733 741-744 764-771 784-786 814-816 822-823 849-851 924 944 950 964-966 975-988 994-995 997-998 1000-1002 1008-1009 1049 1052 1070-1071 1078 1088-1091 1128-1136 1151-1153 1171-1172 1193 1195-1196 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| | | | 1202-1204 1217-1218 1220-1221 1256 1269-1271 1287 1294-1297 1315-1318 1332-1333 1349-1350 1352-1354 1359 1363-1371 1374 1383-1384 1386-1387 1397 1408-1409 1414 1418-1420 1422-1423 1425 1440-1441 1446-1449 1486 1497 1507-1512 1514 1516-1517 1527-1532 1540-1548 1551-1552 1575-1576 1586-1589 1597 1603-1604 1612 1617-1619 1621-1623 1629-1632 1634-1637 1640-1645 1654 1656 1663 1686 1691-1692 1708 1710-1714 1719-1721 1723-1724 1727 1737-1739 1746 1753 1765-1769 1773-1774 1780-1783 1796-1798 1807-1817 1827-1834 1853 1857-1859 1870-1885 1903-1911 1913-1914 1919-1922 1948-1949 1951 1964-1965 1978-1979 2025-2026 2035 2038 2040-2043 2045-2047 2054 2060-2061 2072-2074 2076-2079 2086-2087 2111-2114 2116 2118 2131-2133 2137 2144 2148-2150 2153-2155 2178 2182-2183 2214-2215 2223 2230 2234-2242 2281-2283 2298-2299 2303-2304 2310 2331 2380-2382 2405-2413 2421 2440-2441 2452-2454 2456 2461 2469-2472 2488 2510-2513 2551 2560 2573 2603-2604 2608-2616 2650 2696-2697 2719-2720 2726 2747 2754-2758 2803 2818 2831-2832 2843-2845 2854 2861-2862 2873-2874 2914-2917 2945-2946 2974-2976 3153 3158 3167-3168 3170-3171 3195 3210-3211 3215-3216 3226-3228 3250-3252 3258-3259 3280-3282 3289-3290 3336-3338 3385 3403-3404 3428-3429 3466-3468 3536-3543 3561-3562 3591-3593 3621-3625 3629-3630 3632-3634 3716 3784-3786 3792 3815-3816 3878-3879 3886 3935 3966-3971 4014-4015 4023 4036-4039 4060-4061 4077-4079 4090-4092 4098 4100 4126 4142-4143 4228 4232-4235 4239-4240 4335-4337 4374-4375 4400 4404-4407 4451-4452 4554-4555 4598-4601 4622-4623 4662 4668-4671 4740-4741 4796-4797 4832-4834 4864-4865 4907-4909 4912 4956-4957 5001-5003 5034-5036 5074 5095-5097 5123-5124 5148-5149 5154-5157 5241-5242 5261-5267 5272-5274 5298-5302 5310-5311 5329-5330 5335-5343 5427-5429 5440-5441 5485 |
| testis | GIBCO | ATS001 | 47 81-82 123 136 154-156 175-177 179 227-230 278-283 313-315 341-344 366-367 379-380 456 491-492 574-577 604 652-653 677-678 682-684 699-701 743-744 764-771 784-786 811-816 822-823 826-828 879-881 885- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| | | | 886 906-908 931-936 944-945 950 957-960 969 971-974 993-995 997-1002 1008-1009 1026-1027 1032-1034 1036-1037 1042-1043 1075-1076 1080 1108 1137-1138 1173 1189- 1191 1198-1204 1230-1232 1235-1236 1271 1278-1282 1297 1310-1314 1317-1319 1334- 1335 1349-1350 1357-1358 1374 1397 1403- 1404 1413 1418-1420 1422-1423 1435-1436 1451-1462 1485 1507 1516-1517 1547-1548 1551-1552 1561-1563 1611 1629-1632 1640- 1645 1648 1663 1667-1670 1685 1694-1698 1703-1704 1708 1715-1716 1719-1721 1724 1746 1753 1755-1756 1758 1770-1771 1780- 1783 1814-1817 1827-1829 1848-1851 1853 1865-1869 1882-1885 1898 1925-1927 1948- 1949 1951 1966-1974 1981-1983 2021-2024 2027-2030 2038 2042-2043 2052-2056 2060- 2064 2072-2074 2080-2082 2086-2087 2096- 2100 2118 2144 2146-2147 2153-2155 2177 2186-2187 2216-2221 2231-2232 2234-2242 2254 2267-2270 2275 2283 2310 2331 2380- 2382 2387 2424 2447 2452-2454 2456 2468 2473-2474 2499 2510 2536 2548 2573 2592 2604 2644 2657-2658 2706 2715-2718 2747 2754-2758 2761 2763-2764 2768-2771 2774- 2776 2783 2824-2826 2843 2865-2867 2894- 2895 2898 2945-2946 2961-2962 2989-2990 3008 3013-3014 3017-3020 3029 3139-3147 3167-3168 3195 3204 3212-3214 3217-3218 3226-3228 3242-3243 3256 3285 3289-3290 3304-3307 3339-3340 3442 3558-3562 3576 3588 3595-3596 3628 3689 3691 3707 3723 3735 3795-3800 3810 3871-3872 4014-4015 4040-4042 4060-4061 4071-4075 4114-4116 4121-4123 4126 4136 4142-4143 4230-4231 4241-4242 4252-4253 4335-4337 4379-4380 4449 4465 4542-4544 4549 4581-4586 4598- 4601 4740-4741 4796-4797 4832-4834 4864- 4865 4907-4910 5021-5023 5038-5039 5046- 5047 5107-5108 5284-5289 5372-5373 5387- 5391 5399-5401 |
| Genomic DNA from BAC 63I18 | Research Genetics (CITB BAC Library) | BAC001 | 3895 |
| Genomic DNA from BAC 393I6 | Research Genetics (CITB BAC Library) | BAC002 | 2639-2642 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| adult bladder | Invitrogen | BLD001 | 154-156 175-177 301-303 341-344 652-653 659-660 950 980-988 997-998 1042-1043 1069 1075 1139-1142 1160-1164 1193 1244- 1246 1307 1508-1510 1575-1576 1717 1728- 1734 1746 1805-1806 1870-1875 1882-1885 1903-1911 1981-1983 2004 2006-2007 2038 2060-2061 2072-2074 2118 2191-2192 2273 2283 2294-2295 2344 2639-2642 2721 2747 2818-2819 2914-2917 3112 3212 3280-3282 3424-3427 3470-3471 3536-3543 3664-3665 3691 3760 3791 3795-3800 4014-4015 4082- 4084 4335-4337 4613 4796-4797 4864-4865 4960 5001-5003 5241-5242 5387-5388 5431- 5433 |
| bone marrow | Clontech | BMD001 | 30-31 42 48-50 74-78 114-115 120-123 137 143-165 175-177 213-215 227-230 232 235 278-290 297-303 305-309 313-315 324-325 335 341-344 354 379-380 394-398 435-438 440-441 447-455 462-471 491-492 513 516 520-521 538 551-553 557 561-562 641 652- 653 661-671 674 677-678 680-684 699-701 709-760 763-772 794-795 822-823 849-851 857-859 863-869 882-886 889-897 909-914 916-918 921 924-926 931-936 944-945 950- 956 969 980-988 992-995 997-1021 1026- 1027 1032-1034 1038-1040 1049 1053-1055 1070-1071 1075 1079 1108 1110-1113 1128- 1136 1139-1143 1151-1154 1173 1182-1184 1186-1187 1193 1198-1204 1217-1218 1220- 1221 1228 1230-1232 1249-1256 1264 1269- 1271 1274 1281-1282 1290-1291 1294-1297 1317-1319 1322-1345 1348-1362 1374-1379 1386-1387 1397-1399 1405-1407 1414-1417 1422-1423 1425 1437-1438 1440-1441 1444 1451-1464 1470 1479 1485-1489 1497-1500 1504-1505 1507-1512 1514-1515 1518-1520 1522-1526 1532-1563 1567-1576 1582-1585 1588-1589 1603-1608 1612 1621-1623 1625 1629-1632 1634-1637 1646-1648 1655-1656 1659-1660 1663-1664 1666-1670 1685-1690 1694-1698 1701-1702 1707-1708 1710-1716 1719-1721 1723-1724 1728-1739 1746 1752- 1753 1755-1756 1765-1771 1773-1779 1805- 1813 1830-1838 1853 1857-1860 1870-1875 1879-1881 1894-1896 1913-1922 1925-1936 1948-1951 1963 1966-1974 1978-1979 1993- 1998 2000-2003 2005 2017-2020 2027-2030 2036-2056 2060-2064 2066-2067 2080-2082 2086-2087 2095 2098-2102 2107-2108 2111- 2118 2121-2150 2153-2168 2172 2174-2177 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| | | | 2191-2195 2202-2203 2214-2221 2223 2229 2231-2242 2246-2248 2254 2262 2264 2273 2283 2288-2291 2294-2299 2302 2311-2312 2327-2330 2358 2377-2379 2387-2403 2418 2422-2424 2427 2440-2441 2443 2448-2465 2467-2469 2473-2474 2480 2488 2495 2510- 2513 2519-2520 2528-2531 2560 2572 2592 2598 2604 2628 2644-2648 2650 2656 2677- 2680 2686 2698-2699 2715 2719-2720 2722- 2744 2749-2750 2754-2758 2760-2761 2768- 2771 2774-2776 2781 2783 2785 2793-2820 2824-2826 2829 2843 2846-2847 2863-2867 2873-2874 2888 2891 2894-2895 2904-2905 2931-2939 2945-2946 2965-2973 2976 3008 3011-3012 3017-3022 3029 3041-3049 3054 3100 3102-3105 3150 3166-3175 3181-3186 3188-3194 3204 3208-3209 3212 3220-3222 3226-3230 3235-3243 3245-3252 3256-3273 3276-3277 3280-3283 3285 3289-3290 3299 3304-3307 3319-3322 3341-3346 3372-3373 3402 3406-3407 3422 3424-3427 3438-3441 3446-3449 3456 3466-3468 3470-3471 3486- 3487 3491-3495 3505-3506 3508-3513 3536- 3543 3550-3552 3557-3562 3566-3573 3576 3598-3607 3609-3614 3616-3628 3663-3665 3673-3677 3682 3707 3724-3725 3729-3730 3742-3744 3754 3761 3792 3794-3809 3817- 3821 3826 3828 3836-3861 3867-3869 3878- 3879 3881-3884 3897-3905 3911-3919 3955- 3957 3969-3971 4023 4028-4029 4052 4055- 4056 4082-4084 4094-4095 4101-4107 4109- 4120 4136 4142-4153 4156-4159 4167-4178 4208-4211 4215-4223 4227-4247 4267-4270 4275-4277 4285-4286 4291-4296 4383-4384 4430-4432 4494-4496 4501-4503 4517-4529 4531-4536 4554-4555 4572-4591 4596-4601 4624-4626 4649 4651 4662 4664-4665 4691- 4692 4729 4738-4741 4761-4780 4793-4810 4832-4834 4862-4865 4884 4907-4910 4923- 4928 4930-4931 4933-4935 4937-4943 4945 4961-4985 5001-5003 5038-5039 5050-5052 5080 5114-5115 5137-5141 5148-5149 5153- 5157 5180 5190-5192 5241-5242 5250 5252 5254-5277 5303-5305 5307-5325 5327-5343 5345-5354 5367-5374 5376-5379 5381-5385 5387-5388 5397-5398 5444 5460-5461 5464- 5466 5485 |
| bone marrow | Clontech | BMD002 | 175-177 249-250 254 258-260 301-303 313- 315 324-325 413-414 440-441 491-492 540 574-577 580-581 592-594 599-601 612-620 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| | | | 652-653 724-733 741-750 804-805 814-816 846 849-851 889-897 903-905 910-914 957- 960 970 992 994 997-998 1010-1014 1023- 1027 1038-1040 1089-1091 1095 1110-1113 1128 1202-1207 1217-1218 1235-1236 1256 1271 1297 1319 1330-1333 1348-1350 1352- 1354 1357-1358 1383-1384 1397 1457-1462 1479 1491-1494 1497 1504 1507-1512 1532 1547-1548 1551-1552 1575-1576 1621-1623 1646-1647 1686 1719-1721 1727 1743-1745 1753-1754 1763-1764 1773-1779 1796-1798 1805-1806 1814-1817 1827-1830 1839-1844 1848-1851 1913-1918 1925 1993-1998 2040- 2043 2048 2052-2054 2060-2061 2078-2079 2088-2091 2116-2118 2131-2142 2148-2150 2172 2174-2176 2191-2195 2223 2246-2248 2318-2320 2537-2538 2553 2604 2638 2702- 2705 2709-2711 2713-2714 2739 2781 2796- 2798 2803 2931-2939 2961-2962 3026-3027 3055 3130 3159-3162 3181-3183 3246 3250- 3252 3304-3307 3402 3536-3543 3793 3847- 3849 3925-3926 4024-4025 4060-4061 4209- 4210 4228 4252-4253 4267-4270 4574 4581- 4582 4729 4787 4796-4797 4858 4907-4909 4974 4991-4993 5021-5023 5050-5052 5056 5148-5149 5260-5267 5272-5275 5278-5279 5335-5343 5377-5378 5416 5423-5425 5485 |
| bone marrow | Clontech | BMD004 | 728-733 849-851 1349-1350 1486 1860 2050- 2051 2134-2136 2148-2150 2234-2242 2803 4209-4210 4598-4601 4652-4653 4907-4909 5261-5267 5272-5274 |
| bone marrow | Clontech | BMD007 | 396-398 440-441 453-455 491-492 712-718 764-771 814-816 846 849-851 1096-1104 1146-1147 1315-1316 1486 1497 1522-1523 2134-2136 2148-2150 2223 2803 3250-3252 4598-4601 5001-5003 5050-5052 5310-5311 |
| adult colon | Invitrogen | CLN001 | 1-2 32-34 64 175-177 251 278-283 452 478 814-816 832 870 889-897 944 957-960 1044- 1047 1069 1117-1119 1128 1139-1142 1195- 1196 1217-1218 1317-1318 1386-1387 1511- 1512 1547-1548 1640-1645 1709 1770-1771 1860 1870-1875 1882-1885 1948-1949 1952- 1953 1981-1983 2088-2091 2146-2147 2156- 2160 2174-2176 2208-2210 2254 2347-2348 2511-2513 2604 2629-2631 2737-2738 2831- 2832 2852-2853 2865 3035-3036 3156-3157 3220-3222 3246 3339-3340 3554-3556 3632- 3634 3663 3673-3677 3693 3780-3781 3870 3949-3951 4272 4275-4277 4330-4331 4534 4636-4637 4651 4668-4674 4776 4796-4797 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| Mixture of 16 tissues – mRNAs* | Various Vendors* | CTL016 | 210-211 910-914 995 1128 1479 1617-1619 1626 1784-1790 1913-1914 2901-2903 2979 3831-3833 4796-4797 5001-5003 5075-5077 5154-5157 5414-5415 |
| Mixture of 16 tissues – mRNAs* | Various Vendors* | CTL021 | 175-177 237-240 652-653 801-803 849-851 950 993 1042-1043 1063-1067 1156 1310-1314 1332-1333 1485 1511-1512 1533-1535 1746 2148-2150 2182-2183 2186-2187 2223-2228 2233 2253 2484-2485 2843 2979 3189-3191 3250-3252 4796-4797 4907-4909 5001-5003 5050-5052 5196 5226 |
| adult cervix | BioChain | CVX001 | 1-2 32-34 52 56 70 107-110 123 125 133-134 137 140-142 153-156 175-177 195-196 212 227-230 233 278-283 288-290 301-303 313-315 324-325 335 341-344 365 379-380 394 396-398 491-492 514 520-521 539 583-590 597-598 611 682-684 697 699-701 708 719-722 810 814-816 822-823 840-844 857-859 863-870 873-875 879-881 885-886 889-897 899 903-905 909 915 919-920 925-926 931-936 950-953 957-962 975-988 992-995 997-998 1000-1002 1022 1032-1034 1044-1047 1049 1052 1069 1075 1110-1113 1129-1130 1144-1145 1154-1155 1165-1170 1172-1173 1182-1184 1198-1204 1215-1216 1220-1221 1256 1263 1271 1287 1297 1300-1301 1319-1321 1323-1328 1352-1355 1360-1371 1374 1397 1400-1401 1410 1413 1421 1440-1444 1455-1464 1470 1475-1477 1479-1480 1487 1491-1494 1504 1507-1510 1515-1517 1524 1547-1548 1551-1552 1557 1569-1574 1599-1608 1611 1620 1625 1639 1648 1653-1654 1657-1658 1663 1683-1685 1690 1715-1716 1723 1735-1736 1753-1756 1763-1764 1780-1783 1792-1795 1805-1806 1827-1829 1835-1844 1852 1870-1877 1879-1881 1896 1925-1927 1951 1964-1965 1993-1998 2000-2002 2005 2021-2024 2031-2035 2038 2042-2043 2048 2050-2056 2058-2059 2062-2064 2066-2067 2072-2074 2078-2079 2086-2087 2096-2100 2111-2114 2116 2118 2137 2143-2144 2146-2147 2156-2160 2177-2181 2191-2192 2216-2221 2223-2228 2234-2242 2249 2251-2252 2254-2257 2273 2275 2277 2280-2282 2296-2299 2302 2327-2331 2333-2334 2341 2344 2349-2356 2358 2368 2377-2381 2389-2390 2423-2424 2456 2467 2483 2490-2494 2499 2510-2513 2546 2549-2550 2560 2563 2573-2575 2591 2594-2595 2597 2603-2604 2628-2631 2645-2647 2651-2655 2706 2713- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| | | | 2715 2726 2752-2758 2760 2763 2768-2771 2774-2776 2783 2807 2809 2820 2824-2826 2829 2831-2832 2836-2839 2843-2845 2854 2865-2867 2871-2872 2898 2905 2925-2929 2931-2939 2945-2947 2954 2961-2962 2969- 2976 2979 2981-2983 2985 2989 3009 3017- 3020 3030 3080 3089 3093 3096-3097 3100 3109 3112 3130 3149 3156-3158 3170-3173 3181-3183 3195 3199 3206 3213-3214 3220- 3222 3224-3225 3247-3248 3253-3256 3258- 3267 3280-3282 3285 3289-3290 3292-3293 3310-3311 3319-3324 3341 3345-3346 3349- 3352 3394-3398 3403-3405 3409-3410 3420 3424-3427 3437-3441 3446-3449 3456 3462 3491-3495 3535-3543 3558-3560 3628-3630 3654-3657 3673-3677 3680 3691 3707 3714 3735-3736 3760 3772 3778 3795-3800 3807 3822-3824 3830 3870-3872 3882-3883 3891 3925-3926 3959-3960 3969-3971 4076 4098 4100-4102 4112-4116 4127-4130 4219-4223 4230-4231 4241-4242 4245 4289-4295 4322 4382 4391-4393 4403 4435-4437 4550 4581- 4582 4616-4621 4629-4632 4663 4675 4679 4681-4683 4761-4766 4785 4796-4797 4884 4910 4913 4953 4956-4957 4976-4979 5151- 5152 5177-5179 5272-5274 5284-5289 5293 5303-5305 5335-5343 5421-5425 5431-5433 5464-5466 |
| diaphragm | BioChain | DIA002 | 574-577 1230-1232 1524 1605-1608 2116 2143 2843 3795-3800 4060-4061 4598-4601 |
| endothelial cells | Stratagene | EDT001 | 1-2 32-34 38 45-46 56 70 74-77 137 140-142 165 173 175-177 187-190 195-196 213-215 220 231 278-283 294-295 313-315 330 332- 333 341-344 346-349 364 366-367 379-380 395 445-446 474 491-495 511 520-521 531- 532 545 548-553 574-577 612-620 652-653 682-684 697 704-706 709-711 719-722 801- 803 811-816 822-823 836-837 863-872 879- 881 885-886 889-897 899 903-914 919-920 927 930-936 944 950 954-962 964-966 969 971-988 993-995 997-998 1000-1002 1007- 1014 1017-1021 1026-1027 1032-1034 1036- 1040 1042-1052 1068-1071 1075-1076 1079 1089-1091 1095 1110-1113 1117-1119 1128- 1136 1139-1143 1151-1153 1155-1156 1160- 1164 1172 1192-1193 1198-1204 1217-1218 1220-1221 1235-1242 1244-1246 1249-1255 1281-1282 1287 1294-1297 1300-1301 1315- 1319 1328 1337-1345 1349-1355 1357-1359 1374 1380 1386-1387 1390-1393 1397-1401 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| Genomic clones from the short arm of chromosome 8 | Genomic DNA from Genetic Research | EPM001 | 2639-2642 |
| esophagus | BioChain | ESO002 | 885-886 1639 2223 |
| fetal brain | Clontech | FBR001 | 153 278-283 863-869 1156 1400-1401 1626 1691-1692 1727 2118 2229 2604 2645-2647 2844-2845 3174 3763 3780-3781 4090-4092 4140-4141 4545 4835 |
| fetal brain | Clontech | FBR004 | 855-856 1017-1021 1470 1580-1581 1839- 1844 1978-1979 2052-2053 2084 2171 2249 3197 3451-3455 3713 4960 |
| fetal brain | Clontech | FBR006 | 30-31 39-40 74-77 116-119 130 137 143-148 175-177 187-190 195-196 216-218 223-226 366-367 388-390 400-404 465 491-492 520- 521 557 602-603 607 647-649 652-653 670- 671 676 680-681 685 698 724-727 743-744 760 763 789-793 814-817 824-825 829-831 836-837 849-851 855-856 885-886 889-897 944 994 997-998 1000-1002 1017-1021 1026- 1027 1042-1043 1068-1069 1076 1089-1091 1095 1139-1142 1151-1153 1156 1176 1182- 1185 1192 1220-1221 1228 1230-1232 1332- 1333 1349-1350 1357-1358 1389 1394 1400- 1401 1403-1404 1408-1409 1413 1455-1456 1507-1510 1520 1605-1608 1617-1619 1629- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| fetal brain | Clontech | FBRs03 | 1870-1875 1878 3424-3427 3554-3556 4907-4909 5137-5140 |
| fetal brain | Invitrogen | FBT002 | 32-34 59-60 92-96 124 128 137 180-182 192 195-196 278-283 341-344 436 491-492 520-521 583-590 607 647-649 652-653 677-678 778-783 789-793 822-825 849-854 882-884 950 957-960 964-966 971-974 980-988 1026-1028 1038-1040 1042-1043 1050 1070-1071 1076 1127 1156 1205-1207 1230-1232 1271 1281-1282 1322 1337-1345 1349-1350 1360-1371 1386-1387 1400-1401 1414-1417 1427-1431 1435-1436 1470 1507-1510 1532 1603-1604 1617-1620 1633 1649-1653 1674-1682 1691-1692 1694-1698 1708 1710-1714 1727 1737-1739 1765-1769 1773-1774 1780-1783 1805-1806 1839-1844 1852 1870-1875 1882-1885 1896 1925 1964-1965 1978-1979 1990-1991 1993-1998 2031-2034 2058-2059 2084 2109-2110 2118 2173 2186-2187 2193-2195 2202-2203 2208-2210 2233 2254 2278 2288-2291 2305-2306 2414-2415 2496 2511-2513 2537-2538 2558-2559 2573 2579-2584 2590 2597 2604 2629-2631 2639-2642 2659-2662 2672-2674 2696-2697 2719-2720 2741-2743 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| fetal heart | Invitrogen | FHR001 | 909 1089-1091 1128 1256 1514 1621-1623 3354 4228 |
| fetal kidney | Clontech | FKD001 | 30-31 137 154-156 212 278-283 313-315 326-327 370-371 379-380 491-492 551-553 595 602-604 665-667 680-681 736-740 743- 744 822-823 900-902 950-956 995 1023-1025 1035 1085 1089-1091 1182-1184 1230-1232 1300-1301 1332-1333 1353-1354 1357-1359 1386-1387 1446-1449 1457-1462 1479 1515 1532 1551-1552 1580-1581 1588-1589 1612 1617-1619 1629-1632 1663 1667-1670 1719- 1721 1724 1746 1752-1754 1796-1798 1831- 1834 1845-1847 1896-1897 1925-1927 1951 1981-1983 1993-1998 2035 2045-2047 2111- 2114 2118 2144 2224-2228 2253 2360 2422 2440-2441 2502 2510 2526-2527 2549-2550 2645-2647 2650 2693 2763 2774-2776 2781 2831-2832 2844-2845 2879-2881 2898 2913 2960 2974-2975 2979 3031-3032 3054 3198 3230 3276-3277 3304-3307 3372-3373 3442 3446-3449 3491-3495 3536-3543 3714 3780- 3781 3853 4030-4031 4055-4056 4093 4581- 4582 4679 4864-4865 4907-4910 5001-5003 5038-5039 5050-5052 5142-5143 5148-5149 5329-5330 5372-5374 |
| fetal kidney | Clontech | FKD002 | 313-315 551-553 699-701 743-744 784-786 1017-1021 1173 1182-1184 1403-1404 1753 2055-2056 2116 2118 2223 2253 4598-4601 4907-4909 5001-5003 |
| fetal kidney | Invitrogen | FKD007 | 45-46 491-492 849-851 950-953 1507 1575- 1576 1746 2060-2061 2086-2087 2134-2136 2204-2207 2223-2228 2380-2381 2579-2584 3242 4581-4582 |
| fetal lung | Clontech | FLG001 | 64 350-352 453-455 551-553 736-740 822- 823 863-869 997-998 1000-1002 1035 1042- 1043 1193 1275-1277 1317-1318 1374 1648 1674-1682 1707 1727 1746 1753 1830 1835- 1844 1852 1870-1875 1951 2004 2066-2071 |

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| fetal lung | Invitrogen | FLG003 | 195-196 278-283 341-344 388-390 395 450-451 491-492 849-851 879-881 885-886 950 971-979 995 1128 1193 1237-1242 1269-1270 1386-1387 1450 1507 1514 1605-1608 1709 1746 1780-1783 1830 1835-1838 1848-1852 1860 1865-1875 1990-1991 2010-2013 2060-2061 2072-2074 2094 2174-2176 2233 2253 2283 2526-2527 2579-2584 2594-2595 2836-2839 2844-2845 2888 2896-2897 2913 2951-2952 2979 2985 3008 3123 3149 3200-3202 3212 3258-3259 3280-3282 3466-3468 3508-3513 3536-3543 3605 3629-3630 3691 3749-3752 3793 3840-3841 4016-4018 4114-4116 4258 4330-4331 4598-4601 4897 5102-5104 5119 5276-5277 |
| fetal lung | Clontech | FLG004 | 154-156 971-974 1070-1071 1182-1184 1527-1531 1701-1702 1753 1896 3462 3629-3630 5001-5003 5241-5242 |
| fetal liver-spleen | Columbia University | FLS001 | 1-13 24-27 29-50 52-99 111-113 115 126 133-134 136 140-142 154-156 166-192 195-222 227-230 232-236 241-283 286-287 291 307-310 313-327 330-334 336-361 365-367 369-375 379-383 386-394 396-420 422-431 435-446 453-456 461 474-475 478-481 483-505 507-532 534-545 548-553 557 561-562 565-567 569-577 580-581 583-607 611-620 629-631 633-650 652-653 655-662 682-684 699-701 704-706 709-711 724-727 736-740 743-744 747-750 755-759 773-829 832-835 839-854 857-877 882-886 889-905 909-921 924 927-966 968-969 971-988 990-995 997-1014 1017-1050 1052-1055 1058-1059 1063-1074 1076 1078-1082 1085-1088 1092 1094 1096-1104 1107-1108 1110-1113 1115-1121 1124 1127-1145 1148 1150-1175 1177-1223 1225-1256 1263-1289 1292-1301 1307-1327 1332-1335 1337-1345 1349-1350 1352-1355 1357-1371 1374-1379 1386-1387 1389-1393 1395-1397 1400-1401 1403-1406 1408-1410 1414-1423 1425 1432 1434 1437-1438 1440-1444 1446-1462 1467-1473 1479-1480 1485-1486 1495-1500 1504 1507-1510 1513-1514 1518-1519 1522-1524 1527-1538 1540-1548 1551-1557 1559-1576 1579-1608 1611-1623 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| | | | 4678 4684-4689 4691-4696 4698 4701-4709 4729-4760 4764-4766 4768-4771 4777-4780 4796-4797 4807-4808 4811-4818 4820-4836 4838-4839 4841 4843-4848 4852-4853 4855- 4858 4861 4864-4865 4867-4879 4881-4891 4893-4925 4963 4976-4979 4987-5013 5019- 5041 5043-5065 5071-5073 5075-5088 5092- 5104 5107-5111 5114-5115 5117-5118 5120- 5121 5123-5128 5130-5131 5137-5140 5145 5147-5152 5154-5162 5164-5176 5180-5197 5201 5208 5210-5236 5240-5243 5246-5247 5250-5251 5268-5269 5276-5277 5295-5296 5298-5302 5310-5311 5317-5320 5323-5325 5335-5343 5346-5354 5372-5373 5384 5386- 5391 5393-5398 5402-5410 5413-5415 5417- 5420 5423-5462 5467-5476 5482-5483 5485- 5497 |
| fetal liver- spleen | Columbia University | FLS002 | 3-11 24-27 35 38 42 44 48-50 57 67 70 73-77 85 88 98 107-111 136-142 151-153 165 173 195-196 198 201-205 210-215 219 222 232- 234 236 245 252-254 258-266 277 291 316- 320 332-333 337 354 357-361 365 374-375 381-383 394 406 415-416 418 436-438 445- 446 461 478-480 486 489-490 520-521 527 538 540 543 548-553 574-577 599-601 607 612-620 647-649 677-678 682-685 699-706 709-711 736-740 747-750 755-759 777 788- 793 814-816 818 822-828 833 852-854 863- 869 873-877 885-886 889-897 899-902 906- 914 916-920 924 927-936 946-949 951-956 961-962 969 975-988 990-991 993-995 999- 1014 1023-1037 1041-1047 1052 1055 1063- 1067 1070-1071 1076 1080 1085 1088 1108 1110-1119 1124 1128-1142 1144-1145 1148 1151-1156 1158 1160-1170 1172-1175 1177- 1184 1186-1187 1192-1193 1195-1197 1202- 1204 1208-1212 1215-1218 1220-1221 1225- 1227 1235-1236 1244-1246 1249-1256 1263 1266-1273 1278-1280 1285-1291 1297-1301 1307 1315-1316 1320-1327 1332-1333 1349- 1350 1352-1355 1357-1371 1374-1379 1385- 1387 1389 1395-1397 1405-1406 1410 1414- 1417 1421-1423 1425 1427-1432 1437 1442- 1444 1451-1456 1463-1464 1470-1473 1475- 1477 1479-1480 1485 1498-1499 1515 1536- 1538 1540-1546 1550-1557 1559-1560 1580- 1585 1597 1603-1608 1612-1616 1620 1625- 1627 1629-1632 1638-1653 1656 1661-1662 1664 1667-1682 1685 1691-1692 1694-1699 1701-1704 1706-1707 1709-1714 1717 1719- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| fetal liver-spleen | Columbia University | FLS003 | 210-211 341-344 849-851 1089-1091 1177-1179 1310-1314 1320-1321 1349-1350 1440-1441 1514 1557 1624 1648 2042-2043 2134-2136 2223 2253-2254 2511-2513 2533 2843 2979 4163-4166 4273-4274 4687-4689 4738-4739 4998-4999 5075-5077 5414-5415 5452-5453 |
| fetal liver | Invitrogen | FLV001 | 3-11 52 246-247 255-260 278-283 291 341-344 491-492 596 652-653 709-711 724-727 778-783 814-816 840-844 849-851 882-886 903-905 946-949 964-966 971-988 997-998 1003-1006 1010-1014 1026-1027 1038-1040 1044-1047 1063-1068 1070-1071 1089-1091 1137-1138 1143 1171 1177-1179 1182-1184 1193 1198-1201 1205-1207 1310-1314 1317-1318 1320-1321 1337-1345 1349-1350 1360- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| fetal muscle | Invitrogen | FMS001 | 3-11 154-156 216-218 278-283 313-315 341- 344 388-390 395 478 491-495 511 591 652- 653 704-706 814-816 822-823 889-897 903- 908 925-926 928-929 931-936 946-950 957- 960 980-988 993 1017-1021 1048-1050 1063- 1068 1171 1297-1299 1307 1320-1321 1359 1444 1507-1510 1514 1533-1535 1540 1553- 1556 1585 1605-1608 1639 1694-1698 1710- 1714 1717 1746 1753 1773-1774 1780-1783 1805-1813 1860 1879-1885 1915-1918 2004 2042-2043 2107 2118 2134-2136 2148-2150 2161-2162 2197-2199 2254-2257 2281-2282 2503-2504 2665 2686 2824-2826 2843 2852- 2853 2896-2897 2979 2985 3054 3058-3059 3159-3162 3213-3214 3226-3228 3280-3282 3299 3323-3324 3365-3366 3372-3373 3658- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| fetal skin | Invitrogen | FSK001 | 1-2 39-40 70 92-95 137 157-159 175-177 213-215 246-247 278-283 291 298-300 313- 315 341-344 365 370-371 388-390 419 445- 446 452 478-480 511 516 522-524 538-539 548-553 580-581 597-598 602-603 633-634 647-649 652-653 677-678 685 709-711 784- 786 789-793 814-816 824-829 849-851 863- 870 879-884 903-905 909 919-920 925-926 946-949 957-960 980-988 992-994 997-1002 1010-1014 1017-1021 1035 1042-1047 1050- 1051 1076 1078 1110-1113 1117-1119 1129- 1130 1151-1155 1160-1164 1182-1184 1198- 1204 1237-1243 1256 1271 1290-1291 1307 1310-1314 1320-1321 1323-1327 1351 1355 1357-1359 1380 1385 1390-1393 1400-1401 1414 1418-1420 1432 1435-1436 1450 1457- 1462 1479 1488-1489 1507-1510 1524 1533- 1535 1547-1548 1550-1552 1567-1568 1575- 1576 1579 1585 1588-1589 1611 1617-1619 1621-1623 1653-1655 1663 1686 1688-1689 1691-1692 1694-1698 1703-1704 1710-1714 1743-1746 1753 1765-1771 1773-1774 1780- 1783 1807-1813 1830-1834 1848-1852 1865- 1878 1882-1885 1903-1911 1915-1918 1925- 1927 1954-1962 1964-1965 1981-1983 1990- 1991 2006-2007 2017-2030 2038 2054 2068- 2071 2076-2079 2088-2091 2098-2100 2107 2118 2145 2153-2155 2173 2177 2179-2181 2188 2191-2192 2204-2210 2214-2215 2246- 2248 2251-2253 2267-2271 2277 2280 2286- 2291 2305-2306 2310 2338-2340 2376 2386 2432 2434-2435 2437 2469 2483 2490-2491 2510-2513 2526-2527 2560 2563 2572-2573 2588-2589 2594-2595 2603 2628 2659-2662 2696-2697 2734 2741-2743 2754-2758 2782 2787-2789 2813 2819 2824-2826 2828 2831- 2832 2843-2845 2855-2860 2865 2873-2874 2905 2914-2917 2925-2929 2945-2946 2951- 2952 2955 2961-2962 2965-2975 2979 2981- 2983 2985 2989 2996-2998 3000 3008 3023 3082 3109-3110 3151-3153 3156-3157 3167- 3168 3195 3213-3216 3220-3222 3234 3247- |

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| fetal spleen | BioChain | FSP001 | 175-177 743-744 1171 1202-1204 1457-1462 1753 2060-2061 2116 2143 2223 2253 2728-2729 4167-4168 5001-5003 5335-5343 5444 |
| umbilical cord | BioChain | FUC001 | 1-2 30-31 47 52 70 74-77 100-106 154-156 191 201-205 258-260 267-268 270-272 277-283 298-303 341-344 370-371 379-380 388-390 445-446 457 461 478-480 491-492 557 592-594 605-606 652-653 677-678 743-744 814-816 822-823 847 849-851 863-869 903-905 909-914 919-920 944 950 957-960 970-974 980-988 994-995 1038-1040 1042-1043 1049 1052 1069-1071 1075 1108 1117-1119 1128-1130 1151-1154 1160-1170 1173 1182-1184 1189-1191 1198-1207 1220-1221 1230-1232 1256 1269-1270 1294-1301 1320-1321 1349-1350 1355 1357-1358 1363-1371 1374 1389 1397 1410 1422-1423 1439-1443 1450-1454 1470 1473 1479 1486 1488 1497-1499 1507-1510 1514 1522-1523 1532-1535 1551-1552 1569-1574 1577-1578 1599-1602 1611 1620 1648-1652 1661-1663 1671-1673 1688-1689 1694-1699 1703-1704 1706-1707 1710-1716 1719-1721 1724 1737-1739 1746 1753 1755-1756 1773-1774 1780-1783 1796-1798 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| fetal brain | GIBCO | HFB001 | 3-11 32-34 39-40 42 78 81-82 100-110 116-119 124-142 154-156 165 175-177 195-196 201-205 212-218 220 278-283 286-287 291-296 313-315 335 341-344 346-349 366-367 379-380 388-390 396-398 419 456-461 491-492 511 551-553 557 561-562 574-577 583-590 651-653 676-679 682-694 697-711 743-744 784-786 804-805 814-816 822-825 848-851 855-859 863-869 871-872 882-884 899-902 915-918 927 930-936 944-945 951-953 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| macrophage | Invitrogen | HMP001 | 244 278-283 440-441 445-446 794-795 855-856 995 999 1017-1021 1353-1354 1507 1582-1584 2223 4228 4864-4865 5490-5491 |
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| infant brain | Columbia University | IB2003 | 35 39-40 126 180-182 195-196 244 278-283 296 341-344 350-352 388-390 400-404 413- 414 551-553 557 561-562 583-590 675 794- 796 832 855-856 863-869 900-902 906-908 944 964-966 969 971-974 980-988 997-999 1008-1009 1026-1027 1036-1037 1042-1043 1049 1069 1089-1091 1095 1110-1113 1128- 1130 1139-1142 1155 1173 1193 1202-1204 1297 1315-1316 1334-1335 1349-1350 1353- |

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| infant brain | Columbia University | IBM002 | 133 491-492 682-684 743-744 889-897 1038- 1040 1427-1431 1474 1580-1581 1633 1903- 1911 2025-2026 2146-2147 2188 2310 2376 2726 2787-2789 2904 2992 3212-3214 3224- 3225 3325 3477-3478 3638-3640 3827 3966- 3968 4055-4056 4118 4131 4275-4277 4643 5044 |
| infant brain | Columbia University | IBS001 | 153 197 350-352 459 574-577 743-744 826- 828 871-872 903-905 969 995 997-998 1042- 1043 1068 1127 1151-1153 1287 1349-1350 1559-1560 1694-1698 1773-1774 1848-1851 1978-1979 2054-2056 2111-2114 2143 2200- 2201 2365 2521 2664 2707-2708 2843 2945- 2946 2978 3260-3267 3424-3427 3599-3601 3624-3625 3737-3738 3891 4114-4116 4125 4245 4291-4295 4635 4907-4909 |
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| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| lung tumor | Invitrogen | LGT002 | 32-34 42 45-46 67 96 100-106 116-120 136- 139 153 175-177 179 195-196 213-218 227- 230 278-283 298-300 313-315 324-325 332- 333 341-344 346-349 357-361 365 379-380 393-394 400-404 420 436 474 478 483-485 491-492 513-514 538 548-550 557 574-577 580-581 605-607 611 652-653 682-684 699- 701 709-711 723 728-733 743-744 764-771 778-783 799-803 840-844 852-854 857-859 873-875 885-886 889-897 909-920 924 946- 956 964-966 969 971-979 992-995 997-1006 1008-1009 1023-1027 1036-1040 1042-1043 1048-1050 1063-1067 1088-1091 1110-1113 1117-1119 1128-1130 1139-1143 1151-1153 1155-1156 1160-1164 1172-1173 1185 1193 1202-1212 1217-1218 1220-1221 1229-1232 1235-1236 1244-1246 1269-1271 1300-1301 1315-1318 1323-1328 1330-1333 1349-1355 1357-1359 1363-1371 1374 1397 1403-1404 1408-1409 1418-1423 1432 1434 1438 1440- 1441 1446-1449 1463-1464 1467-1470 1473 1480 1491-1494 1505 1507-1512 1533-1535 1541-1548 1550-1557 1569-1574 1585 1591 1611-1612 1617-1619 1621-1623 1625 1629- 1632 1639-1645 1648 1654-1655 1657-1660 1663-1664 1671-1673 1685 1687-1689 1691- 1692 1694-1698 1706-1707 1710-1716 1719- 1721 1727-1739 1743-1746 1763-1771 1780- |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| leukocyte | GIBCO | LUC001 | 1-2 12-22 39-40 45-47 70 78 107-110 135- 136 154-156 165 175-177 212-215 223-226 231 258-260 267-268 278-283 286-287 313- 315 324-325 332-333 341-344 364 379-380 388-390 394-395 415-416 419 437-438 450- 451 456 462 465 478-480 491-492 511 520- 524 531-532 538 551-553 557 561-562 574- 577 583-590 597-598 602-603 612-620 633- 634 641 652-653 668-669 677-685 699-701 704-711 719-722 728-733 743-744 754-757 760 763-771 784-786 794-796 811-816 822- 828 840-844 847 849-851 855-856 879-886 |

| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| Tissue origin | RNA Source | Library Name | SEQ ID NOS: |
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| leukocyte | Clontech | LUC003 | 1-2 48-50 154-156 195-196 286-287 313-315 324-325 395 520-521 557 602-603 772 784- 786 814-816 822-823 863-869 885-886 906- 908 944 954-956 963 980-988 995 1050 1080 1122 1129-1130 1182-1184 1192 1198-1201 1317-1319 1348-1350 1353-1355 1357-1358 1374 1432 1450 1507 1516-1517 1532-1535 1547-1548 1664 1686 1715-1716 1737-1739 1753 1814-1817 1857-1859 1888-1893 1903- 1911 1919-1922 1950 1984 2010-2013 2035 2038 2054 2058-2061 2116 2118 2125-2133 2178 2191-2192 2223 2278 2572 2574-2575 |

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| | | | 2645-2647 2735 2774-2776 2816-2817 3009 3041-3049 3076-3078 3130 3156-3157 3167- 3168 3170-3171 3289-3290 3341 3403-3404 3635 3908 3941-3942 4030-4031 4055-4056 4275-4277 4691-4692 4756-4757 4796-4797 5001-5003 5148-5149 5275 5383 5435-5437 5497 |
| melanoma from cell line ATCC #CRL 1424 | Clontech | MEL004 | 1-2 52 96 138-139 278-283 313-315 479-480 491-495 511 799-800 822-823 829 847 863- 869 871-875 889-897 944 951-953 957-962 980-988 993 1017-1021 1038-1040 1042- 1043 1129-1130 1172-1173 1182-1184 1202- 1204 1220-1221 1237-1242 1269-1270 1290- 1291 1337-1345 1359 1400-1401 1403-1404 1432 1435-1436 1438 1442-1443 1457-1464 1475-1477 1489 1505 1507 1524 1532 1536- 1538 1547-1548 1551-1556 1575-1576 1585 1603-1604 1611 1617-1619 1648 1663 1688- 1689 1691-1692 1701-1702 1715-1716 1719- 1721 1724 1735-1736 1746 1755-1756 1780- 1783 1845-1847 1876-1877 1882-1885 1925 1954-1962 1981-1983 2005 2045-2047 2058- 2061 2088-2091 2115 2118 2138-2142 2144 2178 2189-2190 2197-2199 2223 2254 2266 2277 2281-2282 2284 2298-2299 2310 2347- 2348 2389-2390 2418 2424 2427 2440-2441 2443 2510-2513 2548 2591 2597 2637 2659- 2662 2781 2783 2814 2824-2826 2843-2845 2857-2860 2898 2905 2945-2946 2955 2969- 2973 3008 3029 3094-3095 3130 3166 3170- 3173 3195-3196 3226-3228 3240 3258-3259 3339-3340 3438-3441 3443 3459-3460 3574- 3575 3577-3580 3589 3599-3601 3635 3658- 3660 3691 3753 3815-3816 3828 3878-3879 3941-3942 3966-3968 4077-4079 4104-4105 4121-4122 4132-4133 4142-4144 4241-4242 4275-4277 4287-4288 4326 4391-4393 4546- 4548 4672-4674 4679 4737 4796-4797 4835 4902 5055 5057-5065 5085-5088 5280 5308- 5309 5389-5391 5421-5422 |
| mammary gland | Invitrogen | MMG001 | 1-2 12-13 39-40 47 62 81-82 96 116-119 126 173 175-177 180-182 195-196 213-215 227- 230 236 246-247 258-260 274 278-283 313- 315 321 341-344 346-349 354 365-367 399 419-420 445-446 450-451 478 491-492 520- 521 538 543 580-581 583-590 602-603 607 629-630 647-649 652-653 670-671 677-678 682-684 697 709-711 728-733 743-744 764- 771 789-793 796 801-803 806-808 814-816 840-844 870 879-881 885-886 900-905 909- |

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| induced neuron cells | Strategene | NTD001 | 313-315 548-553 682-684 814-816 903-905 909 944 950 969 993 1017-1021 1026-1027 1036-1037 1070-1071 1088 1285 1294-1296 1315-1316 1322 1357-1358 1363-1371 1403- 1404 1520 1536-1538 1620 1629-1632 1638 1663 1701-1702 1707-1708 1724 1753 1770- 1771 1915-1918 1925-1927 1950 1993-1998 2017-2020 2025-2026 2058-2061 2083 2121- 2124 2144 2151-2152 2197-2199 2331 2386 2469 2573 2596 2628 2752-2753 2843 2898 2925-2929 2961-2962 2969-2973 3172-3173 3189-3191 3224-3225 3253-3255 3310-3311 3428-3429 3470-3471 3673-3677 3760 3969- 3971 4014-4015 4082-4084 4090-4092 4100 4114-4116 4140-4141 4272 4285-4286 4470 4616-4621 4691-4692 4761-4763 4864-4865 4907-4909 5137-5140 5298-5302 |
| retinoic acid induced neuronal cells | Strategene | NTR001 | 195-196 278-283 388-390 743-744 855-856 995 1038-1040 1139-1142 1418-1420 1533- 1535 1780-1783 1903-1911 2060-2061 2223 2592 3289-3290 3969-3971 4598-4601 |
| neuronal cells | Stratagene | NTU001 | 74-77 195-196 246-247 278-283 294-295 341-344 388-390 491-492 566 652-653 680- 681 743-744 755-757 784-786 801-803 855- 856 863-869 900-902 919-920 950 964-966 995 997-998 1000-1002 1076 1159 1235- 1236 1294-1297 1432 1451-1454 1507 1533- 1535 1605-1608 1648 1667-1670 1688-1689 1691-1692 1694-1698 1703-1704 1746 1753 1765-1769 1831-1834 1848-1851 1900-1902 1925 1966-1974 2060-2061 2088-2091 2095 |

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| pituitary gland | Clontech | PIT004 | 175-177 227-230 491-492 796 822-823 849- 851 992 995 1017-1021 1042-1043 1160- 1164 1182-1184 1202-1204 1215-1216 1220- 1221 1300-1301 1317-1318 1320-1321 1398- 1399 1410 1479 1507 1540 1553-1556 1582- 1585 1591 1625 1648 1657-1658 1663 1708 1753 1870-1875 1925 2060-2061 2068-2071 2118 2447 2604 2696-2697 2715 2774-2776 2843 2871-2872 3021-3022 3100 3203 3331- 3332 3339-3340 3424-3427 3577-3580 3684 3787-3788 3959-3960 4549 5431-5433 |
| placenta | Clontech | PLA003 | 1052 1215-1216 1694-1698 1919-1922 2116 3969-3971 4672-4674 5001-5003 5241-5242 |
| prostate | Clontech | PRT001 | 42 165 246-247 335 511 548-550 675 847 873-875 879-881 889-897 910-914 946-949 980-988 993 995 1008-1009 1038-1040 1049 1128 1154 1157 1173 1182-1184 1202-1204 1297 1317-1318 1352 1357-1359 1398-1399 1414 1457-1462 1485 1498-1499 1524 1553- 1556 1629-1632 1648 1683-1684 1688-1689 1718-1721 1746 1753 1770-1771 1792-1795 1831-1834 1860 1870-1875 1879-1881 1925- 1927 1990-1991 2005 2035 2038 2045-2047 2055-2056 2060-2064 2083 2088-2091 2118 2144 2179-2181 2202-2203 2229 2254 2277 2283 2296-2297 2303-2304 2315 2337-2340 2387 2418 2423 2427 2445 2456 2468 2475 2492-2495 2510 2536 2543-2544 2546 2549- 2550 2574-2575 2591-2592 2604 2645-2647 2649 2659-2662 2712 2721 2749-2750 2760 2857-2860 2871-2872 2894-2895 2909-2911 2925-2929 2951-2952 3005 3013-3014 3017- 3020 3029 3081 3100 3121 3148 3174 3199 3226-3228 3242 3250-3252 3276-3277 3280- 3282 3558-3560 3606-3607 3694-3696 3765 3891 3962 4067 4101-4102 4232-4235 4383- 4384 4461-4464 4533 4546-4548 4581-4582 4796-4797 4882 4886 4899 4907-4910 4967- 4970 5073 5078 5295-5296 5431-5433 |
| rectum | Invitrogen | REC001 | 39-40 61 64 278-283 298-300 491-492 561- 562 652-653 789-793 870 879-881 957-960 997-998 1007 1042-1043 1070-1071 1131- 1136 1159 1217-1218 1235-1242 1272-1273 1275-1277 1317-1319 1363-1371 1380 1386- |

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| salivary gland | Clontech | SAL001 | 48-50 116-119 154-156 175-177 313-315 396-398 491-492 543 591 784-786 826-828 910-914 924 950 994-995 999 1023-1025 1036-1037 1049 1128 1202-1204 1230-1232 1237-1242 1297 1322 1332-1333 1352 1418-1420 1446-1449 1473 1480-1484 1498-1499 1507 1511-1512 1533-1535 1541-1546 1667-1670 1686 1746 1763-1769 1792-1795 1839-1844 1857-1859 1865-1875 1882-1885 1919-1922 1948-1949 1951 1978-1979 2017-2020 2055-2056 2118 2125-2130 2138-2142 2146-2147 2179-2181 2251-2252 2255-2257 2273 2280 2286-2287 2395 2403 2405-2413 2423 2499 2536 2591 2629-2631 2700 2712 2781 2784 2843-2845 2855-2856 2898 2965-2968 3008 3021-3022 3075 3236 3280-3282 3319-3322 3462 3491-3495 3632-3634 3778 3867-3869 3966-3968 4291-4295 4333 4581-4582 4598-4601 4681-4683 4729 4953 5001-5003 5148-5149 5270 5272-5274 5406-5407 5464-5466 |
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| skeletal muscle | Clontech | SKM001 | 1-2 154-156 175-177 216-218 245 313-315 346-349 354 574-577 849-851 928-929 957-960 971-974 1003-1006 1032-1034 1076 1300-1301 1334-1335 1395-1396 1403-1404 1432 1550 1691-1692 1735-1739 1746 1830 2049 2118 2548 2560 2592 2629-2631 2746 2785 2819 2843 3121 3181-3183 3310-3311 3432 3663 3737-3738 3943-3948 4534 5095-5097 |
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| spinal cord | Clontech | SPC001 | 30-31 74-77 123 134 154-156 175-177 213-215 301-303 313-315 421 491-492 520-521 751 796 822-823 849-851 855-856 863-869 871-872 889-897 909 924 927 950-953 964-966 980-988 997-998 1017-1021 1026-1027 1049 1053-1054 1089-1091 1127 1151-1154 1159 1173 1175 1182-1184 1189-1191 1215-1216 1220-1221 1230-1232 1319-1321 1349-1350 1355 1359 1363-1371 1388-1393 1398-1399 1422-1423 1432 1446-1449 1470 1532 1539 1541-1546 1551-1552 1569-1574 1582-1584 1649-1653 1663 1685 1688-1689 1707 1715-1716 1727 1735-1736 1792-1798 1831-1834 1839-1844 1915-1922 1951 1992 2005 2017-2020 2035 2042-2043 2057 2060-2061 2072-2074 2086-2087 2096-2097 2118 2143-2144 2173 2186-2187 2193-2195 2208-2210 |

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| adult spleen | Clontech | SPLc01 | 491-492 548-550 561-562 641 652-653 801- 803 863-869 944 969 971-974 995 1128 1171 1205-1207 1271 1290-1291 1330-1331 1353- 1354 1508-1510 1547-1548 1551-1552 1605- 1608 1621-1623 1625 1694-1698 1743-1745 1753 1796-1798 1827-1829 1848-1851 2054 2066-2067 2098-2100 2111-2114 2179-2181 2193-2195 2537-2538 2604 2925-2929 3017- 3020 3234 3240 3250-3252 3289-3290 3402 3536-3543 3667 3975-3983 4114-4116 4136 4549 4652-4653 4691-4692 4796-4797 4907- 4909 5001-5003 5050-5052 5144 5241-5242 5270 5335-5343 5346-5354 5389-5391 |
| stomach | Clontech | STO001 | 47 134 154-156 286-287 394 440-441 468 707 754 950-953 961-962 995 1041 1050 1070-1071 1075 1160-1164 1182-1185 1195- 1196 1256 1414 1507 1511-1512 1524 1638 1648 1664 1674-1682 1687 1724 1746 1780- 1783 1819 1952-1953 2093 2118 2121-2124 2188 2216-2221 2234-2242 2251-2252 2258- 2260 2273 2424 2464 2511-2513 2522 2548 2626 2645-2647 2650 2664 2675-2676 2686 2726 2820 2842 2898 2957 3008 3114 3172- 3173 3197 3258-3259 3285 3310-3311 3374- 3382 3428-3429 3456 3508-3513 3584-3585 3693 3882-3883 3906 3969-3971 4241-4242 4400 4498-4500 4672-4674 4910 4967-4970 5431-5433 5497 |
| thalamus | Clontech | THA002 | 14-22 52 70 96 131-132 154-156 235 296 313-315 354 400-404 436 551-553 709-711 822-823 829 964-966 969 997-998 1026-1027 1038-1040 1044-1047 1051 1129-1130 1154 1175 1182-1184 1193 1244-1246 1249-1255 |

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| thymus | Clontech | THM001 | 28 39-40 42 52 125 137 157-159 165 175-177 198 235 274 277 284 366-367 394 450-451 491-492 499 516 583-590 605-606 659-660 707-711 764-771 822-823 840-844 847 852- 854 863-869 899 944 950-953 980-988 997- 999 1017-1021 1026-1027 1075-1076 1080 1131-1136 1139-1142 1173-1174 1182-1184 1202-1204 1230-1232 1290-1291 1308-1309 1359 1380 1389 1397 1410 1414 1418-1423 1434 1444 1450 1470 1479 1485 1507 1511- 1512 1516-1517 1524 1551-1557 1569-1574 1597 1611 1617-1619 1659-1660 1663 1686 1709-1714 1719-1721 1727 1746 1753 1763- 1764 1792-1795 1827-1829 1857-1859 1876- 1877 1879-1881 1915-1922 1926-1927 1954- 1962 2000-2002 2031-2034 2038 2049 2054 2060-2061 2098-2100 2118 2125-2133 2138- 2142 2145 2148-2150 2153-2160 2191-2192 2214-2215 2246-2248 2254-2257 2267-2270 2273 2280 2284 2298-2299 2301 2307 2338- 2340 2427 2456 2468 2490-2491 2536 2542 2561-2562 2604 2730 2739 2752-2758 2820 2843 2866-2867 2873-2874 2913-2917 2919- 2920 2954 2974-2975 3009 3025 3035-3036 3088 3094-3095 3117 3149 3170-3171 3210- 3211 3226-3229 3235 3238 3250-3255 3283 3289-3290 3314 3342-3344 3428-3429 3508- 3513 3591-3593 3605 3608 3624-3625 3632- 3634 3636 3689 3691 3723 3772 3778 3780- 3781 3784-3786 3815-3816 3864-3865 3882- 3883 3891 3897-3905 3925-3926 3958 3962 4093 4100 4112-4116 4126-4130 4228 4287- 4288 4581-4582 4598-4601 4652-4653 4662 |

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|---------------|------------|--------------|---|
| | | | 491-492 548-550 583-590 592-594 789-793 814-816 822-823 930 995 999 1050 1068 1143 1202-1207 1230-1232 1297 1323-1327 1351 1363-1371 1383-1384 1388 1425 1438 1451-1454 1507 1551-1552 1582-1584 1627 1663 1688-1689 1691-1692 1719-1721 1746 1753 1755-1756 1765-1769 1792-1795 1839- 1844 1878 1919-1922 1951 1988 2017-2024 2045-2047 2055-2056 2118 2193-2195 2208- 2210 2254 2273 2296-2297 2444 2469 2552 2604 2665 2696-2697 2768-2771 2781 2802 2861-2862 2955 3156-3157 3419 3451-3455 3577-3580 3708 3729-3730 3749-3752 3880 3934 3966-3968 4043-4045 4062-4064 4239- 4240 4374-4375 4629-4632 4666 4796-4797 5024 5148-5149 5181-5183 5389-5391 5485 |

*The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Table 2

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1 | 5498 | C | 1 | 239 | 322 | MGGALLKEPILSPGGGKGKIFFWGPQN* |
| 2 | 5499 | A | 2 | 1441 | 2129 | SVIA*SCRASVASKQS*PTLLPSACARPHA\STVDAPASGGAPRASSPSSDCLWSTSSSSTPLSASASSS/SPPSFNP AADARGSQGPGARGRSCSPSSSERH VRRRVSAARQAGAASAGGGRQAGLAGRGLSA/SRSSARASSSATPALAQSTPSSSESECAPLKSRSGLTSSLSKPAS*ATLGKKGSGSSWRFPPEIHGRHPLSASCWNKSVAAAAAPTGATAPPKAGP |
| 3 | 5500 | C | 3 | 36 | 236 | MGPTIPDXSXFFWRKPITWMPTWEGTSNVGPQPLSSSKSLHSXRGHPAPIPTGQAGPRDSGPGASP* |
| 4 | 5501 | A | 4 | 109 | 300 | GGGKQIPFKGGKFKWGP GPVLKKG EREKPGGNPKKTPWKKASSRPAPRIHPCFT*HAPDPRPLY |
| 5 | 5502 | A | 5 | 2 | 73 | |
| 6 | 5503 | A | 6 | 27 | 375 | EHSGVRQALCFGTASQRPSQQPAPSGPGPPGEPG*ERLCASHKAFISHKQSH*SPQ*PCQAGVTL SRLQT TNSPRPH SQKGLRGPRQTLSLT SQPTACSEN SQGSQSPKRTLS |
| 7 | 5504 | B | 7 | 50 | 204 | XKEGSLCDEYWNPAANLINVCSLFLRQGPR LALMQGEPVDKGCLGVLL ENK* |
| 8 | 5505 | A | 8 | 379 | 623 | ATTVSVPFTAKLLERPGLHLLVFLPNLQFPLQPLVS*LALLRGSTLTKQVPSAPDKPLLVSPPAKHPPVPPSCGPG LQG |
| 9 | 5506 | B | 9 | 185 | 366 | XHPGDGFRPNQEGDERPARKK TWV RDGGPHQGLFRSFHPQFFSRPSRATAHVPAVYFSVEWX* |
| 10 | 5507 | A | 10 | 29 | 308 | WLPPNPGRREARQEEDLGPGWWAPSGPLPQLPSAVLQPTQPGHGPRA SL**SVCFSFADKEGSLCDEYWNPA A/KPH*RLQPLPSTRPEISPL |
| 11 | 5508 | A | 11 | 663 | 1269 | TAGTWAVASLGR LKNCGWKLRKEALMGPTIPDPKSSPLAGLSSPFPWFG RKPITLECPTWERDPRNVGPPAPSP ARKSLPQPTGTTLQPYSPRDKAGPK KTLGPRG/APL*VRRTRPLN*WTPA DLGVRTRGAGPLPDAGTLRPRGA VEPSVSACGKWAPSPTSQGCCEGR CDAVPKHEGLAHPTVLSINVFPVLN QKKKKK |
| 12 | 5509 | A | 12 | 190 | 715 | |
| 13 | 5510 | A | 13 | 270 | 713 | KL TILDCQFTG*QR*KFNG*NLRNR/HSPSRWDGAKPLYKALKL*SSSSSV GAFIFIFTRSRLRAYLFSFAH/LRRPL LAGHLLCSPEQAVELSALLAQTKFG DYNQNTAKYNYEELCAKELSSATL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NSIVAKHKELEGTSQASAEYQVL |
| 14 | 5511 | A | 14 | 1575 | 1968 | REMGFRHVGQTGLELLTSGDLPTSA SQSAGITGVSHHTWPKTLFVLRQSL TLSPGLECSGTISAHCSPHLPCSSNS CAPASRVAESTEAAHH/LCPDNLHISS REGASPCWPGCS*TPELKRPAHPCR DQLGH |
| 15 | 5512 | A | 15 | 185 | 720 | KVSHVYFLHRHGNHPISQTFPHLS PLSIPQONCHCHGPFMSWCWRIKYL GIQLTRDVKDLFKEN*KPLLSKIKED TNKWKNIPCSWIGRINIVKMAILP/K ELEKTTLKFIWNQKRACIAKTILSQ KNKAGDITLPDFKLYYKATVTKTA WE\QNRDIDQWNRIEPSEITPHIYNY LIF |
| 16 | 5513 | A | 16 | 1114 | 2193 | GSFTKRVRRAFKVLRDNPTVAKLS QVKKHWYFTWNHKLKIAKAILSK KNKPGGITLPDFKL*YRATVSKTVW YWHKNRHINQWNRIRNPEANAHTY I*LIFDKGAKNIHWVKTSLFNKWCW EN*ISICKEWEKISANYP SDKGLITR IYKEL/K/QL*EKKSNNLIKKQAKDL NRHFSKEDK*MANRHMKKCSMLIT REMQUIKTTMKYHFTPVKMVYIQA GNDKCWQGCGEKGT FVHC*WECK LV*PL*RTVWRFLEKL/E/LELP*DPA IPLLGIYPK*RKS/CVIKEITVAKIWK QPKCPSTDKWIKKMWYTYTMDYYS ALKKNEILSFPTTWMEKIVILSVIG QSQDKKHCMFSLICGS |
| 17 | 5514 | A | 17 | 149 | 328 | WQDPLQDPCCHQPFHLCLRR*TLH* LRQQ*WPLLRLRGKIMLILLNTHP EHPCVLLDL |
| 18 | 5515 | A | 18 | 615 | 734 | ENSCWTATLQMGKNWQSL*PVLTS YYR*DNSYWREILQV |
| 19 | 5516 | A | 19 | 1 | 181 | MRARRLPWALTVAELGWDTOGG DQTSPGGNDRMSMEAECSTTVSP LSCSIPTGCGQTREEVSARATPPPSL GASLLQTLTPDTHCTGVSA*KLATF FTFVGFLSSMNCLMLSKG*GTAKSF ATFFTFVGLLSSVYPLMSS |
| 20 | 5517 | A | 20 | 1 | 665 | |
| 21 | 5518 | A | 21 | 401 | 1739 | DNSHWRETLQM*RMWQSF*PFFNP C*T*ENSYW/MRNPTNVKNVAKLL AIPQPLLIIR*LILKRNPTNVKNVTKL LSDSQPLLNIK*YMLERNSTNVKNV AKLLIDLQILLYISLFILERNLTSVKN VAKHLTGPQALLNIKDFILERNPSN VKNVAKHLYGLQP*LDIRGYTLER NPTNVKNVAKLLAILQPLLNIREFIL ERNPTNVKNVAKLLAVLQPLLNIREFIL FILERNPTNVKNVAKLLAIPQPLLIIR |
| 22 | 5519 | A | 22 | 618 | 1655 | DIPERNASNVKNVSSHFAVYTKTQ HKCVYTTEKSCCKCECEKTFHWSST LTNHKEIHTEDKPYKCEECGKAFKQ LSTLTTHKIICAKEKIYKCEECGKAF LWSSTLTRHKRIHTGEKPYKCEECG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KAFSHSSTLAKHKRIHTGEKPYKCE ECGKAFSHSSALAKHKRIHTGEKPY KCKEKGKAFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTKHKIHH AGEKLYKCEECGKAFNRSSNLTIHK FIHTGEKPYKCEECGKAFNWSSSLT KHKRFHTREKPFKCKEKGKFIWSS TLTRHKRIHTGEKPYKCEECGKAFR QSSTLTKHKIHTGEKPYKFEECGK AFRQSLTLNKHKIIHSREKPYKCKE CGKAFKQFSTLTTHKIIHAGKKLYK CEECGKAFNHSSSLSTHKIHTGEKS YKCEECGKAFLWSSTLRRHKRIHTG EKPYKCEECGKAFSHSSALAKHKRI HTGEKPYKCKEKGKAFSNSSTLAN HKITHTEEKPYKCKECDKTFKRLST LTKHKIHHAGEKLYKCEECGKAFNR SSNLTIHKFIHTGEKPYKCEECGKAF NWSSSLTKHKRIHTREKPFKCKEKG KAFIWSSTLTRHKRIHTGEKPYKCE ECGKAFSRSSTLTKHKTIHTGEKPY KCKEKGKAFKHSSALAKHKIHHAGE KLYKCEECGKAFNQSSNLTTHKIIH TKEKPSKSECDKAFIWSSTLTEHK RIHTREKPYKCEECGKAFSQPSHLT THKRMHTGEKPYKCEECGK/RF*PI LNPYYT*DNSYWRETLQM*RMWQ SF*EIFNSY*T*DNSYWRETLQM*R MWQSI*PILNPN*TYEDAHWRETIQ M*RMWESF*SILKAYYT*DNSYWR ETLQI |
| 23 | 5520 | A | 23 | 1 | 3476 | MTLNEHAAFKHLFNKAHLAPPLIHL TLSGHSTCFREHRVGAKSNNPPASK GVWALQSARVKFAETTAGQKGMN TTWVFYYPNVASTWWGAMIPVHV VLPGGCHDASTLGDKEKRAGEAVL NVPGFQDSLESHGRIVNCLIPDVQE NNPSTGNESWLKSHQRLGEPTSRR WLITLPVTSRSNSIGHLKGTPGKSKE EIKATVCAPTLKNGFWIAERVMTVS GHEGAASSRALREELRLLFSSCAQG RLTPHIAGYPSKAKLREERSGSNICC SAIFAVLQPLLLIPRGTSQGVDDLQT PTDLQLRVLTVRRKTNKQEGHPHQ NPTCTSPSSKTKDRSTRNVKKDTQ ELNSALRQVDLIDIYRTLHPKSREYT FFSAPHRTYSKIDHTVGSKALLSKR KRTEIITNCLSHHSAIKLELRIKKLTQ NRSTTWKLNLLNDYWVHNEMK AEIKIFFETNENKDTTYQNLWDTFK AVCRGKFIALNAHKRKQERSKIDTL TSQKLEKQEQTHSKASRRQEITKI RAELKEIETQKNLQKINEFRS/W/PW QRHNKKKKFWTNTPEHQCKNPQ *NTGKPNPAAHQKGYPP*SSGLHPW DARLVQHTKINKRNPSYKQNRQK PHDYLNRCRKGL*QNSTALHAKNS Q*IRY*WDVSQNNKSYL*QTHSQYH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SECAETGSIPFENWHKTGMPSLTTP QHSVGSSGQGNHAGERNKGY SIRK RGSQIVPVC R*HDCAFRKPYGLSPK SP*ADKQLQQSLRIQNQCTKTTSILI HQ*QTNREP NHE*TSIHNC FKENKIL RNPTYKGCEGPLQ GELQTTAQ*NK RGYKQMEEHSMLMGR RISYHENG HIAQGNLQIQCHPHQATNDFLHRTG KNYFKVHMEPKKSPHHQGNPKPKA QSWRHHTT*LQ TILQGYSNQNSMV LVPKQRYRSMEQNRALRN NATYLQ LSDL*QT*EKQAMGKGFP T**TVLG KLASHM*KAETGSLPY TLYKN*FK MD*RLKR*T*NHKNPRRKPRHYHS GHRHGQGLHV*NTKSNGNKSQNG QMGSN*TKELLH SKRNYHQSEQAT YKMGENFRNLLI*QRANIQN LQRTQ TNLQEK NKQPYQKV GKGHEQTLLK RRHLCSQKTHEKMLIITGHQRNAN QNHNEIPSHTN*NGNH*KVRKQQG HG |
| 24 | 5521 | B | 24 | 1 | 8442 | MIPARFAGVLLALALILPGTLCAEG TRGRSSTARCSLFGSDFVNTFDGSM YSFAGYCSYLLAGGCQKRSFSIIGDF QNGKRVSLSVYLGEFFDIHLFVNGT VTQGDQRV SMPYASKGLYLETEAG YYKLSGEAYGFVARIDGSGNFQVL LSDRYFNKTCGLCGNFNIFAEDDFM TQEGTLTSDPYDFANSWALSSGEQ WCERASPPSSSCNISSGEMQKGLWE QCQLLKSTSVFARCHPLVDPEPFVA LCEKTLCECAGGLECACPALLEYAR TCAQEGMVLYGWTDHSACSPVCPA GMEYRQCVSPCARTCQSLHINEMC QERCVDGCSCPEGQLLDEGLCVEST ECPCVHSGKRYPPGTSLSRDCNTCI CRNSQWICSNEECPG ECLVTGQSHF KSF DNRYFTFSGICQYLLARDCQDH SFSIVIETVQCADDRDAVCTRSVTV RLPGLHNSLVKLKHGAGVAMDGQ DVQLPLLKGD LRIQRTVTASVRLSY GEDLQMDWDGRGRLLVKLSPVYA GKTCGLCGNYNGNQGDDFLTPSGL AEPRVEDFGNAWKLHGDCQDLQK QHSDPCALNPRMTRFSEEACAVLTS PTFEACHRAVSPLPYLRNCRYDVCS CSDGRECLCGALASYAAACAGRGV RVAWREPGRCELNCPKGQVYLQCG TPCNLTCSRSLSPDEECNEACLEG FCPPGLYMDERGD CVPKAQPCYY DGEIFQPEDIFSDHHTMCYCEDGFM HCTMSGVPGSLLPDAVLSSPLSHRS KRSLSCRPPMVKL VCPADNLRAEG LECTKTCQNYDLECM SMGCVSGCL CPPGMVRHENRCVALERCPCFHQ KEYAPGETVKIGCNTCVCRDRKWN CTDHVCDATCSTIGMAHYLTFDGL KYLFPGECQYVLVQDYCGSNPGTF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RILVGNKGCSHPSVKCKKRVTLVE GGEIELFDGEVNVKRPMKDETHFE VVESGRYIILLGKALSVVWDRHLS ISVVLKQTYQEKVCGLCGNFDGIQN NDLTSSNLQVEEDPVDFGKSWEVSS QCADTRKVPLDSSPATCHNNIMKQ TMVDSSCRILTSDVFQDCNKLVDPE PYLDVCIYDTCSCESIGDCACFCDTI AAAHVCAQHKGKVVWRTATLCP QSCEERNLRENGYECEWRYNSCAP ACQVTCQHPEPLACPVCVEGCHA HCPPGKILDELLQTCVDPEDCPVCE VAGRRFASGKKVTLNPSDPEHCQIC HCDVVNLTCACQEPGGLVVPPTD APVSPTTLYVEDISEPPLHDFYCSRL LDLVFLLDGSSRLSEAEFEVLKAFV VDMMERLRISQKWVRVAVVEYHD GSHAYIGLKDRKRPSSELRRIASQVK YAGSQVASTSEVLKYTLFQIFSKIDR PEASRIALLMASQEPQRM SRNFVR YVQGLKKKKVIVIPVGIGPHANLKQ IRLIEKQAPENKAFVLSSVDELEQQR DEIVSYLCDLAPEAPPPTLPPDMAQ VTVGPGLLGVSTLGPKRNSMVLDV AFVLEGS DKIGEADFNRSKEFMEEV IQRMDVGQDSIHVTVLQYSYMTV EYPFSEAQSKGDILQVRREIRYQGG NRTNTGLALRYLSDHSFLVSQGDRE QAPNLVYMTGNPASDEIKRLPGDI QVVPIGVGPANVQELERIGWP NAP ILIQDFETLPREAPDLVLQRCCSGEG LQIPTLSPAPDCSQPLDVILLDGSSS FPASYFDEMKSFAKAFISKANIGPRL TQVSVLQYGSITTIDVPWNVVPEKA HLLSLVDVMQREGGPSQIGDALGF AVRYLTSEM HGARPGASKAVVILV TDVSVDSVDAAADAARSNRVTVPF IGIGDRYDAAQLRILAGPAGDSNVV KLQRIEDLPTMVTLGNSFLHKLC SG FVRICMDEDGNEKRP GDVWTL PDQ CHTVTCQPDGQTLLKSHRVNCDRG LRPSCPNSQSPVKVEETCGCRWTCF CVCTGSSTRHIVTFDGNFKLTGSC SYVLFQNK EQDLEVILHNGACSPGA RQGCMKSIEVKHSALSVELHSDME VTVNGRLVSVPYVGGNMEVNVYG AIMHEVRFNHLGHIFTFTPQNN EFQ LQLSPKTFASKTYGLCGICDENGAN DFMLRDGTVT TDWKTLVQEWTVQ RPGQTCQPILEEQCLVPDSSH CQVL LLPLFAECKVLAPATFYAICQ QDS SHQEQVCEVIAS YAHL CRTNGVCV DWRTPDFCAMS CPPSLVYNHCEHG CPRHCDGNVSSCGDHPSEGCF CPPD KVMLEGSCVP EEACTQCIGEDGVQ HQFLEAWVPDHQPCQICTCLSGRK VNCTTQPCPTAKAPT CGLCEVARLR QNADQCCPEYENGRLVSVPYVGGN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MEVNVYGAIMHEVRFNHLGHIFTF TPQNEFQLQLSPKTFASKTYGLCG ICDENGANDFMLRDGTVTTDWKTL VQEWTVQRPGQTCQPILEEQCLVPD SSHQVLLLPLFAECHKVLAPATFY AICQQDSSHQEQVCEVIASIAHLR TNGVCVDWRTPDFCAMSCPPSLVY NHCEHGCPRHCDGNVSSCGDHPSE GCFCPPDKVMLEGSCVPPEACTQCI GEDGVQHGFLEAWVPDHPQCQICT CLSGRKVNCTTQPCPTAKAPTCGLC EVARLRQNADQCCPEYENPCPLGY KEENNTGECCGRCLPTACTIQLRGG QIMTLKRDETLQDGCDFHCKVNE RGEYFWEKRVTCPPFDEHKCLAE GGKIMKIPGTCCDTCEEPESNDITAR LQYVKVGSCKSEVEVDIHYCQGKC ASKAMYSIDINDVQDQSCCSPTRT EPMQVALHCTNGSVVYHQVLNAM ECKCSPRKSSK* |
| 25 | 5522 | A | 25 | 364 | 477 | VIEHLVSQDGLDFLTS*SARLGLPKC WDYRREPPRPVH |
| 26 | 5523 | A | 26 | 6838 | 7166 | GSRRPGCHCNSHTGRRSSRHGHLP SPAASRGHPSPSAGPPRS*GARRPSL YAGYEA YLSGGGAGRPGHPWQLLP HASVSQGCCAGQAAGR*RSCTQR RGQSSPGQSQ |
| 27 | 5524 | A | 27 | 817 | 1299 | RKSHIFFFFLRWLALSPRLECSGA ILAHCKLLP/GFKPFSCALSQPSSWD YRHPPRPANFLYF/SVETGFHHVSQ G/GLNLLTS*SAHLSLPKCWDYRRE PPRPAENLSSLTQYLECTQFEIHLGS QTALEGRLVPVTYPLGGVEISGHPV FLLTSSCGR |
| 28 | 5525 | A | 28 | 506 | 761 | DGVLLLLPRLECNSAILAHRNLRPL/ GFKRFSCLTLLSPWDYRHLPPRLAIF FVFLVYVGFHHVGYAGLELLTSR* SARPRPPKIA |
| 29 | 5526 | A | 29 | 71 | 425 | CRRKGVNMNAPLGGIWLWLPLLLT WLTPEVNSSWRYMIATGGSCRVMC YNELGLVSRRLCQRYSPLTLIY GEAKVLFVCGLSLLVHWPNCAPSF RDNT*LLRFLHVIIVLLRPL |
| 30 | 5527 | A | 30 | 263 | 463 | |
| 31 | 5528 | A | 31 | 287 | 2919 | MASFPPRVNEKEIVRLARTGELLAP AAPFDKKCG\RENWTVLAPDGSY FAWSQGHRTVKLV\WSQCLQ\NFL VLHGTKNVTNFKQFKDLPRQNS\DG GSEKIKPREHIDCGDIVWSLAFGSS VPEKQSRCVNIEWHRFRFGQDQLL ATGLNNGRIKIWDVYTGKLLNLV DHTGVVRDLTFAPDGSLLVSASRD KTLRVWDLRDDGNMMKVLRGHQ NWVYSCAFSPDSSMLCSVGASKAV VAAILV*LRLCWHHSHTGAQWC*L GRKSGISGYRAGGDLYHRMK*PCIR LQGVLYVHRCWSMSTFCFSFFLFFF FKVISPTVKYTDS*VN*FSSFMELGV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | *QVKPI*CKVFGFQMVSLCYFLEFF QIPEISYVFDSI*NL YLFSFRNNVLCL CRKKKNQKGLLYSKRRDCLRINLQ AHI*YNRLK*TLESCLELCTVNY*S LESKIVYELILK*LNCFIK*LMIVVS LGKIRWLNFDLLKCNCIIFIK*HFHF VMWFNILLVCQRNFIWL*IFYLLAV SVSLPRLKLVTQAYCKQVIISKGDA NGVTIC*PYVFCLYIF*KSGSFWKKK EKGVCST*PYLFPYILVN*FLE*MDF SIALWLNCIAFILCLGLFLN*HLTET EIEFACLP*LT*RLILI*L*H*AYSLNY S*FIMLNILIKFSSFSIRCAILSSVCLN EAITFAFLQVFLWNMDKYTMMRK LEGHHHDVVACDFSPDGALLATAS YDT*VYIWDPHNGDILMEFGHLFPP PTPIFAGGANDRWVRSVSFSHDGLH VASLADDKM\VRFWRIDEDYPVQV APVSNGLCCAFSTDGSLAAGTHD GSVYFWATPRQVPSLQHLCRMSIRR VMPTQEVQELPIPSKLLLEFLSYRI |
| 32 | 5529 | B | 32 | 51 | 285 | XGDEKGAQAQVAAVLAQHRVALSV QLQEACFPPIRLQVTLEDAASAA SAASSAHVALQVFSELGFPPAVQR WVIGRCL* |
| 33 | 5530 | A | 33 | 38 | 347 | FGVAPGVSLHHPRPHPARATASTR RAWNPQALPQPSGSSAVGSPSPRC HRGRTEW\QCPVMDTITIWNSLGP VLVGEVGSTFPTAGCLGRLPGGSR WSLE |
| 34 | 5531 | A | 34 | 331 | 1257 | FRGCHRGKDRMAARVTHHQPWAQ KHALASWSPPEASTLKGPPEADL PRSPGNLTEREELAGSLARAIAGGD EKGAQAQVAAVLAQHRVALSFQLQE ACFPPIRLQVTLEDAALPHPPAS SAHVALQVHPHCTVAAFPGRFFSE LGFPFAVQRWFIGRCLCVPERSLAS YGVRRDGDHAFLLYLLSA/RSRS/LQ PQDLALKNPQEDGRGTWTLVSPHIG GYPOGPTAQLPPACPSPLPA\SWSCP FRHLHSMPPQKRPCEMCSTQRPCT WDPLAAAST*QPPEVTRGEWPFPH KSDISRPLNSGDLY |
| 35 | 5532 | A | 35 | 616 | 1017 | LYWEKIIFSNLKTPETLFLVMTSNIF HIFWEGNKLPHYTTQFSGFYFILWY FR\DRASL\CRPVWGAVVWS*LTA SNSW\VRCSCLGLPSSWSLSPMPPH SANFKFY*FHLIFVGDGGLAVLFRL VLNSWPQAI |
| 36 | 5533 | A | 36 | 3 | 283 | FYTQNIIFYSVESKLHTSTL*DHYFFF FFETESYSIAQGGVQWGNLGSLLQPP SPGFKQLSCLSLPSSWNYRCAPPCP ANFVFLVEMGFHWIKPG |
| 37 | 5534 | A | 37 | 260 | 569 | RENLDLGEAFISRCLPLHSLAYFLH NLSFKSREMHNMFVKS*QALKFIRR IENNHLFFYYFYFYFERKSLHSPLG NGVGLCLKKKKKNGSYKVLVWSF DSTE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 38 | 5535 | A | 38 | 468 | 849 | TSEEFQQFTIHLTGVLHCHPDLETG GYKTF*WKSLEN*IAFFFFSETESPS APRLECSGSISAHCNLLPGSSDSPAP ASRIAGTTGTHHHARPIFILLVKEGF HHVGQPGLKLLTSGDPPAPASQSA |
| 39 | 5536 | A | 39 | 97 | 448 | GSHEQPWEVVTGSRQPAR*SSR*AI MRKPRAAVGSGHRKQAASQEGRQ KHAKNNSQAKPSACD/GDVAEVTA FRGSLLSWYDQEKRDLPWRRRAED EMDLDRRAYA\KWPTLQDLASASL EEVNQLWAGLGYYSRGRRRLQEGA RK |
| 40 | 5537 | A | 40 | 990 | 1812 | RLPLGRRSPSEAAGAETAPSSLSAA MTPLVSRLSRLWVRWTC\AIMRKPR AAVGS GHRKQAASQEGRQKHAKN NSQAKPSACDGRGRR*DGPGQAGICW SVHLLRA/EATLPRGPVWVWGLWAR *GOVNSVL/DANPFPPVWVSKVML QQTQVATVINYYTGWMPVTPGEEG KGHGSDPR*EPLLWGGCREGFLYH LHP*PCLFLPAWGYRSGPTLQDLGR AFLEEGDQLWAGLGYYSRGRRMP EDTPARNGTAQRSLPQHIRPLNEWP LEWRLDACREP |
| 41 | 5538 | A | 41 | 360 | 652 | IYLAGAQWLTSVILVLWKPRRVDH LRSGVRDQPGQHGETSSLLKIQKLA RRHGACL*SQLLGRWRQENHSNPG DRGCSEL\RCTPAWATEGDSVLKKK |
| 42 | 5539 | A | 42 | 1400 | 1823 | NEKKS VFLRQSL/DSVAQAGVQWC DLGSLQTPPPRFTPFSCLSLPSSWDH RCPPPRPP/RFCFFLYF**RQDFTMLA RLVSNS*LQ/CDPPTLASKSAGITGM SYCTRPNQAGVQWWDLGSLQAPP RFTPFSCLSLPSSWDYRH |
| 43 | 5540 | A | 43 | 227 | 481 | KKKKELEKGNMD*IQSSRR\ETIKM RAKIF*TTNTKLMKKNKTRSLVSEN FNKIGKALARLRKKEKTPITKVRNE TEDITTNFIE |
| 44 | 5541 | A | 44 | 1374 | 1835 | ILPCNKPPWNSMACTTKHLSRSQAY RSAGAFIHWTGEAGVGSALLSLAL QKPWANQGIFPCGGRSQRGVSRN TRVWVQARNWY*VTPTHRVLWMR TAPRPALAASSAAS\PSAVGSPVAA\ PSQPLMTQMATTATEVVVG YAV GHTLSYSENI |
| 45 | 5542 | A | 45 | 1 | 1470 | |
| 46 | 5543 | A | 46 | 62 | 526 | EEKLKKGKSFQEYSGSLLLSIASVGF LSPTDIAIAVPRQWEEMRPLDIV*LA EPEEVEVLEPEEDFEQFLPVINEMR EDIVSLTREHG RAYLRNRSKLWRL DNML\IQIKTQVEASEESALNHPPNP GETAEG\RAAKRCEKAEKARELQ KAK |
| 47 | 5544 | A | 47 | 721 | 1030 | MGPWEPRPQMRT*CLLPLKPNSPPP TPSEE/PGHLPK*PLEVI*WSPSPGFP P/PAFRGQ*ARGHPPPPQWNTPFSP PQQPLSAGKT*PLTPFPALPYLGTG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RK |
| 48 | 5545 | A | 48 | 66 | 386 | PMEIFVDDEANLTLHGVQQYYLKL KDNEKNRKLFDLLDVLEFNQGVIFV KSVQRCIALAQLLVEQNFPAAIAHR GMPQEE/QFKDFQRRILVATNLFGR GMDIERVNI |
| 49 | 5546 | A | 49 | 434 | 858 | CLSHTMDPYSPNLRPPTPPHNRWVI FVKSVQRCIALAQLTSGSRNFPAAIAI HRGDGPREGGGFFRVFRQF*RFFNG RIFVGYQPILGRGMGHSRRVNIAFN YGHAWRVFDTYLAFGVGQRQGRF WATKGFGLFTFCVPMED |
| 50 | 5547 | A | 50 | 1 | 660 | LALARNKSLNLKHIKHFILDECCKM LEQLDMRRDVQEIFRMTPEKQVM MFSATLSKEIRPVCCKFMQDPMEIF VDDETKLTLHGLQQYYVVKLKDNE KNRKLFDLLDVLEFNQVVIFLKSQV RCIALAQLLVEQNFPAAIAIHRGMP QVEERLSSVFSSFKDFQRRILVATNL FGRGMDIERVNI\AFNYDMPEDFD TYLHRVARAGRFGTKGLAITFVS |
| 51 | 5548 | A | 51 | 143 | 387 | QPCLTRY*DTRCTNQ*ETTS*RLCKE PFRPGSFRPNWHLANVVENIERLQL VS\TLRLIEEDSSLN*YSIIHFHSES YR |
| 52 | 5549 | A | 52 | 2 | 1360 | VCVCVCVCVCVRQSLAPLPRLEGS VSILTHCNLRLGLSDSPASASRGA GTTGMCHHTWLMFLFLVETGFRHV GQAGLELQTS\DPALPFPKCWDYR\ VNHARP*HSFYSIRLGDQNVMA GQRPASMPCPVFLVQMSPAAVSTS VREWAPDSQGRHGDGHAKLWGVA DSPAPACPCTFGVTHETGWGSHLPS PKRQS/CYKGSQRPTQPQVIKQAPSS MATIPIHQGDVEGGASWFTPPSAET DPRSGPRTLCREGKCR*LSPYSSIKP GLKMG*IRDFHSTKEKF*WGQNIDL LIFESLLTRRERANDFVVEGPTQL*L V*SIMNANLNSRKAELPNNGTSTA MGSASSFSVCLFYERETPRKAAAH* ENVWELTRRFFIFFEMEFCSSVAQA GAQWCHLGLSLQPAHHEFK*FSSA/S LPSGCDYRHPPPCPANFFYF*VRDGV PSRCPGWPR |
| 53 | 5550 | A | 53 | 218 | 380 | RKMKNSTYAPFAPRPIYSSPPPPQE/P Q*GGRDMAAIW*GALSIPPPVPDLL PLG |
| 54 | 5551 | A | 54 | 76 | 376 | YKIIFVLETCMYKVICRFANNTMHL SYTVIHKDPGKGRGIISPNLFYFIYFE MEF/SLLMPRLCNGT\AILAHRNLH LPGSSNSPASAS*VAEITGMCTMP |
| 55 | 5552 | A | 55 | 97 | 437 | WTRTHRSTCHVAYQEDGLLHLRN TNDPENFPKSYHYHRIIGGASG*QA TAREATHYDGDVIDLDFVTPTPLG TTWGLEGTCENGDSLPA\LMHQSP LVGQPTEDFRNTGGH |
| 56 | 5553 | A | 56 | 22 | 424 | ALGMAHITLFFFFLLLFCDLALSPR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LQCSGTISAHCN LVPPGFKQFSCLSL LGSWDYRCMPPC/RWLT FVFLVET GFHHVGGAGLELLTSGDPPALA/FP KC*DYRR/DPRAWALFVFLT*FFSKL KYHKAKEKWS |
| 57 | 5554 | A | 57 | 514 | 835 | QFIFNVNKINSKTIKDRWGPGTVGF TPVIPQHFGRPQQANHLRSGVRDH PGQQGETPSLLKIQK*AGHGRGHL* TQLLRRLRQENHLNLGGGGCSEPRS RHCTPAW |
| 58 | 5555 | A | 58 | 234 | 457 | SKTENIKYWL VHGELETALHRWRN SKMAY*LGK\QFLINLRTQLPYDSAI PFIGCIPFKYECWTYNKDLFTHVYI |
| 59 | 5556 | A | 59 | 1 | 336 | |
| 60 | 5557 | A | 60 | 192 | 432 | FDENLNSPTWAGHGGSCLSQHFG LRRVDHLRSGI*DQPG*HSKTPFLL/ KNTKISWAWWRTSEIPAAREAEAG ELLELG |
| 61 | 5558 | A | 61 | 81 | 439 | CEHHKAHPPPVS PYQSMAPSFTQRL RPKEQVSPTMPFSLVSTPIHLTSGTP AGLPASIPGPLQSPWPSTTTGTDPKI QGSPARPAQNSPVASS*ATSSPWP ARPPWTP LHSSLPALAA |
| 62 | 5559 | A | 62 | 297 | 561 | SQHFGRRPRQVDHLQSGVQDHPVQ RGETPSLLKIQKLARGGGARL*SQL LRLRLRQENHLNPGGGGCNEPI*HR CSPA WAI E*DSVSKK |
| 63 | 5560 | A | 63 | 3 | 808 | FFFWEPEKAFIEEFEGVSSSSSPSQL GQQRKQDAGVLHSWNSALKNLNV PPPPPGGWCLWGTAALSSSQAGRG SGIGRGGGESGGTG/ASSAEGEAPG GIVSCA*GPGCRSSGAKGLGRLRAS SLQAPAAALIQAAPGVR*TGLGPYL SAVHAGPAAAAAALPGCLS\SPASP AAPVGATPRA\GPLNSENHRCPPGP PGPQFGLGPLGPGPGSGPWVAHSQ NMRAAESAAAAWLSVPSQSPRLSP SSSSSSSPTAWNFS SPRDMAGLR |
| 64 | 5561 | A | 64 | 1005 | 1150 | AWAWVCVSSGLGAPCGDGCCRGR GVASKCCACAGGGCVSVG*GNVCA RA |
| 65 | 5562 | A | 65 | 3 | 230 | LVEMGFHQPGQHGETPSLQKI*NKK \LAGHGGTCL*S*LLRRLSQEDGLSL GGRGFSEPG LCHCTPA*TTEQGLKK |
| 66 | 5563 | A | 66 | 317 | 503 | KKPKPPKPPWEPTTFG/TPAFIPPRGI WFLIAPCGWV*EEGGPSGGPWPWC PLGKTHGEGGKP |
| 67 | 5564 | A | 67 | 523 | 741 | ERGFFFGPHPGGRGKKG*WGPPFP GLKEFSPLRPP*EGGLRGPPPLPG/SF LGFLRKGGFKHGGQGGQNPGGG |
| 68 | 5565 | A | 68 | 498 | 778 | VTINMMTGIVPYISILMLNVNGLSA/ PLERRRLAEWIKIHKPNICCLQEIHL THKDSYRLNVKEWKKIFHTNGNSK *AGVAIVMSEKTD FKATTV |
| 69 | 5566 | A | 69 | 187 | 488 | KRFGKNGFYPCGPGGLKPRALKEPP PLTPQRGGITSSSPPPQPKKTLFFGY WPKKSL*INPQGGLNPSQGGKP\WG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GFPFLDNYGGCWNRPFGPWGGYLK |
| 70 | 5567 | A | 71 | 1006 | 1979 | GLGASILDSTTSTWSWNASRLIGL KNSLFFEME/FSLLLPRLECSGTISA QVNLRLPCSSDSSASASRVAGITGM CHHAQLIFVFLVEKGFHHVGQAGL ELTASGD/PTCLGLPKCWDYR/R*AT APGLFFFFLRQSFTLVAQAGVQWR DLGSLQPPPPPRFKQFSCSLPSTWS WVYRHAPPCPANFVFFFFFFFFLVE KGF\SMLLRLVLNS*PHDPDPPASAS QSAGITGVSHHTRPMSFKNIY\FFFF FFETESRSVAQAGVQWRDLSSRQP PPPGFKRFSCSLSSSSWDYRRVP/PM PG*FCIFRRDGVSPRWSGWSQTPDL K |
| 71 | 5568 | C | 72 | 126 | 472 | MADCCAKQEPERNECFQHKDDNP NLPRLVRPEVDVMCTAFHDNEETF LKKYLYEIARRHPYFYAPELLFFAK SSMNFGMKGRLRLPNRDSSVPVSK NLEKELSKHVARLSQRF* |
| 72 | 5569 | A | 73 | 3 | 873 | HELLSTPLAFGTMKGVTL\ISLLFLFS SAYSRGVFRDAHKSEVAHRFKDL GEENFKALVLIAFAQYLQOCPFEDH VKLVNEVTEFAKTCVADESAENC KSLHTLFGDKLCTVATLRETYGEIA \DCCENKEPERNES/CFCNHKKDNP N/LPPIG*GPEVGC GCGTGFFMDNG RRTFLEKILIMEIGQEGHPYFLWPRE LLFLLLKRVLKLLFTGMLAKLAGL KLACLLAKARWDFRNEGKASSAKQ RLQCASLQKFGERAFAKAWAVTRLS QRFPAEFAEV\SKLVTDLT |
| 73 | 5570 | A | 74 | 849 | 1277 | YNTTKLVPLYLCKMIFLLFCYVYVL RQCLA/SVAQAGMQWHNHSSLKS* PP\GLK*SSHLSLPSSWDYRCVPQRF SLLFIFCRRKGFFPILA*AGLEQLGSR NHLALASHLSVGIIIGVSYHTQPVL AAIAMVLYFVNKLSVLL |
| 74 | 5571 | B | 75 | 120 | 323 | ITRRYA EFSSALVSINQIPNERTMQ LLGQLQVEVENFVLRVAAEFSSRKE QLVFLINNYDMMLGVLM* |
| 75 | 5572 | A | 76 | 154 | 432 | QLPEAGGPGLQEPLQLGELDITSDEF ILDEV DVHIQANLEDEL VKEALKTG VDL*LHSGERTTRD*QLPEAGGPGL QEPLQLGELDITSDEFILDEV DVHIQ ANLEDEL VKEALKTGVDLRHYSKQ VELELQQIEQKSIRDYIQESENIALS HSQITAC |
| 76 | 5573 | A | 77 | 2 | 630 | FFVSGPAAHDLFHAVMGRTLSMT LKHLD SYLADCYDAIAVFLCIHIVL RFRNIAAKRDVPALD/RVTEFWSLM PNRPRTLLVLHDSALTLDY*PGIIN LYSHSFAPEAVVLLFDSFSPSNHCPPT PTTSY*PLN*MMPHSLPSPSNIPCWL TSDSD*AHRYWEQVLALLWPRFELI LEMNVQSVRSTDPQRLGGLDTRPH YVREGKGNKG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 77 | 5574 | A | 78 | 175 | 2385 | QLPEVRLRGMAAAATMAAAAREL VLRAGTSDMEEEEGPAGG\GPGLQE PL\QLGELDITS\DEFILDE\VDVHNQ ANLEDELVKEALKITGVDLRHYSK QVELELQQIEQKSIRDYIQESENIA LHNQITACDAVLERMEQMLGAFQS *PSGSIKL/CRFRTLQEQSGAMNIRL RNRQAVRGKLGELVDGLVVPALV TAILEAPVTEPRFLEQLQELDAKAA AVREQEARGTAAACADVRLDRLR VKA\TKIREFILQKIYSFRKPMNTY QIPQTALLKYRFFYQFLLGNERATA KEIRDEYVETLSKIYLSYRSYLGR MKVQYEEVAEKDDLGMGVEDTAKK GFFSKPSLRSRNTIFTLGTRGSVISPT ELEAPILVPHTAQRGEQRYPFALF RSQHYALLDNSCREYLFICEFFVVS GPAHDLFHAVMGRTLSMTLKHL SYLADCYDAIAVFLCIHIVLRFRNIA AKRDVPALDRYWEQVLALLWSRF ELILEMNVQSVRSTDPQRLGGLDTR PHYITTRYAEFSSALVSINQIPNER TMQLLGQLQVEVENFVLRVGSW SFSFKGREAACVFWIQQLWTWMLG VLME*ERAADDSKEVESFQQLNA RTQEFIEELLSPFGVLRWHL*KEAE ALIERGQAERLRGEEARVTQLIRGF GSSWKSSVESLSQDVMRSFTNFN\ GT\SIIQGALTQLIQL\YHRFHRVLSQ PQLRALPARA*AHSTFHHL |
| 78 | 5575 | A | 79 | 1333 | 1561 | PLFIQLPGLPRMLTQFN\Y*TNHS*SK CQD/HSVCSWVKAFWRAVVAHAC NPSTLGG*GMRITRSGVRD*TDQHG ETH |
| 79 | 5576 | A | 80 | 132 | 356 | KDKIHIIISILKKFDKI*YSLIK\TL*K LGME*TYLNIKVIYDRPTASILSGE KLKSFPLKSGR*QECPLL |
| 80 | 5577 | A | 81 | 108 | 335 | NKDKIHIIISILKKFDKI*YSLIK\TL* KLGME*TYLNIKVIYDRPTASILSG EKLSFPLTSAR*QECPLL |
| 81 | 5578 | A | 82 | 3 | 6742 | |
| 82 | 5579 | A | 83 | 499 | 1018 | PTRVFSITAKLINGGVAGLVGVTCV FPIDLAKHSPQQPALGKPCYKGMIR LPDRRLGRASSAMYRGAAVNLT LGTPEKAIKLAANDFFRLLMEDG MQRNLKMEMLAGCGAGMCQVVV TCPME*PTRVFSITAKLINGGVAGL VGVTCVFPIDLAK\TRRSNQHWESH VTKE*SDCLIEDGSGGG/PSSAMYR GAAVNLT\GTPEKAIKLAANDFFR LLMEDGMQRNLKMEMLAGCGAG MCQVVVTCPMEMLKIQ\QACWTP GRPSSGLGLSTLHLQVLHNWFGFHP QAPLCHPHCLG |
| 83 | 5580 | A | 84 | 3 | 305 | GTRQGCPLSPL*FNTVLEILVRHS/RS SSSSSSSCLTADP/MVLHIENPKGSIK *VLELINEFSQVAGYKINM/QKTVAF LYTNN*LSKKEIKKTIQFILASKRT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 84 | 5581 | A | 85 | 39 | 281 | KPRCIVSFFSMVVEA*ASIVK*EKEK IGNQGTKL**FEEMI/LYIGNSRASA DTLLEIKDFSKISGYRFNIHQSVMLF YFSC |
| 85 | 5582 | A | 86 | 456 | 712 | NIFTYLFIFVTECTVVQAGVQWCD LGSLQPPLPG\SSDPHASTS*VAGIT GVSHGAWLIFFSFFPFLRRSLPLSLQ FGQQSETLF |
| 86 | 5583 | A | 87 | 218 | 468 | NNFFSSRVLLLSRLECNRSRI*AHCN LR/LPGFKRFFCLSLPSSWDYRLLPP RPAFLYF/SV*TGFFHVQASLELL TSDDPPAL |
| 87 | 5584 | A | 88 | 372 | 666 | NVCFIRTGTDCHIIEHNGMKLAITKE KLEHLQ/YVWK/LNRFLNNQGVKEE ITREIRKYFEMNENKNTKYQN*ECV MTTVCRGKFIAANVHIKKQDSNYV R |
| 88 | 5585 | A | 89 | 36 | 350 | KLQLHNLKARIAAIHQAQ*LTPVIPT LWEAKAGRFLEPREVKASLGQ/P** GTHVHKTYKIARAWVAKHLWVPS YFKRLEVRRVALSPRGV/NGCS*RLI LPLPSQP |
| 89 | 5586 | A | 90 | 58 | 375 | VFYNKTTFKVFIIAICSIIYFVCLHSI VI*FFIL/CYCRVSEIFGYRCFIKLLL KSL* [*] L*FVPLFILFACILLF/WLNC YFLRLSTIVFF*KKLLIVLTFFFLYRS IIFS\CFYLLLSFF\CFFGCTL/CSCLC LQLCLFFSFSYFLIHVLR |
| 90 | 5587 | A | 91 | 107 | 355 | DMILYIENPKDSSKNPLGLINKYSK VAGYKINTQKSA AFL*TNLYLKN*P /MRTIPFTIAASSSYLETYLTMEVKD LYTENYKM |
| 91 | 5588 | A | 92 | 31 | 358 | NVKSGQNLTMGEGSVSQGSIFSSLG GHRTVSVVTMVRRCRCPAHRGLSR WLPST\SSGTQ*GP*NC*PNPPITLLR PPRPRQRCPSLCQFPP*TSRQRPSQ PPQGPPEFP |
| 92 | 5589 | A | 93 | 1 | 1253 | MRIPSFLNLQDFEDKMEIKRYRPE GPLATSAQSHVSTAPLISTQIPPHVP PLFLDCRHLTPASLFDQTLIPKKAPS NCVTDSYRKTSEIHPGSLFLILNLQF RTSTSNCCFSGSGKEALTGSIGRERS PLLAQTFFPTLKKSQRSATLECDEE ASLWENPLRDHGLFPASEHRLPLPL NQQKGPPRLRTSPA AHSPNFAG\MP PVASSEGLTSIYSQLSPIG\PPGRRRQ RGCPY*VQLHGDWPLCTAVYT*AR RSVAL*SRFCG*QTRR*TRWQRNPP VCSG/HKLREFPLKLELFPQIQDPIG HQFVISVGQVRGH*STQKLYGPIRS ASPGAD\GGARGRRGFDGSGPPAP NLHPGARALPGSCWSHLPGVRSQE VSFLDSGSGSRVNPPTAEDEAWESG LCSSHPACQEHTKDL |
| 93 | 5590 | A | 94 | 216 | 1374 | RPQGMPPVSSPPPKLLLDPLAQLFS GQQDPQPLEKPHLQCLGRELGSGR RGGGWSPGVENRSQTLFFPGHRAP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | APGDAEGSGP*SFSGDARPTGHLLP PRKG\HL*SSGELRPGRCONS\QAAG/ HRGLGVPRGALGVSLAGSSFPSPR RRPSG*AANNSVASEGAR*ALGRG/ GPEAMP/DEFVRGVSGG*GPRGRSR LLIEW*TEAMFADPTRTAGGVGTD GKLLPVPQGDH*ARPWKPREIRAVS RAGHVG/LPAC*EIPAQSLSGP\RG SAAIFGSCVPHGGSTRAGMVVRVA RGSPRGEQGLVLTR\GTTRTCGMNS SSPLAFSPLKSPG/MGGQLAGP/PGA PSARWSHGGSAGRWCGRGVVGQE LVSWIHRSVTGSPHKFVGCWRQTS |
| 94 | 5591 | A | 95 | 282 | 612 | |
| 95 | 5592 | A | 96 | 19 | 1153 | DLTPGKWDQQEPGRARAPGWRLG AGGGEQSNPLFPAPRTCPRGCRT NWPIKLLCNGKKPEAPGGARGASL SEPSPLPGWPWSTGSEEADLEDRTE\ ERPKGFDSDHVEMLKP*NPKVPNCE GERGCSRAGSTLEPSGESSAQVQE KKDYAQQWF/SNRGQLRPHMPLPT PLGH*AAAGGSGRENVIP\GMCLVS GGDRCC*TPCNPRWEGPSPTPK*PF RQRWRNSRVR\IAHGILADGIHGFG DQLDLGSEEKAPASEGTLEVLPRAN GGVALPVA*RWEDGRRHRLQGKV GDQLSAP\GLPGKSFLSSPPRFPHPS DSL*C*GCRGLGPL*CRGCPRLTSG ASPLPPPPGNLVGGSGPGDPRPSCQ LLPPGKGHL |
| 96 | 5593 | A | 97 | 429 | 945 | KSVLSTLNWAQPRHWPETLPWVPS *PETS\PPPGGS/APPTPDMD*LNSAS PNSAPPAC*NPSACRLSSLPAITPVS QDPT\PSTEQAPKPAFTPWLPPAAS\P FKAQTASKG*PSHMWLPLPLLTTP KPV\PSALLP*APSQPPKGV\QAPS QHPLTPSHRTCSPAGLLTP |
| 97 | 5594 | A | 98 | 178 | 603 | SQHFGPRWTNHLRS*IQDHPG\QHG KTPSLLKILKKKLAGHGGAHL*SQL LGRLRHENHLNPGGGGCSEPR\CHT AAWMTE*DSVSKKKRPGTVAHAC YPSTLGGQGG\RTSRDRDHPCQYG ETPSLLKMQLAGHG\TRL |
| 98 | 5595 | A | 99 | 405 | 689 | GSFLFFCFFF*DRVPPCSP\GWSAVV QQPQLTSALT\SWGSHLSLLSSWEHR DV\PPCPG*FFIFCRDGV/LTVLHRLV SNFWAQ\SILPPWPPKVLGL |
| 99 | 5596 | A | 100 | 3 | 307 | FFFLEPSLACRQAECNAHLAH/CKL NSWFTPF\SLSLRNSWNYRCPPSRL GNFFVFLVETGFHCVSHDGLDLLTS *SVRLSLPKCWDYKGESLHRAQNY LDL |
| 100 | 5597 | A | 101 | 279 | 469 | PKMAQTQKGYLHLILALMCFYFRN TQAKKNLKRDC*RPSRMPKDLACC KSIQNKIKQKIGRKK |
| 101 | 5598 | A | 102 | 265 | 446 | |
| 102 | 5599 | A | 103 | 283 | 398 | NWQEKCTFQIIGGRKRMSFRIILNF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FHN*DRTVCYVP |
| 103 | 5600 | A | 104 | 283 | 397 | NWQEKCSFQIIGGRKRMSFRILINF FHN*DRTVCYVP |
| 104 | 5601 | A | 105 | 2 | 1012 | AEALVESFWKAKQHTKEELKSLQA KDEEKNENEKAKAACSAAAMEEDS EASSSTGDSSQGDNNLQKLGPDVV SVDTDSIRRVYTRLLSNEKIEIAFLN ALVYLSPNVECDLMYHKVYSQDPN YLNLFIVMENRNLHSPEYLEMALP LFCKAMSKLPLAAQGKLIRLWSKY NADQIRMMETVQQLITYKVISNEF NSQNLVNDDDAIVAASKCLKMIYY ANAYAVTKNLGLYYDNRIRMYSER RITVLYSLVQGGQQLNPYLRLIVRCD HIIDDALVRLEMITMENPADLKQFY/ RGI*RRTRWVAAFWDRASEPKANSI GFGGSQLWMPTPVASYT |
| 105 | 5602 | A | 106 | 966 | 3172 | |
| 106 | 5603 | B | 107 | 1 | 2271 | MAGKASESWRKVKDTSCMAVTRE NEKDAKAETPDKTIRSRETYHKN MWETAPMIQIISQGVTPTHENYGS TIQDEIWCLTNFCLDDMLSFVLESC TNHCAYCLNVWYRKRAAAKHLIER YYHQLTEGCGNEACTNEFCASCPTF LRMDNNAAAIKALELYKINAKLCD PHPSKKGASSAYLENSKGAPNNSCS EIKMNKKGARIDFKDVTYLTEEKV YEILELCREREDYSPLIRVIGRVFSSA EALVQSFRKVKQHTKEELKSLQAK DEKDEDEKEKAACSAAAMEEDSE ASSSRIGDSSQGDNNLQKLGPDVVS VDIDAIRRVYTRLLSNEKIETAFLNA LVYLSPNVECDLTYHNVYSRDPNY LNLFIIVMENRNLHSPEYLEMALPLF CKAMSKLPLAAQGKLIRLWSKYNA DQIRMMETVQQLITYKVISNEFNS RNLVNDDDAIVAASKCLKMVYYA NVVGGEVDTNHNEEDDEEPIPESSE LTLQELLGEERNKKGPRVDPLETE LGVKTLDCRKPLIPFEEFINEPLNEA LEMDKDYTFIVETENKFSFMTCAF ILNAVTKNLGLYYDNRIRMYSERRI TVLYSLVQGGQQLNPYLRLKVR RDH IIDDALVRLEMIAMENPADLKKQLY VEFEGEQGVDEGGVSKEFFQLVVE EIFNPDIGMFTYDESTKLFWFNPSSF ETEGQFTLIGIVLGLAIYNNCILDVH FPMGCLQEANGEKRNFSVTWETLT QFLYQSLKDLIGV* |
| 107 | 5604 | A | 108 | 264 | 378 | |
| 108 | 5605 | A | 109 | 297 | 353 | |
| 109 | 5606 | A | 110 | 1034 | 1195 | MQKKMIFQQTAPLNPVQTV*RHP TPKRKECPSLRRQSTLLRMMWYLP CDQWS |
| 110 | 5607 | A | 111 | 1075 | 1826 | LGLQNRNFGYKKHFWVLT DSEPAG VGGGEWFFSLGSRTDRSGAISPLI TLRTLAAGAHQALTKTMMMSD KKRI*VTFLFEFKMGRKAVETTCNI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NNAFGPGTANERTVRWWFT\KLCK GDEGLEDEEP*WDPLEVDSDLL\AR TIKADPLTT\TREVAEEFNIDHSMV FPHLKQIGKVKKLNK*VPHEPSKN KL\FLEASSLILCNNNEPFLSRIVTW DENWILYDNH*QPAQLLD*EAPKPN LHQB |
| 111 | 5608 | A | 112 | 540 | 724 | EAMFYTWEGEWAQEIVGLKKIRL GN\AHAYNPSTLGG*GGQIA*AQEF DTSLDNIARPVS |
| 112 | 5609 | A | 113 | 1 | 370 | QRSRGRGSLRIGQTCLRRDMLSQEL PRLEFPLLLLMLLMP\PPCPAHRA TLFDPTWESLDARQL\PAWFDQAKI GILHWGVLTPSYCIERV*RNWQM EKIPKNVEFMTDDYPPRYTHEDF |
| 113 | 5610 | A | 114 | 151 | 379 | PFYVENP**YTLKNFLELISNYNKV AKYKINIQRSIYFLYASHKQVDFKV QTQ/LPFTLA/SL/RMK*FSISLTK*VQ D |
| 114 | 5611 | A | 115 | 17 | 214 | KQRLSYCIYKTTKTYATYKEIHR/LE VNGCKRIYHANTNQKKAGVAILISD KKHLRQEYYQG*KEML |
| 115 | 5612 | A | 116 | 249 | 675 | QYISVTRCHISMLTLNLNGSNAPLK RYSLTE*IFLNDTTV/CIPRHTDRLKV KG*RKTCYTNRKQKQ*/GAILMPD KTDVMSSSSSSSRK*IIVKGSILQED MTIQNIYTPNTIAP/R*VKLILLGLK G*IHSNTIMVGKFSIR |
| 116 | 5613 | A | 117 | 67 | 373 | FCDCHHFILMFKSPHIWPVGIFSSWL LCFFWACLHHSLSIALLSCTKRYSG LILYFLCSSFEITVSSKSSVSF*RRMV FRNQVLGSRACCCC*GVAAPRFPF |
| 117 | 5614 | A | 118 | 366 | 795 | AWVEQSKVLIKEGGIQLLLTIVDTP GFGDAVDNSNCWQPVIKYFDSKSQ D\YLN AESQVNR CQMPGNRVHCCL YFIAPSGHGPLHN*RLPPSGRIG*YM FVTTWHCLLLRLKPLDIEFTKHLHE K\VNIIPLIAKADTLMPEEC |
| 118 | 5615 | A | 119 | 105 | 702 | AGSSVSLGFCPAAAAHKPRGGALR LPVFRRAQQGPDYALAGVARQPA GTCRRRCNRSHCRAEDPQWPTPAA APAAHSPHMSLGESGLGKLILINSLF LTDLYSPEYPGPSQRIKKPVQVYILV FLIDDKLE*Y*YTQSTCCNFHYAS\Q SWQPAINYIDSKFEDYLN AESRVNR CQMPGNRVQGCLYFIAPSGHGPLH N |
| 119 | 5616 | B | 120 | 7 | 177 | MSVSARSAAAEERSVNSSTMVAQQ KNLEGYVGFANLPNQVYRKSVKRG FEFTLMVVE* |
| 120 | 5617 | A | 121 | 2114 | 2945 | KSVAFLCTNNVQVQAENHIRNVVIS VT\APIHKIKYQRMYP AKEVKEL YR ENYK TLMKEI DD T K K WKNIP/C*W VGRK/LIYRYNTIPIKLSTSFTELEK KILKFIWNQK/HSRIAKAIL/AQKYK AGGITLPDFKLYYKTTVTKTAW/Y Y WYKNRHRDQWNR TENPEIKPYTCN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QLIFDKINKNKQ*GKDILFNK*CWK NWLPICRMTLGPYLSPTYTKITSRW ITDLNVRLQTLNILEENLGKNLMDIS /VGKEFMTRP/PKAYATKTKIDK*DL IKLKSFC |
| 121 | 5618 | A | 122 | 3 | 113 | GLDLLAS*SARLGLPKCWDYRSDW GPGPVCGHLCRG |
| 122 | 5619 | A | 123 | 145 | 540 | FFVFFVEMGFHCVAKAQAYNIFFFF LRWSLALSPRECCGAISVHCKLRL PGSRHSPCLSLPSSWDYRRLPPRPA NFFFVFLVETGFHPC*PGMGLDLLT S/SIRPASA/FPKÇWDYRA*AIAPGK MRLFNSL |
| 123 | 5620 | A | 124 | 739 | 835 | LAKISNSDVLKLSMLHKSENSISHK TGAERNK*YLLIKLKVI*LLTL*VNIC FFQLQFYVK*SFQIYVAWKVLIRQS Y*FLPVIFSIYFFYL*LIFV/CDTFCF *SHFLLFIFYVYFNLVTMRITYNILEL *HFNLNLFQLKFNHHPKFYCIYIAL L/CFMLLM*QIISLFIVYHVTDLLITF YAFAF*IM*KIKSRVTNQNYNRTVF MFVYVYLPPEFVYSYSLLIYLSY CLEFIYFNLKDLTLPECQFRDKWIF FQF*KKIRKCLNFS/CHF*RISFPAIYF SIDRFLHYFKYIIHCLLAFKVSAREIS C |
| 124 | 5621 | A | 125 | 48 | 492 | HPTGPGRRSHPRPCPRRSLTSLAPSP WPPGSLQRSLLDPQRSPPWRPRTQAC TRSAHALRHTIPRSTLGVTVGLEAA PPPQHLRAKGT/PPVPGAQPPGPRP WPTQLRERPSPEPPPPGLGLPGSKTP ALPARPRVG*MGPKAQPHTPF |
| 125 | 5622 | A | 126 | 536 | 669 | YLNVGNNWVG\PMHTSNPSTSGG* GGWST*GQELKTILTSLVKHS |
| 126 | 5623 | A | 127 | 793 | 829 | GRCHLAHGGVQGSRIKPPQLGAWG RRQRDIGNRGSRLWGEKEEKAGE RKDEPALARSTSQAPSRLHPCIFNPL GVRYPRWALHPQLCAPP*AHVSVS TQIPRQRPQVAVTSLVPPISG*FRAP QGKLPNGQMLYGRHPHPLQAPPTA RASPSHVLTLTGTEQPPRA*THSPEK W*GVPAWLRTSPRPRPVGRREQVT LIWKPKQN*SAESPPSHRAYPEIPFR LLCLQPRGTGPVLLLGP*SSKCPEPPC TKSKPGWGKACSPLTGPCLPSP/PDL PSVPSPSPVLPDPNRTATASRNPTV TERYLNASLCWSQPDLPQGPIITDM PSAPAVPLTSDNCPSMSPAPSGKAV RQMPPGTWWGSG |
| 127 | 5624 | A | 128 | 322 | 386 | IRCFALRFSSLLSFIHLY*DT*HPDT* HPDIQTPGHL/HTQTPDTRTPGHPDT ETPDTQTLRRLTPRHLD*HSDTQT PDTQTPGHSTPRNL |
| 128 | 5625 | A | 129 | 323 | 516 | AGGRFPSWDPFSSRGSQASKPVRMP PTR*MRR/RGRQPCPGHRRRTQLFA VSAPSRDLQNCSERF |
| 129 | 5626 | A | 130 | 238 | 583 | MADKQISLPAKLINGGIAGLIGVTC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VFPIDLAKTRLQNQQNGQRVYTSM SDCLIKTVRSQGYFGMYRGAAVNL TLVTPEKAIKLAAANDFFRHQLF*GR AEA*PCLKRLLGGFWG |
| 130 | 5627 | A | 131 | 3 | 492 | SSGLGCAGTRDSQLSIRGLSSTRRS GGGGDGDGTPARDLQLGWLHLLH GSGDRRGIEECAIKRKDQGVNQKK KKKRTSKLGRMSSCSNVCGRQAQ AAAEAGGYQRYGVRSYLHQFYEDCT AS\WEHEDDFHILRSPTRRS/SYIFE GVDSFSGTLL*YLAWTG |
| 131 | 5628 | A | 132 | 1 | 245 | GPGTGPEPWTPYS*EGDPRGRPRPR PLGPPP/TAHAADGSYRHSASGPGS WTSPFPSPGGGEKSGRTGQRVWKF GFWSWLCH |
| 132 | 5629 | A | 133 | 554 | 1049 | GRTGGGLGLLHGHTRLADTDLLDR GMLKDTLAQAPPPLGEAYCHQGP GPWAGGGALSPGTRLQAGIQG/P/PE PQLPQLRPEPRP*PP/AQVVAGCGPA DLPPGGCPGCSGCSPHR*TAFIKTSA NPATLAGVGWG*GHPEGVPHTASE TGSDLQL*PTAIGHTGGPW |
| 133 | 5630 | A | 134 | 798 | 1083 | DPVGKGNVELPGRIAHCFHCLPVLH VCLSLSVLCVCFVLFWCFSTSLF*RII VFERYLTFLVCVLCC*GLCFICTCF YCSLVF*LFASCFLYSS |
| 134 | 5631 | A | 135 | 71 | 484 | EIFCYCVKYTYIQTHAPFKFFRFIYL FRDRVSL*PRLECCGVVLAHCNLR/ LPGPK*SSHLSLLSSWDYRRTPPMPS WFLCFS*RRGPHHVIQVGLELLGSS SLPALASQCWDYRREQPWPG*KVF LSSAYCLFHLTLY |
| 135 | 5632 | A | 136 | 186 | 434 | SQHFGRRPRQLDAPRSGI*DQPGQHG ETPSLLKIQKLAGHGGRRL*SQLALE RLARQENHLKPGGGGCSEPRSRHCIP AWVTERD |
| 136 | 5633 | A | 137 | 1638 | 1904 | GGWITRSGDRDPSLAKHGETPSLLK IYKKLAGRGGRSL*SQLLRRLRQEN GINPGRACSKPRSHHCTPAWATG DSASKK*KIKKKVV |
| 137 | 5634 | A | 138 | 421 | 1155 | KICGSYYPLFLLATFSEESFQSMLIK TTLSLNVGLVLSWKR\VQGAS\GKL QGLSEFCESQGAQNLTLRALRLLHD LQIGEKLLVKVDAKTKAQLDEWK AKKKASINGNARPRNCHLMTDEEA LDEETKRRDQMIKGAIEVLTREYSS ELNAPSQESDHPARKKKKEKKEAIF RRFPVAPL\IPYPLITKEDISAIEMED DYIDLISREISIFRDTHKRSYGD*CK MKLSAWKVTRNRINWKKRK |
| 138 | 5635 | A | 139 | 338 | 395 | |
| 139 | 5636 | A | 140 | 340 | 1248 | RPLVLANCIQEVIKRIVDMQVPLISG MQ/AWFNIVKQINVIYHLNIMKDEN HIISIHGEKAFHKIQHPVIMEILNKIE REGVYLNNTKTIHEMTTAEITSQGK WNAFPVGSHMMQE/CLSPLLFN/LIL AVLARAMK*/QKEIKLIEIRKKEVKL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; v = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YLFVDDMIFCAENHKESTKILLELS NIFSGFAQYSISTKN*LNHFTFNNKQ L*KKILK/QLPLAGELK/RKKYLKIN VKRSEVFTLKSTNIDAND*KHI*RH NPY*WFGKINIVK*LYNNPM*FRFN MISIKIPISFC*RNKKQAGKMAHVC WPG |
| 140 | 5637 | A | 141 | 47 | 411 | |
| 141 | 5638 | A | 142 | 1 | 343 | GRLQAITDKRKIQEEISQRLKIEED KLKHQHLKKKALREKWLLDGISSG KEQEEMKK/RKSTKEEAILKKLSIE RTTEDIIRSVKVEREERAEESIEDIYA NIPDLPKSYIPS |
| 142 | 5639 | A | 143 | 460 | 976 | LLRIGKEAELGGRGRLPGHSQIKRK LQEEISQK/RV*KLGEDKLKHQHFE DK/VPLREKWLPWNPASGKEPGR D*RSQNQPRPSTQIPGS*NKVSRLRLE KENQDLEKAELQISTKEEAILKKLS IERTTEDIIRSVKVEREERAEESIEDI YANIPDLPKSYIPSRLRKEIN |
| 143 | 5640 | A | 144 | 79 | 533 | SSIMTFLESSAVPPHWTGQDGRVC WTGWIPQCQAGSAPE/RS*VFINSAG QKSADTGWSSSKPQN*HLSSFHQA VVGMIQPSHSQFLMKRKAASPRKL EWEH/LQPLHPMTLLYR*DGKPFR* VLLSTYTYCSSRDRPKSSGKNARRF PAHGSS |
| 144 | 5641 | C | 145 | 354 | 416 | MKESPGGELPQTGKKPVFLF* |
| 145 | 5642 | A | 146 | 3 | 145 | SSSSDFAGQTL*STQTVQN*FKKVL KPGRLYPVPIATMGIKEPLIS |
| 146 | 5643 | A | 147 | 214 | 464 | FCGLLLHPVSADF*PAELINTQEPQ ERCQLDTGESSRVQHTLPSCPVCQG GTAELSRNVMIGASELKCLHPSPKL EYILPGN |
| 147 | 5644 | A | 148 | 246 | 730 | SSIMTFLESSAVPPHWTGQDGRVC WTGWIPQCQAGSAPE/RS*VFINSAG QKSADTGWSSSKPQN*QLSSTGAAL PLASLSRERAWVDDGKHRLTTPMT VPQRAVQQL*ETSG**DWRQKVQIF QQA VVGMIQPSHSQFLQREDVIML RPFGLHLSWEENGs |
| 148 | 5645 | A | 149 | 12 | 288 | FGGGYIPTWGKGEGILALELNHDIS REFCSAPALASRPPPTPPPLLPPT/PP LPAPRSPADATPRRVGGPLR*ALKP RAPGPGWSRRRCRSWW |
| 149 | 5646 | A | 152 | 106 | 344 | KQILLPPRLEG/NGQNSG*WKFPLP GPSLFSCPSFQTSNGYGPQQAIF WKFKIKTGFHGV TREGLNFLTSGSA PLGS |
| 150 | 5647 | A | 153 | 38 | 349 | RTAKSGSTKFSLSNSKYGTVLAVLF MKKILVRLSPKKNDQTVKYIKRPL TSLKIREIHIKTALLYLLE*KLKLF DDTCH**A\WRNYCWRVCVLIQPL WRQMW |
| 151 | 5648 | A | 154 | 220 | 970 | ESRTRGAEAAAGLAPSCTSPQAHGPA PLPTHVCCGVAIGMEPGHTAISPWW ELAVHLTGLVSSHDA LGMMPSQQG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; v=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | *QWGRQRGLASGN*GRMSFPNSWP VTPICAARLPPGLLLICGFDGAGHSD RSEGF*GLRFPFCFKRQ/RSHSVSQA RV*WCDHGSLQPPSSGLKHPPVSA SQVAGTTGMWHRAWLVCLFETES CSVAQARVQWRDLGSLQPLRPGFK QSSCLSLSSWDYRHHVAPCLASLFV CLRRS |
| 152 | 5649 | A | 155 | 193 | 369 | HLN**FSNLIFFETESPSVTIRGIISAH RNPRLPGSSDSPTSASRVAGTTDT |
| 153 | 5650 | A | 156 | 626 | 1017 | FDSCLFLFCFVCLRQ\SSVAQAGVK WHGLSSLQVPPPGFTPFWSLSLRSS WDYRHPSPHLANVFCFLGFFVFLVE RGFTVLARIVSIS*PHDPPTPASQN AGITGVSHCAWPTLVCLNAKFSIVV FVHKD |
| 154 | 5651 | A | 157 | 1 | 336 | TVSQAPSPESNPHGRRGDYHRKLIG QTFEWV/VRRHGGRAIGPRLSRVTK AAGARPPPEPKDFGFPEAARRVMGIT PVLDLGRQPVRGALVELRGAHGWR AGGGTGSCGIPARL |
| 155 | 5652 | A | 158 | 2 | 320 | VVAVSQAPSPE/SEP*FPVTRGHHGR HGDYHRKLIGQTFEWV/VRRHGGRA AIGPRLSRVTKAAGARPPAGAGEG/ LDRVGFDLINARIPPAK GANGSSPPR GACDRPEVI |
| 156 | 5653 | C | 159 | 177 | 380 | MPTGADPLRGGDACIYQIKTNPVSP SPAPAGGRAPAALVTLDNLGPIARP PWRRRPIRTSAPINFRW* |
| 157 | 5654 | C | 160 | 1 | 417 | MDATCHGCLQFQIMRNKKFQLLSP SSQHFRMTASGGKQLLCRTGQKM EHPIPXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXGRPV * |
| 158 | 5655 | C | 161 | 1 | 403 | MDATCHGCLQFQIMRNKKFQLLSP SSQHFRMTASGGKQLLCRTGQKM EHPIPXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXX* |
| 159 | 5656 | A | 162 | 513 | 1086 | QPQVASSYSAGQGRRWNTPSLGKIT RSGDRDHPG*HSETPSLLKIQKLAG CGGRHL*SLLRRLRQENGVN LGG GGCSEPRLRHCTPAWATE*DSISKK REKKKKKKERKKKKRKKKKWKKKE RGRGEAGEEQGEEGERRRDKKKK EKKEREETREEGRRRRRRRKKKRR RRKKKEERTTKRRRRTRKKK |
| 160 | 5657 | A | 163 | 2 | 935 | WRRSTPAPSATSASPSRCL*SQLLG RMRQENRLNLGGGGCSEPRSCHCT LASPAGTQSCSRCTSQQGVQSDIPC TAAAPETAPRRGSAGGTWCRRRAP P |
| 161 | 5658 | A | 164 | 34 | 1026 | LLALGQSSCL*SLLGRMRQENRLN LGGGGCSEPRSCHCTLASPAGTQSC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; v=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SRCTSQQGVQSDIPCTAAAPETAPR RGSAGGTWCRRRAPP |
| 162 | 5659 | A | 165 | 45 | 69 | RKNQRIYQIARKRLNEMARISPLRS MIILNVSGLNFPKRCRLAEWTUSSP DPIICCL/QKTHFTG/KDIYRLKIKGW KKIFHANGSQ*QTAMMNTNRERTK GYTK |
| 163 | 5660 | A | 166 | 48 | 72 | RKGQRISEIAIKRLNKMARISPLISII LNVSGLNFPKRYRRAEWTUSSPDP IICCL/QKTHFTG/KDIYRLKIKGWK KIFHTNGSQ*RTAISQSAMCNNNRE RVKGFPK |
| 164 | 5661 | A | 167 | 118 | 639 | ATVPSQQLIFDKDSKAIQWRDTLFN KWCY*IN*ISTCKKLDIDSYLAPRT KINPKRILDLNVKPKTIKCLQENTGE NCWDFGSGKHFLDMTPKMQSTK*Q ISKLIKI*NFSSKTQHFALLIIRIF*KTL LTGSKYKATTWKK/VFVNHIPDKRL ISQIYQELFRTQTKNPTSDW |
| 165 | 5662 | A | 169 | 435 | 808 | KNLCNNKKFHRDEGWAQCLTPVIP ALSEARSRLYHLR\SGVRN*PGQHG *KHGLYWIMQNLAGRGGTCL*SQL LGQLRQENSLNLQGGGCSEPRSRHC TPAWVTERDSVSTTTTKIFTRMNLN R |
| 166 | 5663 | A | 170 | 167 | 197 | VKFHKIKLDGEDTTYGGFDGPGLM YVYLISSDGH*FTQLHQEL |
| 167 | 5664 | A | 171 | 45 | 259 | ARMNSKLALAA*ALQKRSLRHQSNV FSMFDQSQIQEFKEAFNMIDQNRDG FIDKEDLHDMLASLGELGQGQG |
| 168 | 5665 | A | 172 | 90 | 468 | IMKLLTRAGSFSRFYSLKVGPVAKAK ATAAPAGAPPQPQDLEFTKLPKGW LIAPLENYPPG**IGWFIKAGT*SEDF NALGTTTHLLSTTCSVTNGASSFTIT RGIESADGPLTVTASREYMDHTVE |
| 169 | 5666 | B | 173 | 89 | 186 | XLKYFQTVTDYGKDLMEKVKSPEL QAEAKVLL* |
| 170 | 5667 | B | 174 | 85 | 298 | XLEGALVRRQAKEPCVESLVSQYF QTVTDYGKDLMEKVKSPELQAEAK SYFEKSKEQLDTPDQEGWERELV* |
| 171 | 5668 | C | 175 | 279 | 533 | MAKDLMGEGPRTPELHAERQVFTF EKFKGSSLTPLDPRKAWERELGLTS LELIFRGNFGNHSLATPVESFPRTIW SFQTPGWAF* |
| 172 | 5669 | C | 176 | 260 | 389 | MDFFAQKKKKKVCMYVHMSTQR WLPNETNQINVLGFLNFLSC* |
| 173 | 5670 | A | 177 | 84 | 1008 | KVCCRYRKANGGKGSPVQEVDPDG APEGAPLQQGPAPGWLPLPTTQSVS APPGGESPTENQPMFKQTDPMKS FWTKMGSPTLPSPNSV/AVSHFSPH FISN*EWEQNQPLSLVLSGRGDELH SDGGQKTQGLDKQQLPRGWHGLV SFGRAACSKLGKNLRPQEIKWSSKL HLPIPESQC*SPLVGVEQWGGKLG VGLLLQPKGGIPTALSPCALPAGHP TLPYGNAGTDLRLHTEPEGPHGEP GLPARWGQDGMERWAAAGLGKG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YLLQASRGVVGSETGQVGFLFGKKT KSNRLIAVNDSVHFL |
| 174 | 5671 | A | 178 | 79 | 336 | NCCNTIKSISEKP/LANSIR*AKKQEG FFQISGIRQGCLLSSFLFILEVLARG NR*D/IKCIQIGKKKVKLSLFSETMR FNIWKRLR |
| 175 | 5672 | A | 179 | 3 | 370 | SVCVRAHESVVKSEDFSLPAYMDR RDHPLPEVAHVHLSASQKALKEK EKASWSSLSMDEKVELYRIKFESF AEMNRGSNEWKTVVGGAMFFIGFT ALVIMWQKHVGL\ASKWDYEKNE WKK |
| 176 | 5673 | A | 180 | 24 | 1173 | RAVAAGSGGRMLATRVFSLVGKRA ISTSVCVRAHESVVKSEDFSLPAYM DRRDHPLPEVAHVHLSASQKALK EKEKASWSSLSMDEKVELWVLKG PTGAPSSSRKRVCDRASAHFWAYC LESSLAQEGCSAGVSGHCARAPVY VLTSHLALPADRIFC*APFSVLSGGS LSAYLLGKT*LTVNY*KKLITMHSV WDERGRKITGLNRP*YCNSKK*FC SFNLHLKRTVCIFFLPCPVTCLRGHV CARMCVNMWPGLVYPSALCFL HKCGFGEKWLNVAAEAGAADLCAC KWLSSLPPVYRIKFESFAEMNRGS NEWKTVVGGAMFFIGFTALVIMWQ RHYVYGPLPQSFDKEWVAKQTKR MLDMKVNPIQGLASKWDRV |
| 177 | 5674 | A | 181 | 1 | 738 | RRSQRYPFPLHGDRAAGCGRSLPR SRGAPRRGLALFRSRDTGCRGRSRQ GSGGRMLAYQGYFTLVGKRAISTS VVCVRAHESVVKSEALFASQPYMH RR*HHPCPEVAHVHLSAQPEGT* KEKEKAFLEASLSMDEKVEVVFAL KFKE\SFA*RLNKGAPNRVGKDRFV WAGAIVSFNRVFTALRLSCWQKH YV\YGPLPRKSF*QKSGLAKQTQEG CLDNEGEPPSQGLASK\WPYEKNE\ WKK |
| 178 | 5675 | A | 182 | 82 | 395 | ICSFAPSSIFWGSFTGTCSSTSVRA AAPPGTPQRPSMDAHTGRKGRLS *TSFFTWSMVTALLGVWTSVSVVW FDLADYDD*L*ALAIYD\ADGDVRF LRGLSH |
| 179 | 5676 | A | 183 | 134 | 594 | VITLTIVSPALVANNASARGLTLPAP/P LPTGSRRTGAPSWEPDGLGSSLASC *NPPGAPGPKS*SQTGRPAPALASR LSGPLLQLPCFLSVPRSPERAPGPRH KLLLLQSLMAVSFISQFKCHLPGEV LPDRAAPGGSWPGDSRALTKSPCT |
| 180 | 5677 | A | 184 | 3 | 404 | |
| 181 | 5678 | A | 185 | 2 | 851 | AAAPAPAPAPTPTPEEGPDAGWGD RIPLEILVQIFGLLVAADGPMPLGR AARVCRRWQEAASQPALWHTVTL SSPLVGRPAKGGVKAEEKLLASLE WLMNRFSQLQRLTLIHWKSQVHP VLKLVGECCPRLTFLKLSGCHGVTA DALVMLAKACCQLHSLDLQHSMV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; ▽possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ESTAVVSFLEEAGSRMRKLWLTYS QTTAILGDLLGSCCPQLQVLEVSTGI NRNSIPLQLPVEALQKGCPLQVLR LLNLMWLPPKPPGRGVAPGPGFPSLE ELCLASSTCNFVS |
| 182 | 5679 | A | 186 | 2 | 568 | EFGKDSCGNISAALPPLSAQVFTAPE ADPHPLEVSGTTPRVEGESSL* LHITCDTLGLVSTLGSSTLGAQRCSVG MSACLPGLFLLFPAGRYQRRGHP SRPGMGRKEVTAKAVRVGLAPATL SVSLVDLSLSSPNPSCPSVSPQLVGE CCPRLTFLKLSG\CHGVTCLTLWSC LAKACCQFHKPW |
| 183 | 5680 | A | 187 | 2 | 333 | ARDSTSTTEMNPQVLFQRV**QFLLI TTSWRKVISQTFGRLVDTGSKL/TV QMPRISSPSVRVAACGGQVIDGVLL KVQLTVDP*T*WTDLVIFS/SAFE*VI GIDILGSECS |
| 184 | 5681 | A | 188 | 2 | 363 | AREVFTQHSHTLYH*TIHTGEKPYK CIECGTAFGVRSCLSIHLVVHTG*LP YRCHECGMVFMNRNTHLVRHQLIHT GEKPYMCNECGRAFIHNSNLATHQ AIHTGEKPYICTECGTVFTQN |
| 185 | 5682 | A | 189 | 361 | 1026 | RKYLPPRPTFNAEALPLKVRIWGRG LISKLYH*LYQEL*L*LYQGLITILLE KKLI*KLDKNLNRHFSKEDIQMANR HMKMYSTSLNREMOIKTTMRYPS PQLKYLLSQKTGNNKC*RGCGEKG TLVH/WWKCILVQPLWRTVWRYL/ RKLKIELPYNPAIPLVGIYPKERKSV Y*R*ICSMFTVALLAIAKIWKQSKCP SADEWINKIWIYAYTTEYYSAIK |
| 186 | 5683 | A | 190 | 158 | 366 | FIISMNFVFLYFVFDLSINEILLGLKE WSIYLSS/DHSLSSLCSFYLLLLMFFL CMLLLLLLCSSIIIS*P |
| 187 | 5684 | A | 191 | 10 | 284 | |
| 188 | 5685 | A | 192 | 3 | 438 | LFISLLSISEKIIENCWV*LSAARS*A LRKLAF*ATRSFF*ARDILGRFHLF F/CNFFLGLLFIDWILSYSSMSFLIHL LHPAGQQASTICCSIIQANLHTIF WQFVCIRCADYHIPLYTGISNLNDI SVCHTNYHPVIGVW |
| 189 | 5686 | A | 193 | 497 | 752 | DGVLLLLPRLECNSAILAHRNLRPL/ GFKRFSCLTLLSPWDYRHLPPRLAIF FVFLVYVGFHHVGYAGLELLTSR* SARPRPPKIA |
| 190 | 5687 | B | 194 | 922 | 2057 | YPNRFPLVMDSEKQRNFNAESTIGS HIHGPRIVAGLHAPTLMEDEDEDALQ ETVRASIRKEQRNSRHDGGDGIRKA HAAIPRESRSMKRSPRKEVKKRW NRPKMSLAQKKDRVAQKKASFLRA QERAAES* |
| 191 | 5688 | A | 195 | 1492 | 1790 | SQTLGGRGGQITKSGDREHPG*HSE TPSLLKIQKLAGHNGCLWSQLIRR LRQENDMNPGGRCSEPRSCHCTP AWVTEQDSISKKKKQKQKEGLGGS A |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 192 | 5689 | A | 196 | 178 | 572 | QAGSCTRTSQPRDSRGSDIQPVGLA FGRTPAELQELHLSSPRPGRGAVWA CGSLEPGPLPLLSITSGSQPSLQLSSL PQSPLFCPLPPF/PPPRPPPRVGLVPPP *LTHVPGLQPTGRPPSPSRSPAPPP Q |
| 193 | 5690 | A | 197 | 209 | 684 | PWDCVHACLRGGWHSANRGHFRI GGPGRPKAPFLPFPASLKVQALIPYP GVHPGRPLHPCVPRRMQRLCGTRD PEKLASCDIVVDVGGEYDPSRHRY DHHQRSFTETMSSL/DPLGSRGKTK LSSAGLIYLHFGAQ/VLAQLLGTSEE DSMVGTLYDKMY |
| 194 | 5691 | A | 198 | 2 | 720 | IPGCMIRHELLPPCRELLMGHRFLR GLLTLLPPPLYTRHRMLGPESVPP PKRSRSLMAPPRIGTHNGTFHCDE ALACALLRLLPEYRDAEIVRTRDPE KLR\SCDIVNVVGGEYDPSRHRYD HPQRSFTETMSSLSPGKPWQTKLSS AGLIYLHFGHKL\VAQLLGTSEEDS MVGTLYDKMYENFVEEVDAVDN GISQWAEGEPRYALTTTLSARDARL NPTWNHPDQDTEAGFKRA |
| 195 | 5692 | A | 199 | 209 | 684 | PWDCVHACLRGGWHSANRGHFRI GGPGRPKAPFLPFPASLKVQALIPYP GVHPGRPLHPCVPRRMQRLCGTRD PEKLASCDIVVDVGGEYDPSRHRY DHHQRSFTETMSSL/DPLGSRGKTK LSSAGLIYLHFGAQ/VLAQLLGTSEE DSMVGTLYDKMY |
| 196 | 5693 | A | 200 | 2 | 720 | IPGCMIRHELLPPCRELLMGHRFLR GLLTLLPPPLYTRHRMLGPESVPP PKRSRSLMAPPRIGTHNGTFHCDE ALACALLRLLPEYRDAEIVRTRDPE KLR\SCDIVNVVGGEYDPSRHRYD HPQRSFTETMSSLSPGKPWQTKLSS AGLIYLHFGHKL\VAQLLGTSEEDS MVGTLYDKMYENFVEEVDAVDN GISQWAEGEPRYALTTTLSARDARL NPTWNHPDQDTEAGFKRA |
| 197 | 5694 | A | 201 | 94 | 660 | LHLKNSDGYCLIVYQKRFIPVTFIHF CFLILSLKFNNIPLNIFANGEKYFVY KFTYSYVVKFLTCAFVELPVNCLFI SFSHFFLMSFVIFL**ILGMLYVLVL LIFNFTYICIVIAFY*LFVVIQTFLHFY LLKFINLFL*SFSGFCVLLRRVIPRI YICFIRILYNTSITLFTYLEE*FSFDM |
| 198 | 5695 | A | 202 | 3 | 347 | FFEMEF/SLLLPRLECNGVILVHCNL RLPGSNDSPASAS*VAEIIGVCTASS *IFVFGTLTQ*KSRLVDQAGLELLA PASSDPILTSQSAGITGVTTDIQPPF FLSSFANTEWT |
| 199 | 5696 | A | 203 | 32 | 403 | APIPDAMGHFTEEDKATITSLWGKV NVEDAGGETLGKLLVVPWTQRFF DRFGNLSSASAIMGRR*VKAPG*NV VLTSLGDALMHLDDLKAPLANLRER T/CDQGCWVNPENF*LLGNVLVTVL AI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 200 | 5697 | A | 204 | 94 | 361 | FCQLDSLYTESQSLDSTVL*LAEHM KFIKTSY*GALDTFTKHLQMSVDA YE**MISILNPSSLSERQSLLLFIVLD LSLVPYLLIFE |
| 201 | 5698 | C | 205 | 265 | 408 | MTLSCSNLVFFFLFKITVFIMTMVTP QCKGGPDSVCFSTLFVNKCPV* |
| 202 | 5699 | A | 206 | 10 | 419 | MRGGHSWARKGGMRGLIRNERES GGGEQTD*ASKLKRGNSNRITPFAY MDTY\ASSSSSSSSSSSSSSSSSSSSASKLE AELGQTGLLPIPLGGGGGAFSTKTV RSGESEGGLWKQRKRWLEGRRCGR VSGWECGGAEAMK |
| 203 | 5700 | C | 207 | 165 | 248 | MDTYXXXXXXXXXXXXXXXXXXXXX FQARS* |
| 204 | 5701 | C | 208 | 337 | 428 | MILRVDDFVPLALLPQSFPHRSHYD PNPAA* |
| 205 | 5702 | A | 209 | 531 | 1860 | PSKPPNQCFLSLSQATSAGTHLSQD TESLTQVAKGIS*GSQGHGGGTLM RGGHSWARKGG/H*EGSSGMRGRA VEGNKQTRLLN*NGEIQTEPLLHT WTLTVQMRKVTPREGELSCPRASK LEAELGQTGLLPIPLGGGGGALSTK TVRSG\GVRGVFGSRENDGLWKVD VEGSVAGSRAGA*AMKGEPKQIPK LTL*S*P*ENPNGNAVVSFS*ARGKL*/ SFTKTLAGPAGAPAPAPPP\GPRWPP PA/DCGHTRPPLPSESLEAELKAGDS PSLALDSLSP*PPPTPPAGPRRSQGPP GAPAGALGSRCPRQVVKQTTLGS* RGRAGAGNTRRRGSGPHAAPIGSV DLRSGAPATAGPCGRAASVGAGPR RGRGGRGLPAPPWGT*GAPKGPRR RGPAGWSQTGSARPCGPWASRGGP KPRPCVHGGRRPGDAPGVVTAPRC GR |
| 206 | 5703 | A | 210 | 32 | 452 | |
| 207 | 5704 | A | 211 | 38 | 618 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSS\PSAIMGNPKVKAHGK KVLTSLGDAIKHLG*SQRAPFAQA* SELALVTKLHVDPGGTFKLLGEML LVTRFWAIPFSAKEFHPWRLQA\SW QKQKMAEDGDLELASALVPSRLPL SSLAHECRAFQGYGFILASNYK |
| 208 | 5705 | A | 212 | 137 | 368 | DGVYLWTHRPYCGLGSLNFGSVIIV LP*VKAYGWMVLTSLGDAIQPLAD PECSF\GQLRELRCMDLHVDPEDFR LLGK |
| 209 | 5706 | A | 213 | 60 | 317 | FPCLVCCTLQENSGKPILCPRRTTAQ LGPRRNPAWSLQAGRLFSTQTAED KEEHLHSIISSS*SVQDYTSKHKFQA STYKH*SIA |
| 210 | 5707 | A | 214 | 3 | 406 | HEDKLCTVATLRETYGEMADCCAK HEPERNECFLOHTDYNANLSRLMR PEEDVMCTAFHDNEETFLKKYLYDI ARRHPYFYDPELLIFANRHKAFTD CSQAGD*AAWLVPKLDDYLYEL*A |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TSCIIISKCANL |
| 211 | 5708 | A | 215 | 1 | 2953 | MKWVTFISLLFLFSSAYSRGVFRRT PLGPASSLPQSFLKCLEQVRKIQGD GAALQEKLCAATYKLCHPEELVLLG HSLGIPWAPLSSCPSQALQLAGCLS QLHSGFLYQGLLQALEGISPELGPT LDTLQLDVADFATTIWQQMEELGM APALQPTQGAMPAFASAFQRRAGG VLVASHLQSFLEVSYRVLRLAQP GGGDAHKSEVAHRFKDLGVEEDFT ALVLIAFAQYLQQ*PFEDHVKLANE ATEFAKTCVADESA\ENCCKSLHTL FGDKLCTVATLARETYG\EMADC\C AKQGT*GEMECFFATQRMNDPNLP PIGWRTRGWMWMLHCFHFDNEGD IF*KKYLLWKLPGRTSFTFYGPPELL FLWLKR/RIKAGFLQEC\CQGWLD*S WPACLAAGSDELSGMKGKAS\SAK QRLKASLQKIWEKELSKPWAVAR LSQRFPAEFAEVSKLVTDLTKEVHT ECCHG\DLLECADDRA\DLA\KYICE\N NQDSISSKLKECCAEKPLE*FHCLA EVENDEMPADLPSLAADFVENKD VCKNYAEAKDVFLGMFLYEYARR HPDYSVVLLRLAKTYETTLEKCCA AADPHECYAKVFDEFKPLVEEPQN LIKQNCLEFEQLGEYKFQNALLVRY TKKVPQVSTPTLVEVSRNLGKVG KCKKHPEAKRMPCAEDYLSVVLNQ LCVLHEKTPVSDRVTCKCTESLVNR RPCFSALEVDETYVPKEFNAETFTF HADICTLSEKERQIKKQTALVELVK HKPKATKEQLKAVMDDFAAFVEK CCKADDKETCFAEEGKKLVAASQA ALGLTPLGPASSLPQSFLKCLEQV RKIQGDGAALQEKLCAATYKLCHPE ELVLLGHSLGIPWAPLSSCPSQALQ LAGCLS QLHSGFLYQGLLQALEGI SPELGPTLDTLQLDVADFATTIWQQ MEELGMAPALQPTQGAMPAFASAF QRRAGGVVLVASHLQSFLEVSYRVL RLAQP |
| 212 | 5709 | A | 216 | 1060 | 1259 | TKFGQHKGKTPSLLKI*KLAGHGGAH LKSQLPGRHENHLNPGGGGCSEPR LCHCTPAWVTKRDCLKK |
| 213 | 5710 | A | 217 | 2 | 354 | SAAAGQGEENQLEASLDALLSQVA DLKNSL/EEFHLQVGERVWPADLLN TLNKVLKHEKTPFRNQVIPLVLS DRDEDLMRQTEGRVPVFSHEVVPD HLRTKPDPEVEEQEKQLTTV |
| 214 | 5711 | A | 218 | 90 | 329 | |
| 215 | 5712 | A | 219 | 2 | 632 | QPSFLCVILVYLGDQVPPIGAEKRRS TLEASLDALLSQVA*SEELSGEFHL QVGDEYGRLTWPSVLDSICLAFLD SMNTLNKVLKHEKTPAVP*PGHHSS GCCLQDRR*KISCRQT*KDGCLFSA H*GKSLDHLEKPSLDP*KLEEQEKQ LTTDCSPAFGADAAQKQIQSFE*NV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FQTF LGENQQRGSEDSWRFSGR SRLLTPTDT |
| 216 | 5713 | C | 220 | 309 | 479 | MIHYSSSY SFKSSRELHIKFKFPVST SCGAFGSKIKWKVLSEVVEETQESE QPEVL* |
| 217 | 5714 | A | 221 | 76 | 525 | PQPLGPQPQQRPSRLASCCGAAAPC SWVEGAIGHAPPHGLPIMSNGYRTL SQHLNDLK KENFSLKLRIYFLEERM QQKYEASR\EDIYKRNTTELKVEVES LKRELQDKKQHLDKTWADVENLN SQNEAELRPQFEERQQETEHVYELL EK |
| 218 | 5715 | A | 222 | 534 | 1310 | PRNEFTQQFCFIDSFFLVTLKIEALQ CSHRSRSGEKVPFVQTYSLRAFEK PPQVQTQALRDFEKHLNDLAKKENF SLNVRIYFLEERMQQKYEASREDIY KRNTTELKVEVESLKRELQDKKQPS GLKPWADVENLQPVQNEAELRRQ FEEPAQQETEHVYELLENKMQLLA RRNSRLATE*TMRGWQLLVERQRK GV*TWKLSGET*RESPKNWGRCPR EPQVKPDPLHLRPLAQKGKDLKKI MLGSPNHIKNASDQ |
| 219 | 5716 | A | 223 | 32 | 360 | TGSKIRNIKG I HIGREEMKLILFTNYI LVCRE/NPKIMFKLLALISRY*ATVA GCNIYIPPTPKLNFDIVG*ILLAKKLF TNANNIRYLGINLIINDGHHSKEI YIISL |
| 220 | 5717 | A | 224 | 2 | 761 | APTPTGQRVVRATPAQSAPVRLRRR SYDVNNPIPSNLKSEAKKAAKILRE FT\ETSRNGPDKNPGSTVIAKAKIG LANSCLLNQSPGSLVTFORGGPGVL VARL\PDGK\WSSPFS\ALGIAGFGG GFEIGI*GIQTLVIILEF/DDPCC*EAF AKGGNLTG GNLTVAVGPLGRNLE GNV\ALRSSAAVFTYCKSRGLFAGV SLEGSLIERKETNRKSVQVKVILIE SVMRK*YFKS*YNLQSTFIYSFYNM WF |
| 221 | 5718 | A | 225 | 299 | 541 | SQHFGRLTQADHLKS*VQDRPGQH GEIPSLQKIQKLAGHGGASL*SQLLG RLRQENHLNPGGGGCSEPARTPGWA TE*DSV |
| 222 | 5719 | A | 226 | 198 | 660 | LLLALLFNTVLRFTVCLFLFQAPILK SPCCSAARVDRRKSIWVDGL*ICSR LSK*VIC*LGTFKFVVQILQHTLSN *L/HLNIEKN*GLTG*VSILCKCLFYH SL*PLL*VKCSLRPGVVTHTCNLSTL GGRGGRIT*VQEFETSLGNIVRHRI |
| 223 | 5720 | A | 227 | 1 | 347 | GERLAGRRRKMAVESRVTREEIGN DS*KPIDREKTCPLSLRAFTTNNGR HHRMDDFSRGNVPYSELQTYTWM DATLKDLTSLAQELYPQATLNGTH FTFAVALTHATPPGSRVND |
| 224 | 5721 | A | 228 | 3 | 225 | SCQGERLAGRWRKMAVESRVVTQE EIKKEPEKPIDREKTCPLLRVFTTN NGRHHRMDEF SRGRWSKAPGKQK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GP |
| 225 | 5722 | A | 229 | 1984 | 2676 | |
| 226 | 5723 | A | 230 | 2 | 590 | GCRNSARGKMAVESRVTQEENKKE PEKPIDREKTCPLLLRVFTTNNGR\H HHRNGRVSPRGVNPSTELQIFPLGW MPTLKELTSLVKEVYPEARKKGTH FNFAIVFNRCLKVPGYR*FSFLQS* GGLASTHVWAERGLDDSHPELQSR K\QIGDYLDIA\TPPNR\APPPSGR MRPYLNSNFTYLFIFYFFPSVM |
| 227 | 5724 | A | 231 | 1 | 291 | |
| 228 | 5725 | A | 232 | 3 | 320 | AKNRLQILKFCLHFKERKTVLPSKH AVPEVIEDFLCNFLIKMGMTRTLDC L/QASEWYELIQKGVTELRTVGNVP DVYTQIMLLENENKNLKKDLKHYK QAAEYVIF |
| 229 | 5726 | A | 233 | 209 | 461 | |
| 230 | 5727 | A | 234 | 104 | 609 | RQPGTRGTRRTRWRLEGAYYLEQV TITEASEDDYEYEEVTC*F*IPDDNF SIPEGEEDLAKAIQMAQEQTDEIL ERKTVLPSKHA VP*VIEDFL/RCNFL DQNGELTRTLDCFQSEWYELIQKG VTELITVGNVPDVYTQIMLLENENK NL*KDLKHYKQAAEYVIF |
| 231 | 5728 | A | 235 | 222 | 502 | TSLIKHYISNLFTFINSVEYKQ*WFL LWLCVSLKC*LGQAWWAQACNLS TL*GPRWAADHLRSEVRDRTG\QH GETPSL/LKNTKISWAW*WVPV |
| 232 | 5729 | A | 236 | 565 | 779 | APGVRD*PGQHGENLSLQK*KLKK LAGHGGIHLCFQLRRPRQKYRLSP EGQDCSE/PMVCTLA WATEQDPVS |
| 233 | 5730 | A | 238 | 656 | 923 | VPVHRGKERGGIQDLDEIATPTLLS KSSSFFKTSYCTDFFLFLTESCCVTR LECSGMISAHCSLCLPGSSNSAPTSP VSHNKDRLLHL |
| 234 | 5731 | A | 240 | 171 | 373 | AWLCANKTLFLNFYLFETRSC/SLS RLECNAIIAHCSLLLPGPSDSPTSA SQVAGTTRTCHDTQPI |
| 235 | 5732 | A | 241 | 915 | 1283 | QRQGRGLWDNEEGEIGTKYSSFKI DTVEKLFLGGGRSRVKPRGSNKAR DPPSPSPAWEVGPQLGVPLKSPCG LHLGLAAVPLYDPRGGGPHTPPHTP P/PTPHPPHPPHPPHTKHTPTNTQ |
| 236 | 5733 | A | 242 | 555 | 767 | NKKDLFSLRSGDQKSKVKTSEGPRL /PLRGIRENP/CPVPAPGGPRHCLAC GGITPVSAIITRISCPLYSN |
| 237 | 5734 | A | 243 | 2 | 744 | GTMAVFVVLLALVAGVLGNEFTIL KSPGSVVFRNGNWPPIGERIPNVAA LSMGFSVKEDLSWPGLAVGNLFHR PRATVMVMVKGVNKLALPPGSVIS YPLENAVPFILDSVANSIHSLSFSEETP VVLQLAPTEERVYMRKANSLFEY LSITFLQLHNRLFQKNSVLTSLPLTS LNNNELHLLFF/S*LQPLH*ISNFLS CDKHFTQKMIVLINNHSNLPMLPTK FGNPFLTQSFPSPNLSLKPFSA |
| 238 | 5735 | B | 244 | 385 | 544 | MTGSPEDDETGYPLRSPGQERSST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | EKPMDNAATSGIRSPGIGQFPFRKTTDPX* |
| 239 | 5736 | A | 245 | 1 | 449 | GNEFSILKSPGSSVFRNGNWPPIGER IPDVAALSMGFSVKEDLSWPLAV GNLFHRPRATVMVMVKGVNKLAL PPG\SVISYPLAENVDLLFLSELQVLH DISSLLSRHK\HLAKGSILPDLYSLAE RAGFGMEIGKRYGEDSEQFRDASKI |
| 240 | 5737 | A | 246 | 2 | 1230 | GAGRVRARHLLTLRLSPCPAGPFRV APQCCGRRGTMAVFVLLALVAG VLGNEFSILKSPGSSVFRNGNWPPI RE\RDPPDVAAL/SPMGFSVKEDLSW PG\LA VGNLFHRPRATVMGDG*RG VNKTWLYPQGSV\SYPLENAV PFS LDQCLQIP\HFLIFLEETSCLFLQLGF PVRE\RVVLWL GKANFSV*RTFSVT LRQLR/NIRLVFKENSVSSVSLPLNS LSRNNEVDLLFLSELQVLHDISSLL SRHKHLAK\DHSPDLYFTGSWAGLA DEIG\KALLGEDSEQFRDASKILVD\ ALQKFADDMYSLYGGNAVVELV TVQSF\DTSL\IREGQGTYSLEGKTS GTPASPYNLAYKYNFEYSVVFNMV LWIMIALALAVIITSYNIWNMDPG YDSIIYRMTNQKIRMD |
| 241 | 5738 | A | 247 | 1547 | 1965 | AQGRFQALCSLVAVRAWGWPLSG NSFSCGNSQC\TKVNRSVTTRRTAP MGPTRRMRVWLAASWRMAGRIVG GMEASPGSFRGKPAFERTRSTSVGR HHQRQPLRS*NHRFQDPTKWVAYV VRPTSAARRPAPCGPSKKA |
| 242 | 5739 | A | 248 | 403 | 734 | MAVQAGTQCLVQQLHSGFLQHLW LDHCRPRKMLTEVLLEVAPA*DQA LLAGWEDVCGSREAHGLD\GRPKG RGLVSSSTATSKSAVSALYRGCLTI WTTWARTVLA\SEPLR |
| 243 | 5740 | A | 249 | 1 | 552 | MVWSSQRCCRKHCGAAGPGTV CQ LVRPLLTD RMVCAGYLDGKVDPAR PQKNTDTSVSNAGRFTDIWMPVLE EFKAVGIERQNVGPGLNGEAHPGR GRVRSCLREVPWQVSLKEGSRHFC EQLWWGTAGCCLPPTASPVSGIKA L/YESELADARRVLDETARERARLQ IEIGKLRAELDEVNKR |
| 244 | 5741 | A | 250 | 63 | 497 | LPDVEKLGRRRGRKMDSVEKGAAR LR\PNPRGRPSRGRPPKLQRNSRGG QGRGVEKPPHLAALILARGGSK\GIP LKNIKHLAGVPLIGWVLRALDSG AFQRCACARVGGAAWAGVGRGSR AAGGAGASGATALGRGPSLMPGM C |
| 245 | 5742 | A | 251 | 1 | 349 | GTRAVVCGRRLISVREQIRHFVMP EINTNHLDKQQVQLLAEMCILIDEL DN\QAYCETKKNCHLNENIEKGAAL KQTL\LLSDLCRHFRFAEKSTLFKEV QTSVIPYFLVGSSSFK |
| 246 | 5743 | A | 252 | 2 | 423 | LRWSL/DSVAQAGVQWGDLSLQA PPPGFTPFSCLRLPSSWDYRCQPPRT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *≡Stop codon; ≡possible nucleotide deletion; ≡possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | *RRGFIVLARMVSIS*PCDPPASASQ SAGIIGM/SHRARPGFPT/CQTTQEPG GTTSHGYRIPPP*QDLC*LPQFPERG SGSQRC*DKPGSPSL |
| 247 | 5744 | A | 253 | 891 | 1564 | SPRALAANPWWMVTSVSSRVKQSC TQQGGFVPLAQVHSPUISELYALV SLFFYFLFDICRARILSGSFCILRTLL LLLFLRRSLNSVTQAGVQWRDLGS LQAPPPGFTFSLSLPSSWDYRRLP PRPANFVFLVETGFHRDETRIVSI SIGPRDPPASASQSAGITGVNHRAW PTFCIFCRDRVSSCWPGWSRSHTPG LKRSSCLSLPKFWDYRHKLPYP |
| 248 | 5745 | A | 254 | 6 | 338 | MEPSCGLGSEALALTQTWAGSHSL KYFHTSVSRPGRGEPRFIYVGYVDD TQLVRLDND/APSPKMVPRAPWIEH EGSKIWDRETHIAKDTRQIFRVNLR TLRSYYDQIEAGD |
| 249 | 5746 | A | 255 | 2 | 424 | |
| 250 | 5747 | A | 256 | 25 | 486 | EFHRLRENPPWCLSPADKTNVKA WGKVGAAHVRSMCAEALERMFLS FPTTKTYFPHFDLSHGSAQV*GATG KKVADALTNAVAHVDDMPNALS ALSDLHAHKLARVDPVQLSSS*SHC LLG*PWPAHLPRPSFTPGGCTPSLG QVSWAFC |
| 251 | 5748 | A | 257 | 230 | 358 | FLIILRRSLILSPRLECNGSVPAHCSL/ RTPGFKRFSCLSLSSS |
| 252 | 5749 | A | 258 | 75 | 188 | |
| 253 | 5750 | A | 259 | 340 | 535 | FRFKALFDLFLVEIASCCVAQAGV QWCDLSSVQPPPGSSDSPTSASQI AGTTGALQHAWLIF |
| 254 | 5751 | A | 260 | 1618 | 1962 | DRVSLSPRLECSGTILAHCKLR/LP GFTLFSCLSLPSSWDYRRLPPRPAN FFVFLVEMGFHRVSQ/AMGLDLLT SGDPPASGLSKCWGLQGVSNLRPS QASPSFKGIKGPQTLRA |
| 255 | 5752 | A | 261 | 3 | 395 | |
| 256 | 5753 | A | 262 | 152 | 514 | LATLLGPWSCARVPSVPALLTPPPL AGPPPPQPLLQRLCSGPRLLLLSLGL SLLLLVDCVIGSQNSQLQEELRGL RETFSNFVASTEGPGSRALSTQGRA MWGRKMEVRLEFPVWRKQQ |
| 257 | 5754 | A | 263 | 138 | 1072 | |
| 258 | 5755 | A | 264 | 1 | 488 | |
| 259 | 5756 | A | 265 | 1 | 2105 | FRAASCAPPSWRMELRSGSVGSQA VARRMDGDSRDGGGGKDATGSED YENLPTSASVSTHMTAGAMAGILE HSVMPVDSVKTRMQSLSPSSQSPV PSIYGALKKIMRTEGFWRPLRGVN VMIMGAGPAHAMYFACYENMKRT LNDVFHHQGNSHLANGIAGSMATL LHDAVMNPAEVVKQRLQMYNSQH RSAISCIRTVWRTEGLGAFYRSYTT QLTMNIPFQSIHFITYEFLQEYNPH RTYNPHSHIISGGLAGALAAAATTP LDVCKTLLNTQENVALSLANISGRL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VVPMGPLLPNALERGGDGTAHRK AVCGDIREVWELDRLLPCDIRDGAF ITMPFHICYAQNREGELLRPAELAD GAAPRELGPQGGGPEDGWGQPRW RRRQGPPEGREDYENLPTSASVSTH MTAGAMAGILEHSVMYPVDSVKPR ARPRLLAALRRGRRSGEHRWLRRR LGSRGTRSLKLCTVLPRWPFLAGA AHTCAVSEGVPRRGSPHHAGAEKR VALARPRALGTWCVAAAPRVISGT WGRQVFSRLVAALYRFDSPWDPL SEGSCTSSPDFGSPSRREAMTFAFSF CLRGGRHMPSLREHYWARMSHER HKDWANVGGTITVLSEPNFLINNTR LARNRTPWARHDNWCHHWQHVSP ESSLDCVRLQGLPWMAAAEVEMK LPAGHMHMPVSFPNRSPLGAGCIN |
| 260 | 5757 | A | 266 | 882 | 1299 | |
| 261 | 5758 | A | 267 | 1 | 2607 | MAFAWWPCLILALLSSLAASGFPRS PFRL LGVANGIEVYSTKINSKVTSRF AHNVVTMRAVNRADTAKEVSFDV ELPKTAFITNFTLTIDGVTYPGNVKE KEVAKKQYEKA VSQKTAGLVKA SGRKLEKFTVSVNVAAGSKVTFELT YEELLKRHKGYEMYLKVQPKQL VKHFEIEVDIFEPQGISM L DAEASFIT NDLLGSALT KSFSGKKGHVSFKPSL DQQRSCPTCTDSLLNGDFTTTYDVN RESPGNVQIVNGYFVHFFAPQGLPV VPKNVAFVIDISGSMAGRKLEQTKE ALLRILED MQEEDYLN FILSGDVST WKEHLVQATPENLQEARTFVK SME DKGMTNINDG LLRGISMLNKAREE HRIPERSTSIVIMLTDGDANVGESRP EKIQENVRNAIGGKFPLYNLGFGNN LNYNFLENMALENHGFARRIYEDS DADLQLQGFYEEVANPLLTGVEME YPENAILDLTQNTYQHFDYGSEIVV AGRLVDEDMNSFKADVKGHGATN DLTFTEEVD MKEMEKALQERDYIF GNYIERLWAYLTIEQLLEKRKNAH GEEKENLTARALDSLKYHFVTPLT SMVVTKPEDNEDERAIADKPGEAS YQPPQN PYYYVDGDPHFIIQIPEKD DALCFNIDEAPGTVLRLIQDAVTGL TVNGQITGDKRGSPDSKTRKTYFGK LGIANAQMDFQVEVTTEKITCGTG\ RA\STFSWLDTVTVTQDGLSMMINR KNMVVSFGDGVTFVVVLHQVWKK HPVHRDFLG FYVVD SHRMSAQTHG LLGQFFQPFDFKVSDIRPGSDPTKPD ATLVVKNHQLIVTRGSQKDYRKDA SIGTKVVCWFVHNNGEGLIDGVHT DYIVPNLF |
| 262 | 5759 | A | 268 | 1 | 1842 | |
| 263 | 5760 | A | 269 | 3 | 377 | |
| 264 | 5761 | A | 270 | 1 | 621 | MTKRCLDHRGEWLPAGGGGGHTE GTRCLHHAPVTWVGIEVDIFEPQGI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SMLDAEASFITNDLLGSALTKSFSG KKPVWLRGRHTPKGNLDSEVLAGL SPCPIPLAGLTVNGQITGDKRGSPDS KTRKTYFGKLGIANAQMDFQVEVT TEKITLGTG\RA\STFSWLDTVTVTQ DG*APLQGLQGGLQGEGDHSGPQP NPGALSEPELV |
| 265 | 5762 | A | 271 | 3 | 2722 | FSDGLCMVALSHLGSALQLGSLCFP RSPFRLLGKRSLEPGVANGIEVYST KINSKVTSRFAHNVVTMRAVNRAD TAKEVSFDVELPKTAFITNFTLTIDG VTYPGNVKEKEVAKKQYEKAVSQ GKTAGLVKASGRKLEKFTVSVNVA AGSKVTFELTYEELLKRHKGYEM YLKVQPKQLVKHFEIEVDIFEPQGIS MLDAEASFITNDLLGSALTKSFSGK KGHVSKPSLDQQRSCPTCTDSLNL GDFITITYDVNRESPGNVQIVNGYFV HFFAPQGLPVVPKNVAFVIDISGSM AGRKLEQTKEALLRIEDMKEEDY LNFILFSGDVSTWKEHLVQATPENL QEARTFVKSMEDKGMTNINDGLLR GISMLNKAREEHRIPERSTSIVIMLT DGDANVGESRPEKIQENVRNAIGG KFPLYNLGFGNNLNYNFLENMALE NHGFARRIYEDSDADLQLQGFYEE VANPLLTGVEMEYPENAILDLTQNT YQHFYDYGSEIVVAGRLVDEDMNSF KADVKGHGATNDLTFTEEVDMEKE MEKALQERDYIFGNYIERLWAYLTI EQLEKRKNAHGEEKENLTARALD LSLKYHFVTPLTSMVVTKPEDNEDE RAIADKPGEDAEATPVSPAMSYLTS YQPPQNPYYYVDGDPH/FSIIQIPEK DDALCFNIDEAPGTVLRLIQDAVTG LTVNGQITGDKRGSPDSKTRKTYF GKTGASPMAMGFPGWVETTEKIT LLEQARCRAFFSWLDTVTVTQDGH FLASSRRLSMMINRKNMVVSFGDG VTFVVVLHQ/VCWKKHPVPTVDFL GFYVVDSHRMSAQTHGLLGQFFQP FDFKVS DIRPGSDPTKPDATLVVKN HQLIVTRGSQKDYRKDASIGTKVVC WVFNHNGEGLIDGVHTDYIVPNLF |
| 266 | 5763 | A | 272 | 1168 | 1626 | RAGRGGEGHKLNSYGGRRARSQG HLLSSALSPFVSAASYQPPQNPYYY VDGDPHFIIQIPEKDDALCFNIDEAP GTGLRLIQDAVTGLTVNGQITGDK RGSPDSKTRKTYFGKLGIANAQMD FQVEVTTEKITCGTG\RA\STFSWLD TVTVT |
| 267 | 5764 | A | 273 | 534 | 690 | FVIFSPCSIAMATKENMTSQRGML KSIHMKMNTL\ANRFPA\VNSLIQRV NL |
| 268 | 5765 | A | 274 | 3 | 946 | TTKMAAGTSSYWEGEARRPPDLRK QARQLENELDKLVFSKLCTSYSH SSTRDGRDRYSSDTTPLLNGSSQD RMFETMAIEIEQLLARLTGVNDKM |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AEYTNAGVPSLNAALMHTLQRH RDILQDYTHEFHKTKANFMAIRERE NLMGSVRKDIESYKSGSGVNNRRT ELFLKEHDHLRNSDRLEETISIAMP TKENMTS\QRGMLKSIHSMNTLA\ NRFPAVNSLIQRINLRKRRDSLILGG VIGICTILLLLYAFHLMGHLQGLLTA TAFTPWSGIRKHRREKLTVLIISLTS RMNARLTVMDSVTWSG |
| 269 | 5766 | A | 275 | 269 | 476 | VMAVLPSGTALKTNWEPGRDLQC NGSSLLLSGAPHIVSLLGFRIRAKTG RARC\HACNPNTLGGRGGRI |
| 270 | 5767 | A | 276 | 2 | 424 | |
| 271 | 5768 | A | 277 | 3 | 452 | |
| 272 | 5769 | A | 278 | 3 | 498 | PTLLVPTDSERTHHGSCFLPDKTNV KAAWGVGAHAGEYGAEALERM FLSFPTTKTYFPHFDL\SHG\SAQV\K GHG\KKVADALTNAVAHVDDMPN \ALSALSDLHAHKL\R\DPFNFKLPS H\CLLVTL\AAHLPAEFHPLRWHALP GTSFLGFLSTVADLPNTR |
| 273 | 5770 | A | 279 | 333 | 538 | IFSSLWLFFILSIKDFILFYFLFLAQRS SVTRLECSGTISAHCNLCNPNSSDF RVLRLGNRLRLKIKK |
| 274 | 5771 | A | 280 | 192 | 607 | GRLWGCVSKKSVGCLPHPGCLWA AFLTLDACGLPSSPWMPVGSPLPHG CLWAAFLTLDACGLPSSPWMPVTW FPWGLPKLRDPKPPSNLMTRPVSEP PVLSPSPSPTPSATRPTHFPSLKGPA HRPAHVFPFNPCFVP |
| 275 | 5772 | A | 281 | 17 | 363 | GLESEFLLRGLLRPGEQDSALASAV PGSLAQTLPPWS/PLW/TMSFPAHA APHPACCHCLSY/PVSCPVSVPSSLP LGCPLQLLPSCPNPCYPSPAVPTYCP AGKEEKRRSPSCQACS |
| 276 | 5773 | A | 285 | 96 | 389 | QGPAAENMAAKMFEFIGKFGALV DAGGVVNSALYSVDAGHRAVVFD RFRGVQDIVVGKGTWLPWLQKS/ IIFDCRSQPRNVLVFTGSKDLQIGNL H |
| 277 | 5774 | A | 286 | 1 | 390 | FFYFFFLERDFLFLFYFIFFAVLLLLP NLECNGAISAHRLRLPGSSDSPAS ASQVAGITGMQHHAWLSFVFLVKT GFVHLGHAGLKLPTSDDPPTAASDI VGITGMIPPVAGPKQRHFCARSVLV PFI |
| 278 | 5775 | A | 287 | 16 | 546 | QLNGRSIRHEVMSHRKFSAPRHGSL GFLPRKRSSRHRGKVKSFPKDDPSK PVHLTAFLGYKAGMTHIVREVDRP GSKVNKKEVVEAVTIVETPPMVVV GIVGYVETPRGLRTFKTVFAEHISDE /CRLPLRQKKAHLMEIHVNGGTVA EKLDWARERLEQQVPVNPVFGQDE MIDVI |
| 279 | 5776 | A | 288 | 1 | 625 | CKFIRVMAHTRLRLPLRRKKAHL MEIQVNEGTVAEKLDWARERLEQQ VPVNQVFGQDEMIDVIGVTKGKGY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KGVTSRWHTKKLPRKTHRGLRKVA CKDGLIKNNASTDYDLSDKSINPL GGFVHYGEVTNDFVMLKGCVVGT KKRVLTLRKSLLVQTKRRALEKIDL KFIDTTSKFGHGRFQTMEEKKAFM GPLKKDRIAKEEGA |
| 280 | 5777 | A | 289 | 1 | 903 | |
| 281 | 5778 | A | 290 | 38 | 482 | |
| 282 | 5779 | A | 291 | 1 | 1131 | |
| 283 | 5780 | A | 292 | 1 | 1329 | STHASDGVMShrkfsAPRHG\SLGF LPRKRTSRHRGKVKSFPKDDPSK\p VHLTAF\LGKAG\MTHIVREVDR\p GIHRCNKKERWWRA\THCMRPPP MVVGGHLVG\YVET\PRGPPGPFKT CLLLEH\NDELPRGVFYKEFGH*NL KKKAFTK\YCKEIGKDED\GKKPAW KKDFQQH*KKLLAQVHPCSIAQTQ\ MRLPL\ROKKAHLME\QV\NGGT VA\EKL\DWAREKLE\QQ\VPVNPSV LGRMRMID\VIGGDQRAKGYKGGS PS\RWHTKKAAPAKTHRG\LRKVG LVLGAWHP\ARVAFSVG\RAAGQK GYPSTALEINKKIYKIGPGVTLsRA GSLIKEQCLHLNYDLSDKSINPLGGF VHYGEVTNDFVMLKGCVVGTKKR VTLRKSLLVQTKRRALEKIDLKFI DTTSKFGHGRFQTMEEKKAFMGPL KKDRIAKEEGA |
| 284 | 5781 | A | 293 | 238 | 326 | HTYKSDTRYERHACWGALL/CNYM RQECLDSRFVDRPMPVFRLVSVIG TSILYMKAFMHMPFK |
| 285 | 5782 | A | 294 | 2 | 358 | GWGMSLGGAGVEGMEVGTSDLGF FSGQRALSPWVSPVPPGLCAWRKD SPVEQKPQGPSLPLSALPYLWG/AP WPPAGPQTRGLGPFRGTGSPPSIPIS RAQKDSWPWPVPSTPACFSAPG |
| 286 | 5783 | C | 295 | 56 | 175 | MASXNRQQFFXNTPXKLLKSPHCNI YRLLSAKSQGKFWK* |
| 287 | 5784 | A | 296 | 1178 | 1515 | KKFMKILEHMFEGFFSFLNFFIFSG GRRSALTARGGSEVAANLGLTCNL HPPGFKRFSCRLRSSWDYRRPPPR PANFVFSVETGFCYVGQAGLKLLT SSDPPASAFPKC |
| 288 | 5785 | A | 297 | 136 | 251 | IHQEKPPNIFSVKKRHYD*PGQHDP LASASQSAGITGV |
| 289 | 5786 | A | 298 | 118 | 337 | IHQEKPPNIFSVKKRHYD*PGQYGK TSLLLKIQLAGYSGTCL\KSQLLRR VGREVIQLALKIRAPIWKIECL |
| 290 | 5787 | A | 299 | 160 | 437 | KRDTTSLGQYGQNPASLLKIQLAG Y\SGTCL\KSQ\LRRLRHQNRLNLG GRG\GSEQRSCHLHSGGHSETVSK KKKKRERQQWRQIGTCMP |
| 291 | 5788 | A | 300 | 61 | 1302 | FSGSCVPPRTCGLCWISTGQSGVVS VSSTRLEESEGTQPPSPSSDTGSEGE EDDEGEEHGLGGQNEVGIIPTTLEFL ENHGKNILLSNGNRTVTRVASYNQ GIVVINQPLVPQLLVQVRIDFLNRQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | WTSSLVLGVITCAPERLNFPASACP SNGQPGCCGAVGSSTTSQAGLSSQI CEKFGPNLDTCPGTLGLRLDSSG GLHLHVNGVDQGVAVPDVPQPC ALVDLYGQCEQVTIVNPEPGAASG KSAGTQGDMEKADMVDGIKESVC WGPPPAASPLKSCEYHALCSRFOEL LLLPEDYFMPPPKRSLCYCESCRKL RGDEAHRRRGEPPREYALPFGWCR FNLRVNPRLEAGTLTKKWHMAYH GSNVAAVRRVLDRGELGAGTASILS CRPLKGEPGVGFEEPGTNC |
| 292 | 5789 | A | 301 | 1 | 936 | |
| 293 | 5790 | A | 302 | 1 | 1023 | |
| 294 | 5791 | A | 303 | 1 | 867 | |
| 295 | 5792 | A | 304 | 1 | 569 | SGRVAMGRRRAPAGGSLGRALMR HQTQRSRSHRHTDSWLHTSELNDG YDWGRLNLQSVTEQSSLDLFLATA ELAGTEFVAEKLNIKFVPAEARTGL LSFEESQRIKKLHEENKQFLVVYRG DQTNWNQNTTPEELKQAEKDNFLEW RRQLVRLLEEEQKLILTPFERNLDFW RQLWRVIERSDIVVQIVDA |
| 296 | 5793 | A | 306 | 846 | 1070 | RVGDRSEREIVILKTNFTYFQVFPKA GCGCFSFLFSFFLSFFFLRGETESRSV ARMKCSGVISAHCNLCPLGSS |
| 297 | 5794 | A | 307 | 118 | 340 | KFQTEVSHFFLCNLICSYFIFLL/CS FLLIHF/LYSLFFFLFCFMFFLFIMY /LFFVLLIRYSYIKSLLFLMSCN |
| 298 | 5795 | A | 308 | 42 | 352 | TRGPRVPHSGSASSPAQKSGCTG/P* NSALARPALVSFRAMPNSRGW/PQG EQR/PGSPHHRSPGHWKRVHVPPA AQRGPGAGGCHQGTGPEAQAHAQ VRPPAQGG |
| 299 | 5796 | B | 309 | 796 | 3180 | VAEAPGLVDVPGGHPEPQSCEKLE NTGGKIGHRKKMPYSTPAPCVSPLK LDLWLSVRERTPDGSLTLLHCATS DPQGQALCPGGSPQHQLAGQLV VHELFSVLQEICDEVNLPLLTSLQP LLGIARNETSAGRASAEFYVQCSL TSEQVRKHYSGGPEAHSTGIFFV ETQNVRRLPETEMWAEPCPSAKGA IILYNRVDVVLASTPMRICPPAAMP LLPLRLCRLWPRNPPSRLGAAAGQ RSRPSTYYELLGVHPGASTEEVKRA FFSKSKELHPDRDPGNPSLHSRFVEL SEAYRVLSREQSRRSYDDQLRSGSP PKSPRTTVHDKSAHQTHSSSWTPPN AQYWSQFHSVRPQGPQLRQQQHK QNKQVLGYCLLLMLAGMGLHYIAF RKVKQMHLNFMDEKDRIITAFYNE ARARARSVPALFCSLLPVQEPHFGIP IPTTQAPVSQPDAPGHQRKVVSVID VYTRATCQPREVVVPLTVELMGTV AKQLVPSCVTVQRCGGCCPDGGL CVPTGQHQRVMQVLGTWGNQGQ MQILMIRYPSSQLGEMSLEEHSQCE CRPKKKDSAVKPDSPRPLCPRCTQH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HQRDPDPTCRRCRRRSFLRCQGRG LELNPDTCRFSLSTAGSLLQLTDV WWLLGRLKISLVGEQAQPDHSSHE SQPRCTGRVLSICLSAVATATGAEG KRKLQIGVKRVDHCPIKSRKGDV LHMHYTGKLEDGTEFDSSLPQNQPF VFSLGTGQVIKWDQGLLGMCEGE KRKLVIPSELGGATLVFEVELLKIER RTEL* |
| 300 | 5797 | A | 310 | 61 | 674 | GCGTLGPLQWDFPEPGCKGMMAPL AEGQSSAHISVWGNLRTFCVSTKKI PVDSGASGSPTQVSASLTCSAQAA LDIELGTGLGNNLVSFRGDAKQAG AGLRVKNKAGSPSTRSPEGHWKR VHVPPAAQRGPGGWGLPPRAHGPE AQGAHQVRPPA\QGPQPPAGSGAG RQGSRLWLVRPPVGPDPDRPAC HPSRWHPAVAA |
| 301 | 5798 | A | 311 | 89 | 1166 | |
| 302 | 5799 | A | 312 | 1 | 2094 | MGAPAVQSSSGPAGARPRKAGVER RAEPAGPGLPETTRKSPQILGFSLR AVVWDLFPGSKQIVRRKLPIPGQAV LVQADVATLTSRRVLHACGLVPLE MPCIQAYGTPAPSPGPRDHLASDP LTPEFIKPTMDLASPEAAPAPTALP SFSTFMDGYTGEFDTFLYQLPGTVQ PCSSASSASSTSSSSATSPASASFKE EDFQVYGCYPGPLSGPVDEALSSSG SDYYGSPCSAPSPSTPSFQPPQLSPW DGSFGHFSPSQTYEGLRAWTEQLPK ASGPPQPPAFFSFSPTGLS\PSLAQS PLKLFPSQATHQLGEGESYSMPATF PGLAPTSPLHLEGSGILDTPVTSTKAR SGAPGG\SEGRCAVCGENASCQHY GVRTCEGCKGFFKRTVQKNAKYIC LANKDCPVDKRRRNRCQFCRFQKC LAVGMVKEVVRTDSLKGRRGRGPS KPKQPPDASPANLLTSLVRAHLDSG PSTAKLDYSKFQELVLPFHGKEDAG DVQQFYDLLSGSLEVIRKWAENP GFAELSPADQDLLLESFALELFILRL AYRSKPGEGKLIFCSGLVLHRLQCA RGFGDWIDSILAFSRSLHSLLDVP AFACLSALVLITDRHGLQEPRRVEE LQNRIASCLKEHVA AVAGEPQPASC LSRLLGKLPRLCTQGLQRIFYLK LEDLVPPPPIIDKIFMDTLPF |
| 303 | 5800 | A | 313 | 858 | 1143 | QLVPCCPPTQRTVQKNAKYICLAN KDCPVDKRRRNRCQFCRFQKCLAV GMVKEGVWL/RVRPTGARVGLSGV RPPGPPGFCPGGPTGGHVLFPPHL |
| 304 | 5801 | A | 314 | 190 | 330 | ERIKKQDLSICCLQVTHFTFKDSQRL KVKGWKK\IFHTNKNQKRIWT |
| 305 | 5802 | A | 315 | 190 | 324 | ERIKKQDLSICCLQVTHFTFKDSQRL KVKGWKK\IFHTNKNQKRI |
| 306 | 5803 | A | 316 | 85 | 310 | CAWHVNILIGKRLNTPYRSGTRQG CMLLPFLFNTILKDLVTALKNQDIK GKQIK/EEIKLSLFTMITRVDKNQS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 307 | 5804 | A | 317 | 33 | 494 | |
| 308 | 5805 | A | 318 | 1 | 612 | |
| 309 | 5806 | A | 319 | 113 | 551 | LLWRESAVTALWGKVNVDVGGK ALGRLLVVYPWTQRFESFGDLST PDAVMGNPKVKAHSKKVLRGAFS GGLAHL/DNLKGTFAHTEVSLHCD KLHVGSWRTFRLG\NVLVCCCWA HSLLGKEFQPHQLQACLIKIGWL VG |
| 310 | 5807 | A | 320 | 221 | 376 | DRVSIPRLESSGAILAHCNFR/SGFK QFSCSLPSSCDYRCVLPRRALCSSC |
| 311 | 5808 | A | 321 | 32 | 452 | |
| 312 | 5809 | A | 322 | 72 | 570 | SRRAWVSFTEEDKATITSLWGKVN VEDAGGETLGRLLVVYPWTQRFED SFG\NLTCASAIMGHPKV\VHGKK VLTSLGDA\EHLDLKGTF\AQLSEL HCDKLHVDPENLKLGNVLETALAI /HFSAKQFTPEVQASWQKMGD\GV ASALCFTKHLDFMCMMQSFQR |
| 313 | 5810 | A | 323 | 35 | 359 | |
| 314 | 5811 | B | 324 | 102 | 431 | MIIYRDLISHDEMFSDIYKIREIADGL CLEVEGKMVSRTEGNIDDSLIGGNA SAEGPEGEGTESTVITGV\DIVMNH LQETSFTKEAYKKYIKDYMKSIGK LEEQRPD* |
| 315 | 5812 | A | 325 | 132 | 708 | RRRRLPSVAIMIIYRDLISHDEMFSDI YKIREIADGL\CLEV\EGKMVSRTEG NIDDSLIGGN\ASAEGPEG\EGTRST VITGV\DIVMNHHL\AGNKFSQKEAY KKYIK\DYIEIQFKGETLKEPEDQKR VKPFYDRGLQE\QFKHILG*FSKTYQ FFIG\ENMNP\DG\MVALLDYREGWV *PHI*FSFKDGL\EM\EK |
| 316 | 5813 | A | 326 | 1 | 5796 | |
| 317 | 5814 | A | 327 | 3 | 467 | |
| 318 | 5815 | A | 328 | 73 | 1593 | |
| 319 | 5816 | A | 329 | 57 | 1358 | RRKVAMDLIPNLAVETWLLAVSL VLLYLYGTRTHGLFKRLGIPGPTPLP LLGNVLSYRQGLWKFDTECYKKYG KMWGTSSLFPHYPSSEALGGSC VRLLLCVTP**TRT*GCCVSYN*GT YEGQLPVLAITDPDVIRTVLVKECY SVFTNRRICATTSTIKMQTHSVTMW LPPAVLQSQHGVCFL*QSLGPVGF MKSALSLAEDEEWKRJRSLLSPTFTS GKLKEKRHHKIH\YKMSLTAPCWRK PYPSGT*VCTFNYSIFGAYSMDVITG TSFGVNIDSLNNPQDPFVESTKKFL KFGFLDPLFLSIILFPFLTPVFEALNV SLFPKDTINFLSKSVNRMKKSRND KQKHRLDFLQLMIDSQNSKETESHK ALSDLELAAQSIIFIFAGYETTSSVLS FTLYELATHPDVQQLQKEIDAVLP NKVRG |
| 320 | 5817 | A | 330 | 870 | 1150 | HRLDFLQLMIDSQNSKETESHKALS DLELAAQSIIFIFAGYETTSSVLSFTL YGTGPHPDVQAGNCKREIDAVLP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NK\APPTYGAVGTDGSYL |
| 321 | 5818 | A | 331 | 144 | 377 | RRCKGISTSCHCIITNEIFIFIFFEAE SHSVARLECSGAVLAHCKLCLPGL RHCPASATREAEAREWLETRSRL Q |
| 322 | 5819 | A | 332 | 3 | 323 | DRVSLSPRLECNGMISTHCNLHF PGSSDSPDTP/SQVAEITGVHHHAQL IFVFLVETRFHHIGQAGLELLTSSDL PTSASPSAGIIGVRHCAWARITFQRT KCFSI |
| 323 | 5820 | A | 333 | 187 | 450 | NYVSQKRKKLNSPINYKEIEFIVLK LPK\KKPLGPNGFTAIFYQTFKKGM \TPILDHLLQKIDVTLPYLFYKTDFT LTLKPKTIQKTRA |
| 324 | 5821 | C | 334 | 122 | 292 | MMCSMTLSFIFSFMRLCRSIRASS WNSPWFRVSGCPSFTEYWWKVLM MVYMLRSS* |
| 325 | 5822 | A | 335 | 295 | 931 | VLSRKCQRSLTAFSSKCPNSWFSITQ TECKTMTCGMPQHVTQQ*RPINTS HQYSVKLGHPRHPETRGRFKELVR\ KDLQNFLKKENKNEKVEIHIMEDL DTNADKQLSFR/EEFIMLMGEA*PG AFPRRKIARGLTEGPGVHHHKPGPG GGAPPKDHSGPRFTVGHGHGHSTW WPRPQATNHGGQATLPLPNHRPRG LLCQTVLAVGLGAGAK |
| 326 | 5823 | A | 336 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 327 | 5824 | A | 337 | 3 | 556 | HSLFGTSEVINKLRSPDAMGHFTEE DKATITSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIH GQPPKSRHMGKKVLTSLGDAIKHL\ DDLKGHLLPKPEVNCTCDKAALLD PEELSSFLGEMLLG/VPVFGQSHFRA KEFHPWRLQGFPGISRRWQKMVT\ GVASALVPSRYH |
| 328 | 5825 | A | 338 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 329 | 5826 | A | 339 | 38 | 547 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSA\SAIMGNPKVKAHGK KVLTSLGRCHKSTWDDLKG\TFAQ A*SELH\CDKLHVDPPGGTFKLLGK MLLG*PV\LAIPFSAKEFHP*RLQAS WQKQKMAEDGDLELASALVPSRY H |
| 330 | 5827 | A | 340 | 168 | 330 | SSLGLDLVCGDMAKCTKKVRIISKY GTRYGASLRKMVK\RIAITQHTKYI CSSRA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 331 | 5828 | A | 341 | 2 | 355 | ARATMVLSPADMTNVKAAWGKVG AHAGEYGAEALERMFLGLTTKTY FSHFDLSHGSAQVKGHCМКVVDAL TNAGINVDNL\PNAL\DTLIDLLTPIF CRSLNLFYLISNSLFIISVH |
| 332 | 5829 | A | 342 | 176 | 410 | AGLLPDP/TITARMNVGV AHSEVNP NTRVMNSRGIWLAYIILVGLLHMV LLSIPFFSIPGGWTLTNVIHNLATYV FLHT |
| 333 | 5830 | A | 343 | 469 | 708 | |
| 334 | 5831 | A | 344 | 49 | 351 | ATSPDIAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLDGYPWTQR GFDSFGNLNYTSDVMVDPKFMGHG MKVLTYLGDALCDLDDTNGNFAH VSTVMC |
| 335 | 5832 | A | 345 | 665 | 921 | AKKKEKKTGALSARRQPNPPTQNT PHPHPPNPTPHHPPPPSPPTPHSPPP FLILQKLLIAVTIFDPTYCVISYSW VIMTFNKL |
| 336 | 5833 | A | 346 | 2 | 341 | HEEGFVNPGARFCLPEAAAVRRPPG EATVIMSDQEAKPSTEDLGDKNEGE SIKLP/VLAHDRTEHFNVKTTTHLT SLPQSYCQIQAVPLNSLTLLFARPTT AAHHTPPELPMQ |
| 337 | 5834 | A | 347 | 209 | 397 | VSLWQEA MRLPKNTPEEKDRRTAA LQEGLRPVSVPLTLAENGAF LWS DMENLSDIYWYASE |
| 338 | 5835 | A | 348 | 87 | 356 | IHFYRVKIFFHILCFYIFIQICHYSFIF YFFCRQG/HLSRLEGSGAILAHCNL CLLGSNDPPTSASRVAGTAGTHHH AWLIFVFFIETGY |
| 339 | 5836 | A | 349 | 3 | 204 | KMEARKQRESMRGREAREKEKG YERSSEGERVVERNIGHKRRRDAK REARWEKIHGAKEARNRYK |
| 340 | 5837 | A | 350 | 3 | 341 | HERHEIPIIKMSHRGPWLMVDFLSY KLSQNGYSWSQFTDVEENTTEAPE RTELDRITPLAINGNRSWHLADSPA VNGTTGHSSSDARDVIPMAAVQH ALWEASDEFELRHR |
| 341 | 5838 | A | 351 | 67 | 541 | EAPARRALCGRVPSEAQRDGHQAP LLSRRRL*AFFVADGIFKAELNEFL TRELAEDGYSGVEVRVTPTRTEIIL ATRTQNVLGEKGRRIRELTA VVQK RFGFPEGVELYAEKVATRGLCAIA QAESLRYKLLGGLAVRRCAGNQSE DHACLG TNW |
| 342 | 5839 | A | 352 | 3 | 495 | |
| 343 | 5840 | A | 353 | 1 | 459 | EDGYSGVEVRVTPTRTEIILATRTQ NVLGEKGRRIRELTA VVQKRFGFPE GSVELYAEKVATRGLCAIAQAESLR YKLLGGLAVRRACYGVL RVIMESA AKGCEGVVSGKLRGQRANS/MKFG KAGGFPGLVNYCALVGPLCAYT GVVGH |
| 344 | 5841 | A | 354 | 1 | 885 | SWSTHASVSAERGGKMAVQISKK GEFVADGIFKAELNEFLTPQLAED GYSGVEVRVTPTRTEIILATRTQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *~Stop codon; /~possible nucleotide deletion; ~possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VLGEKGRVIRELTAVVQKRFGFP RRASVELYAEKVGHYRSCVAIAQG RSLCVYKLLRKGFACAGGPCYGV AAGSIMEKWGPKAFCVWWSGKT SEEQRA*IP*SFVEWP*WIHSGDPV* LTNVDTAVRHVLLRQGVVLGVKVK IMLALGTQLGKIGPKKPLPDHVASIV EPKDEILPTTPISVEQKGGKPVTAH GPTRSPQPNRVSLAAVFWSLDVAL |
| 345 | 5842 | A | 355 | 1 | 284 | SLFLYTANSRLGPLVSPAFMPHRISC NVTKGLPHDHYACLQEIKSSYKFYR YFETQQQSVQPCLSRTHQKSRLN NVYSAVRRLQVHMKALLNE*VSPA FMPHRISCNVTKGLPHDHYACLQEI KSSYKFYRYFETQQQSVQPCLSRTH QKSRLNNVYSAVRRLQVHMKAL LNE |
| 346 | 5843 | A | 356 | 1 | 1404 | |
| 347 | 5844 | A | 357 | 1 | 771 | |
| 348 | 5845 | A | 358 | 3 | 913 | |
| 349 | 5846 | C | 359 | 461 | 667 | MRMTMMMMMIHLKLILMMMM KSMEPLLEGAYDPADYEHLPASAEI KELFYISRYTPQLIDLGTN* |
| 350 | 5847 | A | 360 | 76 | 158 | |
| 351 | 5848 | A | 361 | 1 | 2313 | |
| 352 | 5849 | A | 362 | 788 | 926 | PSPELPEGDFEGFFPQKLQ*SCLPTL QKKKNNNNNNNNNNNNNNNEK |
| 353 | 5850 | A | 363 | 168 | 447 | TGTPGYACNSQNLGGPTGGISRSPV *NQPGQKGETPGFLKIPKLTRGGGR ALQFQVLGRVRPENPLNLGGQNFN* PKLCPCTSTWGKIRLPF |
| 354 | 5851 | A | 364 | 637 | 1258 | VLFLRKPTPAACLGHALSHRNLGPS AANSPSVLGKPAPSWSHVPATVLP GQQGTPCDMRVSGTVRVGSTVMST TSIPALPHLGSTSVGPPQPGGHEKQ MITWCKDRLQLTHSDEGFGVGFFQ TTMYILASKMCTGAQRSGCWALRV PQEDGKNQLIRFYCMYVCIYFETES HSVYVQAGVQWRDLDSL*PPSPEFKR ISCLSFLSSW |
| 355 | 5852 | A | 365 | 217 | 481 | KCSFQM*YRLKNYNNNHSHPFISIL FLISSNIQNNFGSRYN*NHLKMYKT EAQRLTCSMLHKSNPFLFILNRMFL TRNLLGPHSLVP |
| 356 | 5853 | A | 366 | 1 | 245 | PVPRGGSKLLTHHLAPLTLPKAGDS GVNPRVPPFLSPPAIWGPCKILGL AKTPVPRFPLGKKFFPSP*FPPFFPK NKTL |
| 357 | 5854 | A | 367 | 145 | 196 | |
| 358 | 5855 | A | 368 | 120 | 173 | |
| 359 | 5856 | A | 369 | 138 | 321 | NECLLSFFSV/PNSSLLK*KS*ASA VAHTCNPSTLGG*GGWIT*GQEFET SLANMVKPLY |
| 360 | 5857 | A | 370 | 1536 | 1629 | KSQKACNPSTLGG*GGWIT*AQEFT TSLANT |
| 361 | 5858 | A | 371 | 11498 | 11651 | LKNNFKKCTMWAIGMVADTCNPST LGGRGGWIT*GQGFKTSLANMMKP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | CLY |
| 362 | 5859 | A | 372 | 15 | 272 | RLKAATLKMPGSAAKGSEL SERIES FVETLKRCGVPRSED TARVTLLM MRWIFNDHRWIPP*ELVDPYIYFPW PCSTLSCWDWS |
| 363 | 5860 | A | 373 | 433 | 612 | QAPLQKPTVRR*K*VREIRGRD*VE E*IEEWYR*RSGRETRRGRESGR*ER GEVDREERKRE*GSRVRRGRERRG RERRGRERGGEESQEGKREKRKRE RRGREKRGREERKRAKEVFKDGER PRAKVGIVLKRQ |
| 364 | 5861 | A | 374 | 785 | 1178 | ALGCPGCPLLA VSGKDHNSSTQPAT HNSRDRRERRKEERERRGRERGEE IEEGKR*RSGRETRRGRESGR*ERGE VDREERKRE*GSRVRRGRERRGRE RRGRERGGEERQEGKREKRKRERR GREKRG |
| 365 | 5862 | A | 375 | 1969 | 2208 | GANPIHDLHPHDLTTSHRPHIFIFFE MESRSVTQAGVQWHD LGSLKSPPT GLKLFSCLSLPSG*NYRCTPSHLANF CIF |
| 366 | 5863 | A | 377 | 171 | 442 | GKKWSFSLQNW HVQAY*LSCNRY CSLKDHD FITPSDGGPDIFLHICDVE GEYVPVEGDEV TYKMCSIPPKN EKL QAVEVGITHLGP GTQH |
| 367 | 5864 | A | 378 | 3 | 775 | SVHSSAHASERVAEQNGLQGQAMS SVPSPPPQPPTHQA\GVGLLDTPRSR ERSPSPLRGNVVPSPLPTRR\TRTFSA TVR\ASQGPVYKGVCKCFCRSKGH GFITPQLMAAPDIFLHISDVEGEYVP \VEGDEV TYKMCSIPPKN EKLQA VEVVITHLAPG TKHETWSGHVISF LGDGGSTPCPVLVGRLCGEEAADT GDDILPHETGLQRGNGPSHVSPGGK GYGGAGVGC GVFAISTAYGPLQQ PLHHLKSIKSI |
| 368 | 5865 | A | 379 | 7 | 316 | APSPDAMGHFTEEDKATITSLRGKE NVEDAGG*TLGRLLDDYPWTHRIL DS*GKLLSDYAIMGKQDDKEHA EK ELPSLEDALAHWADASASGHWP SD VPCAYR |
| 369 | 5866 | A | 380 | 61 | 304 | ARTWNSVRMASSGMTRRDPLANK VALVTASTDGIGFAIARRLAQDGAH VVVSSRKSQNV DQV*VST*LASV*L IYLMCVLP |
| 370 | 5867 | A | 381 | 2 | 281 | |
| 371 | 5868 | A | 382 | 2 | 558 | HSLLERLRLSISFLVQTPIGHSTEED\ KATITSLWGKGEMWKNAGRKKPL GRPPGLSLPQWTPRG SF EQALGNL VSSCPPAPSMGKPPQKSKGTMAKK GA*PSLGKMPIKAPLDDLKGT FAP A*SELHC DKLH/VLDPENFKLLGN VLVTVLAIHFGKEFTPEVQASWQK MVTAVASALSSRYH |
| 372 | 5869 | A | 383 | 3 | 368 | EFFCGLCVKSEISLHLFCLANFFPSL KPOITSSGEMVPLLPCQS*EWRRKD ESSTLPPPPSSGAECCTWLRPSPSTS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PCPCLPHPYVQGSLCETQSHLTVNP ASSSYRISPPPLISSRTRY |
| 373 | 5870 | A | 384 | 179 | 455 | EFGWGGGKSLGLPRAGLD*IGGSLG FIPLLSTPVSHSHAFSVGAILALIFLL ESLAFQWLLLLSSSHFLYFSLLFFRQ SSFCFLTEEQKKKK |
| 374 | 5871 | C | 385 | 22 | 423 | MKAAVLTALXFLTGSQARHFWQ QDEPPQSPWDRVKLHELQEKLSPLG XEMRDXRAPMWTXXNASGPLQRR VRXLWPRALRLSRRTAAQTWPSTT XRPPSILSTFSEKGQARVRGTSKA CXPLLESXKGXVS* |
| 375 | 5872 | A | 386 | 1 | 671 | SGRIQEVPHGPFMRKAAVLTALA\VL FLTGSQARHFWQDEPPQSPWDRV KDLATVYVDGLTEDSGKDSVTSTFS KLRE*LGPVTQEFWDNLAEKETEG RQEMSKDL\EEVKAKVQPYL\DDF QKKWQEEMELYRQKVEPLRAELQE GARQKLHELQEKLSPLGEEMRDRA RAHVDALRTHLAPYSDELQRRLAA RLEALKENGARLA EYHAKATEHL STLSEK |
| 376 | 5873 | A | 388 | 24 | 499 | HTDTYPHPHLIARPQGFPELKNDTF LRAAWGEETDYTPVWCMRQAGRY LPEFRETRAAQDFFSTCRSPEACCEL TLQVRGPQKRERFMPSVCHLATCL LFPTPLRRFPLDAAIIFSDILVVPQA LGMEVTMVPKGGPSFPESLREEQDL KRLLDPEMV |
| 377 | 5874 | A | 389 | 109 | 750 | HTDTYPHPHLIARPQGFPELKNDTF LRAAWGEETDYTPVWCMRQAGRY LPEFRETRAAQDFFSTCRSPEACCEL TLQPLRRFPLDAAIIFSDILVVPQAL GMEVTMVPKGGPSFPPEPLREEQDLE RLRDPEVVASELGYVFQAITLTRQR\ LAGRVPLIGFAGAPWTLMTYMGFI LTWTQNMWAPLWMLCINTHVCFD RTECIPLSSTTNTDD |
| 378 | 5875 | A | 390 | 1 | 295 | PQTOREPAMVLSPADKTNVKA WGVGAHAGEYGAEALERMILFFT TRTYFPRLDLSLLSDPV*FPVITEAF ARTYSGVIADLLSNTEPHMIQMAAS |
| 379 | 5876 | A | 391 | 112 | 310 | |
| 380 | 5877 | A | 392 | 49 | 615 | RAQRGCSQSCGKMNARGLGSELKD \SFPVTELSASGPLES\HDLRLKGF\S CVKNELLPSHP\LELS\EKNFQLQPR LK*NFTLEETFQGSILLPLKITGGDF QGQCRQV\QRLPFSFQAPNLSTGMV FEGGNDETIWDLEDIL**SHHKSEV HGESHTFDGWEYKPWVYCNSAGS WKPRAILFIVIFVL |
| 381 | 5878 | A | 393 | 167 | 1955 | LCPHVVEGMWEVPVISLMRALIPF MRASPSRVRRAATPAAVTCQLSNW SEWTD CFPCQDKK/YTVM TLSAIQT IQGNILIS ETLIMSAMAGFPNKYRHR SLLQPNKFGGTICSGDIWDQASCSSS TTCVRQAQCGQDFQCKETGRCLKR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HLVCNGDQDCLDGSDEDDCEDVR AIDEDCSQYEPIPGSQKAALGYNILT QEDAQSVYDASYGGQCETVYNG EWRELRYDSTCERLYYGDDEKYFR KPYNFLKYHFEALADTGISSEFYDN ANDLLSKVKKDKSDSFGVTIGIGPA GSPLLKFIFTRIFTKVQTAHFKMRK DDIMLDEGMLQSLMELPDQYNYG MYAKFINDYGTHYITSGSMGGIY ILVIDKAKMESLGITSRDITTCFGGS LGIQYEDKINVGGGLSGDHCKKFG RARKAMAVEDIISRVRGSSGWSG GLAQNRSTITYRSWGRSLKYNPVVI DFEMQPIHEVLRHTSLGPLEAKRQN LRRALDQYLMEFNACRCGPCFNNG VPIEGTSCRCQCRLGSLGAACEQT QTE/G*GAKADGSWSCWSSWSVCR AGIQERRRECDNPAPQNGGASCPGR KVQTQAC |
| 382 | 5879 | A | 394 | 94 | 276 | |
| 383 | 5880 | A | 395 | 25 | 1876 | ILQGPACTHLLQFPEYIALFLQGN VRGLLAEMFAVFFILSLMT*QPGV TAQEKGNQRRPATPAAVTCQLS NWSEWTDPCFCHDKKYRHRNLLQ NKFGGTICSGDIWDQASCSSSTTCV RQAQCGQDFQCKETGRCLKRHLVC NGDQDCLDGSDEDDCEDVRAIDED CSQYEPIPGSQKAALGYNILTQEDA QSVYDASYGGQCETVYNGEWRE LRYDSTCERLYYGDDEKYFRKPYN FLKYHFEALADTGISSEFYDNANDL LSKVKKDKSDSFGVTIGIGPAGSPLL VGVGVSQSQTSLNELNKYNEKK FIFTRIFTKVQTAHFKMRKDDIMLD EGMLQSLMELPDQYNYGMYAKFIN DYGTHYITSGSMGGIYIYLVIDKA KMESLGITSRDITTCFGGSLGIQYED KINVGGGLSGDHCKKFGGKTERA RKAMAVEDIISRVRGSSGWSGGL AQNRSTITYRSWGRSLKYNPVVIDF EMQPIHEVLRHTSLGPLEAKRQNL RALDQYLMEFNACRCGPCFNNGVP ILEGTSCRCQCRLGSLGAACEQTQT EGAKADGSWSCWSSWSVCRAGIQE RRRECDNPAPQNGGASCPGRKVQT QAC |
| 384 | 5881 | A | 396 | 2 | 307 | QAGV**WDLGSLQPLPRLKQFS/CI LNPGNLSKEF*STKETKQNFVGHQ SQTSKFAISLIQHPINMRSGTKTFM MV*GNKQRSKFPIWTFKIFDMLPS |
| 385 | 5882 | A | 397 | 374 | 665 | GAQGLSLSPRLECNGAILAHCNLC PGSSNSPGSAS*VAGTIGMHMHARL MFVFLVESGFHHVGQAGLELLTSSD PPASASQSAGIRGISRRAGLDF |
| 386 | 5883 | A | 398 | 202 | 425 | RLGGVEEGWGKGRSLVLHLKCGV QILLMTLTGKTISL*LDPSTIVNVK ALIHDIERIPDHEMLIFACKQLE |
| 387 | 5884 | A | 399 | 202 | 418 | RLGGVEEGWGKGRRLNLRLRGGL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HIYMITILDLNISLEDMPNPTI*NVK AMILSNNGIHSHE*RLIFEGMR |
| 388 | 5885 | A | 400 | 144 | 433 | |
| 389 | 5886 | A | 401 | 1 | 3135 | |
| 390 | 5887 | A | 402 | 79 | 929 | PVAQGMLRWTVHLEGGPRRVNHA AVAVGHRVVSFGGYCSGEDYETLR QIDVHIFNAVSLRWTKLPPVAPGEV CHPWASS\VVPYMRVYGHSSVPSDD TVLLWGGGRNDTE\GPCNVLYAFDV NTHKWFTPRVSGTVPSARDGHSAC VLRKIMYILGGYEQQADWFSNDIH KL |
| 391 | 5888 | A | 403 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 392 | 5889 | A | 404 | 50 | 562 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDA\EHDDLKGTFQAQLSE LHCDKLHVDPENLKLGNVLETAL A\HFGAKILPFKGRLPGRRWQKMV TGVASALCFTKHLDFMCMMSQSFQR |
| 393 | 5890 | A | 405 | 228 | 420 | TPEADALYSHNPGGNLDRHTASKPS ALLQPGPAWQRGSACSLQILPESRV GFPTGPP*ARKVSI |
| 394 | 5891 | A | 406 | 653 | 940 | KWKKINVFFETGSRSAQAQARVQWC HLGSLQP*HPRLKEPPASASQTAGT TGMHHHAWLS*VSFVKMRLGHIIQ DIRRLMDSINMPHYMHQAPPMCQ |
| 395 | 5892 | A | 407 | 795 | 1802 | CRLHTQQIQRLETASGFLRMKGKNS VQLQEGWERFQDPGNHITRPRPFLP SDPHPTLMCLQGPPTGKGPGKSRAT GTCAAEGA\DETSYF*NAFQLPLYK LIKIIRKKEK*K*KSCT*KRVRWSKL CPRDWAAARTEAPPTGLESRQPVC QDPPPLPTAACIPP/CWLGSF*KRM ND*QTKITPWG*FPHHPRL/PPSSSPS NSSSSPSSPSKLSSSSMASPVKYST ARGTIRSRKKCPISKSEANVNSESSS SDSPSPDATDLPFNGLKKLKKDSL TCFVIVLTVPRPLCFCFFLMVLTVTF FPFFQSIHVPSQSTISGPSKEKGSALS GSDFIL |
| 396 | 5893 | A | 408 | 342 | 515 | |
| 397 | 5894 | A | 409 | 3 | 333 | AAWLLLGAATGLTRGPA/PRPSPPR ALTPA*GPLAAFTAARSDAGIRAMC SEILRQEVLDKDGFRDILLIKVKFGE SIEDLHTCRLLIKQDIPAGLYVDPYE LASLRERNITEEKTSWRRLWLPSDN |
| 398 | 5895 | A | 410 | 877 | 1206 | QGGQSSLGTAGPEPDSPGDPGSAAE QSAREGRRAHGSNV*PPPARSTDG PAPGPHIPATRREAREPGPLPRSGPP SPAPLTGVRARGGEGRGGPAREPG RRPEEQPGGR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 399 | 5896 | A | 411 | 238 | 326 | LHSGPGVVVT*YRKMTSLWAGCSR HACNPSTLGSRGIQITRGQEF |
| 400 | 5897 | C | 412 | 194 | 474 | MWKMHHMCERHGSTVLAIYLRQQ MPQHFFSHSSQYIHILANENYLGLSP FLLKHKFFIKCCIPASSNAHADFRR ARRKETAAPQPCRRPAAR* |
| 401 | 5898 | A | 413 | 1 | 88 | |
| 402 | 5899 | A | 414 | 65 | 191 | |
| 403 | 5900 | A | 415 | 131 | 363 | EVKMAGFLDNFRWPECECIDWSER RNVVASVVAGILVSEKDWLVTCPY LLPWKLMPVPLN*EWLSRTTYFTAV LYR |
| 404 | 5901 | A | 416 | 146 | 567 | EVKMAGFLDNFRWPECECIDWSER RNAVASVVAGILFFTGWIMIDAA VVYPKPEQLNHAFTCGVFSTLAF FMINAVSKLLQVRGDSYGKAAVLA GRTGARVWAFHWGFMLMFGSLIA SMWTLFGAYVTPKYLMFIRD |
| 405 | 5902 | A | 417 | 17 | 369 | KL TGFLGLGVPPKPVIPFKNRPIGPG PWVPPVIPAPLEAQVGGSPSPEIGAP PGYKGEPPFFLKPKQFTRQCGQPPL SQVPWSFRPKKGLNPGSRAFH*LRS RPCSTWATKPNFVS |
| 406 | 5903 | A | 418 | 553 | 673 | RRIKGGVQWLTPVISVLWEAAAG D*LEASSRLYATPPD |
| 407 | 5904 | A | 419 | 2 | 427 | HVIKVLHDDWIFTPFIQGP*SM/CSS KNESRHIGS*RVTG*LLEVLKSL*S FGRLNALNMKSL/TSEVQEE*RKLN KTHRVRQDFDKDRKLAVGQSESPG HPTSEKPPSTSSSAGCMLCSLHISRG FQLRRKRQLNGKCCPIQ |
| 408 | 5905 | A | 420 | 82 | 371 | RRHSVACTPHPSSQVLKSL*SFGR NALNMKSLKAKFRKSDVN*IKLIEC KEPSTEN*LLARVKVLVIRLPRNLL QPHRLLAVCYAAAYISPLAFS |
| 409 | 5906 | A | 421 | 103 | 430 | SFGRNALNMKSLKAKFRKSDTNE WKNDDRLLQAVENGDAEKVASL LGKKGASATKHDSEGKTAFHLAAA KGHVECLRVMITHGVDVTAQDTTG HSALHLAAKNSHHE |
| 410 | 5907 | A | 422 | 87 | 283 | SFGRNALNMKSLKAKFMKSDTNE WKNDDRLLQAV*NGDAEKVASL LGKKGASATKHDSEGKTA |
| 411 | 5908 | A | 423 | 2 | 424 | |
| 412 | 5909 | B | 424 | 108 | 395 | VGAHAGEYGAEALERMFLSFPTTR TYFPHFDLSHGFCPGLRGHGKEGGR RADQRRGQRGTTCPTSLALSDLHA HKLSGGTRFNFQAPKATGLLG* |
| 413 | 5910 | A | 425 | 2 | 334 | |
| 414 | 5911 | A | 426 | 236 | 649 | |
| 415 | 5912 | A | 427 | 76 | 322 | TNSPCYVVFGENSFFS*IIENKKQENK VQQAGIRLYGALLTKCPRLYSKQIH PALLRRLQHGVLDLVYFEDILDKLIG HGPSGV |
| 416 | 5913 | A | 428 | 988 | 1223 | RGERADHLRSGIRDQPGQHGETPSL LITQKLAGLGSACL*SQLLGRLRQE NCLNAGVGGCSEP*SRHCTPAWAT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | ERDS |
| 417 | 5914 | A | 429 | 57 | 349 | ERESPFAPRLEGKGANLG*WKAPLP GLSPFSGLSLPRGTGNYGPPQPPVNF F*F*GETGFPRLTREGLNLRPSENPA LVKPQNKVAPKHGVEKPGGK |
| 418 | 5915 | A | 430 | 291 | 594 | SWLFRLGAMAHAYNNSSLGGQSGR IVWAQEFNTQPGQHRGD ^p GLYK*FF FLISQCDGMHLWSQLLRRLRQKDH LNPRAQGCSEL*LHCCAPAWVTEQ DLSQ |
| 419 | 5916 | A | 431 | 27 | 361 | RGPTVTPQIMAVEDVASTGADPCD LDS DGLLHEILTSPILLLLGLCIFLL YLIVR*DQPAANGDSDDD*PSPLPR LKRRDFTPDDLRRFYSVQDPRILMD FNCKVFDVTK |
| 420 | 5917 | A | 432 | 196 | 555 | SPSMNPRKKVDLKLIVGAIGVGKT SLLHQYVHKTFYEEYQTTLGASILS KN*SYWVD ^t TLKVTDLGD ^t TGGQER FRSMVSTFYKGS DGCILTFD ^t VDLE SFEALEFWPGGGLAQNGPNEA |
| 421 | 5918 | A | 433 | 1 | 685 | EIKYHSLPRLECRGEISAH*NLCPLG SSDSPATAS*VAGITGMRHYAQLIFL FLVET*FHHVGQGWSRTPDSNDPPA SASQGAGDYRRD |
| 422 | 5919 | A | 434 | 56 | 335 | KCSPKILLTSESTSSNPCLIDTNASDF HFLSQVLE*VVSPKGSKEALCCILR HLGYETRESCPWCP SQFRYITFDMG SYVGPVLHHSCQALSL |
| 423 | 5920 | C | 435 | 24 | 332 | MKGRTFISLLFLFSSAYS RGVFRRD AHKSEVAHRFNDLGEENFRALVLIA FAQYLQQRPFEDHV ^t TYAQLQLFV KPMVKWLTAVQNKNLREMNASCN TXMTTH* |
| 424 | 5921 | A | 436 | 130 | 599 | |
| 425 | 5922 | A | 437 | 1 | 404 | |
| 426 | 5923 | A | 438 | 3 | 647 | FSLLSTPHAFGTMKWVTFISLLFLFS SAYS RGVFRRDAHKSEVAHRFKDL GEENFKALVLIAFAQYLQQCPFEDH VKLVNEVTEFAKTCVADESAENC KSLHTLFGDKLCTVATLRETYGEM ADCFLAQHKDDNP ⁿ LPRLVRPEVDV MCTAFHDNEETFLKKYLYEIARRHP YFYAPELLFFAKRYKAA ^t TECCQA ADKAACLLPKLDEL ^r DEG |
| 427 | 5924 | A | 439 | 323 | 899 | MMRVFLSEKALSSSYLEMYLSTPH AFGTMKWVTFISLLFLFSSAYS RGV FRRDAHKSEVAHRFKDLGEENFKA LVLIAFAQYLQQCPFEDHV ^t KL ⁿ VE AKQEPERNECF ⁿ LQHKDDNP ⁿ LPRL VRPEVDVMCTAFHDNEETFLKKYLY YEIARRHPYFYAPELLFFAKRYKAA FTECCQAADKAACLLPKLDEL ^r |
| 428 | 5925 | A | 440 | 1 | 1206 | SFSLSTPHAFGTMKWVTFISLLFLF SSAYS RGVFRRDAHKSEVAHRFKD LGEENFKALVLIAFAQYLQQCPFED HV ^t KL ⁿ VEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MADCCAKQEPGRNECF LQHKDDNP NLPRLVRPEVDVMCTAFHDNEETF LKKYLYEIARRHPYFYAPELLFFAK RYKAAFTECCQAADKAACLLPKLD ELRDEGKASSAKQRLKCASLQK/PR NLGKVGSKCKHPEAKRMPCAEDY LSVVLNQLCVLHEKTPVSDRVTKC CTESLVNRRPCFSALEVDETYVPKE FNAETFTFHADICTLSEKERQIKKQT ALVELVKHKPKATKEQLKAVMDD FAAFVEKCKADDKETCFAEEGKK LVAASQAALGL |
| 429 | 5926 | A | 441 | 28 | 1587 | |
| 430 | 5927 | A | 442 | 1 | 1652 | GTMKWVTFISLLFLFSSAYSRGVFR RDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPLEDHVKL VNKDD NPNL PRLVRPEVDVMCTAFHDNEE TFLKKYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK LDEL RDEGKASSAKQRLKCASLQK FGERAFKAWAVARLSQRFPKAEFA EVSKLVTDLT KVHTECCHGDLLEC ADDRADLAKYICENQDSISSKLKEC CEKPLLEKSHCIAEVENDEMPADLP SLAADFVESKDVCKNYAEAKDVFL GMFLYEYARRHPDYSVVL LRLAK TYETTLEKCCAAADPHECYAKVFD EFKPLVEEPQNLIKQNC ELFQGE YKFQNALLVRYTKKVPQVSTPTLV EVSRLGKVGSKCKHPEAKRMPC AEDYLSVVLNQLCVLHEKTPVSDR VTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQTALVELVKHKPKATKEQLKAV MDDFAAFVEKCKADDKETCFAEE GKKLVAAASQAALGL |
| 431 | 5928 | A | 443 | 1 | 1515 | MKWVTFISLLFLFSSAYSRGVFRRD AHKSEVAHRFKDLGEENFKALV LIA FAQYLQQCPFEDHVKL VNEVTEFA KTCVADESAENC DKSLHTLFGDKL CTVATLRETYGEMADCCAKQEPER NECF LQHKDDNP NLPRLVRPEVDV MC/H/YPNAAQNPW* TGDHAFQLW KSMKHTFPKSLMLKHSPSMQIYAH FLRRRDKSRNKLHLLSL*NTSPRQQ KSN*KLLWMISQLL*RSAARLTIRRP ALPRRVKNLLQVKLP*AYS RGVFR RDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPFEDHVKL VNEVTE FAKTCVADESAENC DKSLHTLFGD KLCTVATLRETYGEMADCCAKQEP ERNECF LQHKDDNP NLPRLVRPEV DVMCTTKCCTESLVNRRPCFSALEV DETYVPKEFNAETFTFHADICTLSE KERQIKKQTALVELVKHKPKATKE QLKAVMDDFAAFVEKCKADDKE TCFAEEGKKLVAAASQAALGLTCEA CQEPGGLVVPPTDAPVSPTTLYVED |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ISEPPLHDFYCSRLDLVFLLDGSSRLSEAEFEVLKAFVVDMMERLRISQKWVRVAVVEYHDGSHAYIGLKDRKRPESELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKIDRPEASRIALLMASQEPQRMSRNFVRYVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVLSSVDELEQQRDEIVSYLCDLAPEAPPTLPPDMAQV |
| 432 | 5929 | A | 444 | 2 | 1848 | RFSLLSTPHAFGTMKWVTFISLLFLFSSAYSRGVFRDDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLPRLV RPEVDVMCTAFHDNEETF LKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAAACLLPKLDELRE*LNLQKHVLLMSQLKIVTNHFIPFLETNYAQLQLFVKPMVKWLTA VQNKNLREMNASCNTKMTTQTSPDW*DQRLM*CALLFMTMKRHF*KNTYMKLPEDILTFMPRNSFSLKGIKLLQNVAKLLIKLPACCPKLDELDEGKASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTD LTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLKQNCLEFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKLPSC**SC\CLLPKLDELDEGKASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTD LTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLKQNCLEFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKLPSC |
| 433 | 5930 | A | 445 | 1 | 3780 | MKWVTFISLLFLFSSAYSRGVFRDDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOH/KCFLOHKDDNPNLPRLV RPEVDVMCTAFHDNEETF LKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAAACLLPKLDELDEGKASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTD LTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLEK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SHCIAEVENDEMPADLPSLAADFVE SKDVCKNYAEAKDVFLGMFLYEY ARRHPDYSVLLLLRLAKTYETTLEK CCAAADPHECYAKVFDEFKPLVEE PQNLIKQNCLEFEQLGEYKFQNALL VRYTKKVPQVSTPTLVEVSRNLGK VGSCKCKHPEAKRMPCAEDYLSVV LNQLCVLHEKTPVSDRVTKCCTESL VNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVEL VKHKPKATKEQLKAVMDDFAAFV EKCKKADDKETCFAEEGKKLVAAAS QAALGLTPLGPASSLPQSFLKCLE QVRKIQGDGAALQEKLCAATYKLCH PEELVLLGHSLGIPWAPLSSCPSQAL QLAGCLSQLHSGFLYQGLLQALE GISPELGPTLDTLQLDVADFATTIW QQMEELGMAPALQPTQGAMPAFAS AFQRRAGGVLVASHLQSFLEVSYSR VLRHLAQP |
| 434 | 5931 | A | 446 | 2 | 2255 | STPHAFGTMKWVTFISLLFLFSSAYS RGVFRDAHKSEVAHRFKDLGEEN FKALVLIAFAQYLQQCPFEDHVKL NEVTEFAKTCVADESAENCDSKSLH TLFGDKLCTVATLRETYGEMADCC AKQEPERNECGTMKWVTFISLLFLF SSAYSRGVFRDAHKSEVAHRFKD LGEENFKALVLIAFAQYLQQCPFED HVKLNEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGE MADCCAKQEPERNES/CFCNHKKD NPNLPRLWRPEVDVMCTAFHDNE ETFLKKLYENCPERHPLPFMAPG NSFSFAKRYKAAFTECCQAADKA ACL/LCPKLDELRG*KGRLRSAKQR LKCASLQKFGERAFAKAWAVARLSQ RFPKAEFAEVSKLVTDLTKEVHTECC HGDLLCADDRADLAKYICENQDSI SSKLKECCEKPLLEKSHCIAEVEND EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSV LLLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCLE FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSCKCKHPG AKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD KETCFAEEGKKLVAAASQAALGL |
| 435 | 5932 | A | 447 | 1 | 477 | FYNRVLLLLLPRLEC*GVIFPHRNHL PGSSDSHALAFRTVTGITGTCHHACLI FVLLVETRFLHVGQAGLELLTSSDP PSSASQSSGITGVGHCAAGPTAHFLP HKVLRRLSTKLPSGMSPETIHPRRHA EKSCLSFSLYLFHLTSSCSFIHPFSIL TFKC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 436 | 5933 | C | 448 | 141 | 390 | MAKFSLCPPVKERGEKAHWEXXX XXNKATNSICEVSTFMXXXXXXXXXX XXXXXXXXXXLNIHYESDWVISKLIP GCIKMTEAITC* |
| 437 | 5934 | A | 450 | 345 | 462 | NQRSTARGKELLQDTRALKKNS*R VIKYSKQQAQTCEG |
| 438 | 5935 | A | 451 | 1538 | 1709 | SKCKLKQDPSHAGTSLQSQLLRRLR QENPLRPGFQGCSEL*SYHCTPARV TEQDPIS |
| 439 | 5936 | A | 452 | 243 | 353 | YSYHIRVHVHHTHPLHACP*LHTVR YT*NSTHTHTYF |
| 440 | 5937 | A | 453 | 2 | 366 | SLPASDRPPISSPLATSGTIFSAISCF WDLPAFLWLAPSCQPTMSSQIRQN YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART |
| 441 | 5938 | A | 454 | 2 | 797 | LIGKFAPRGPRIRQRRGGPARVWSL CFKQVFGTEQDPGILFPASGPPSDFL LRLQTSQTIFSAISCFGLPAQHRFLW LAPSCQPTMSSQIRQ\NYSTDVEAA VNSLVNLYLQASYTYLSLGFYFDR\ DDVALEGVSHFFRELAEE\KRKGYE RLK\MQNQ\RGG\RALFQDIKKPA EDE\WGKTPD\AMKAAMALEKKLN QAL/LWDLHALG\SARTDPHLCDFL ETHFLDEEVKLIKMGDHLTNLHR LGGPEAGLGEYLFERLTLKHD |
| 442 | 5939 | A | 455 | 2 | 331 | FFVFCFGKRGLAVFRVEGKGMNPG *RNLWLPGLKNFSGTLWRGGNNK PGPPLQPKFGFLKKKGFSPPGGGGF KIPNLEIGPNKGPKGWE*RA*PPNPS PSNFFNKPWVG |
| 443 | 5940 | A | 456 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 444 | 5941 | A | 457 | 38 | 533 | APSPDA\MGHFTEEDKATIT\SLWGK VNVE\DAGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHG KKVLT\SLGDAIK\HLDDLKG\TFQA A*SEPAPVTKLHVDPENFKAPGEM LLVTR/VLAIPFSAKEFHP*RLQASW AE/MMGDLQLASALVPSRYH |
| 445 | 5942 | A | 460 | 3 | 198 | GIPGSSFCGLCGDVPKPV*RADGS C*DGVAPRLLRPRGFRGGRCGPVLD SLAGQRGAESGCRG |
| 446 | 5943 | A | 461 | 649 | 1185 | ETCLAFMYQRTCSADSKRYTWQLF LEKGPMGYHPLHF*VFLGFFFFFFFET VLAVLPQAGSVGGHNHSSIASSNHP RA*ANPPHLVAGDYKLTAQPGLKF/ VFLLETGFSYVCPGWVSGSLGSNGP PAPAFQRHRAKFVSFVPCCHHAQQK GSIPFNELTFINWVMLGGASSLSWEI VNSS |
| 447 | 5944 | A | 462 | 1 | 298 | NKEILARPNGSSPEFPPLWGLRQVD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PPESGVQSPASPHGKTLFLLKKPTLT GQGGPNPVFPVLRRVKPQGPLNPG GGGFH*PKSCPCPPEWGAKLDPVF |
| 448 | 5945 | A | 463 | 179 | 351 | RHVGIKHGDHEATEKFIDEFAKVIA DKHLTLEQVYNANETSLF*HYYPR KTPITAAE |
| 449 | 5946 | A | 464 | 1 | 327 | PGVPMQRAEFEQPYKRSRCDDSPRT PSNTPSAEADWAPGLELHPDYKTW GPEHGCSFLRRGGFDKPVLLKNIRE NEITGALLACPDESSFENLGVSVLR* T*KLLNYYYS |
| 450 | 5947 | A | 465 | 261 | 452 | GDLRVTGAPSVSLSP*LGLP*VSRP* VPSPLASGTSKPLARFPEEAVGFSPR GLCLLISFPGL |
| 451 | 5948 | A | 466 | 362 | 991 | PSRHLSWLWGSTGCRNAHVQLAG GAGARAGEERPCFPRPELAGTVSPG DKSLRQFGEKGGGGHERMQGPHHS SKESGGQSHGEDPSLEASPPKPESPA SQVPMKSPPVIPGETAHGLP*VSRP* VPSPLASGTSKPLARFPEEAVGFSPR GLWSAMQAGVCDQGICAIRNSPQT TQGGRRP*ERRCRYMHVTTEKAAF TPSAPRECLPH |
| 452 | 5949 | A | 467 | 24 | 436 | RFIVLVHYISAPGELCRGWGSPKME GWGKRTSCQSLPKAGRSPGSLSRD EYCGHRLPDNV*ATGGGQGPAPG MGVRNPSPAPRTSPGWRVPSNTAP QLLGCFGGQTGRVPFIQPDPSSSSG MRNSPPGRGCLESA |
| 453 | 5950 | A | 468 | 2 | 424 | |
| 454 | 5951 | A | 469 | 3 | 452 | |
| 455 | 5952 | A | 470 | 2 | 467 | PDSSGPHRLRENPPWCLSPADKTNV KAAWGKVGAVHGEYGAELERMF LSFPTTKTYFPHFDLSHGSAQVKGH GKKVADALTNAVAHVDDMPNALS ALSDLHAHKL RVD PVNFKLL\SHCL LVT\AAHLPAEFTPCGGTAS\DKF LGFLKQRC |
| 456 | 5953 | A | 471 | 61 | 346 | VRARVSPAAAMGCTLSAEDKAAV ERNKKIDRNLRDREKAAKEVKLL VLGAGESGKSAIGKPMIIEEGYIQ DEWKPFKGIVYSNTLQAIIGT*KAA VERNKKIDRNLRDREKAAKEVKL LVLGAGESGKSAIGKPMIIEEGYI QDEWKPFKGIVYSNTLQAIIGT |
| 457 | 5954 | A | 472 | 828 | 1066 | QAQWLTPCNAQH FARPRRANHLRL GV*HQTGQH GKTPSLLKEKYKKKK KVASRSHMSVIPTMWKAEAEELLE PGRQRSQ |
| 458 | 5955 | A | 473 | 180 | 350 | EPMAKGKTESPGPKRCGP*I*WVIS QRGTLRFRGAGLFFMGEFLRLGENL LEIPRGA |
| 459 | 5956 | A | 474 | 1689 | 1856 | GRCHITCVKSHGAAFDTTFILFY FILFYFILFIF*TESCSVTQAGVQRGN LGSL |
| 460 | 5957 | A | 475 | 115 | 324 | SNFQLSRKLYF*FFQGKSKHNEYFI FE*T*ILHFLNLGIVIYNYGTSFRKNR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MKRKWVNDKMGQQQKHG |
| 461 | 5958 | A | 476 | 310 | 633 | RFSLGEQECEVCYRLRPTPGWTPGE TAGVAGREPLVCSPPPPPASPCAPP KVRSDMGPOPCAS*WPSGLTKGP SCFPVASHGGITPGQWPGEETS KERSSATK |
| 462 | 5959 | A | 477 | 2 | 293 | PAAERSCLRVTFAACPASMEPKRI REGYLVKKGSVFNTWKPMWVVLIE DGIELYKKNCNSP*GMIPLRGITLT RPWLDFGRRKCWFTKSSIQYL |
| 463 | 5960 | A | 478 | 387 | 511 | WDIPFISDIYIILITGYLTTY*NVLH WKKIIFYIALIVL |
| 464 | 5961 | A | 479 | 130 | 240 | KNEQDPRDL*DNDKWPNIHVIGVPE EDKDNGTERVFD |
| 465 | 5962 | A | 480 | 116 | 423 | GIRCPGPRESLLSQFILSMRQAGQ DWQPEAYTLRICQLEVFSTCVSSLL HPVCRSQ*LPMEPEVIPGWNGKPRG HWPVQIFKSFTHTGTPNLAGPGCCCG VR |
| 466 | 5963 | A | 481 | 64 | 343 | QLL**LSSTWEGQLAAKELDEQRGI GC |
| 467 | 5964 | A | 482 | 61 | 342 | QPQDTMGHLTPEEKSAVTDLWGK VNADEADGEALVTLLGVYPWTQR MFESFGDLDTPEADMGNPKVKAHG WKVL*AFIDGPAHPDQLKGNLCT |
| 468 | 5965 | A | 483 | 557 | 816 | SRHFERPWVDHLRLGV*DQPGQHG ETPSLQKIQKLARSGGTHL*SSYL G*SGKNHLNPGSQGCSEP*SCHCTP GWVTEQNSVSKK |
| 469 | 5966 | A | 485 | 277 | 322 | FFF*VYHVWFLFSFLICRFMPFAKFG NF*PLFLEIFFHPYSFSSL*YEW*SFC YCLRGLLCFHVYPLFLVYFSLFFILV NFC*LFFSSLILFFCHMQSTVELVQ |
| 470 | 5967 | A | 486 | 31 | 309 | FLELGP GKPF GNM YDADDDMQYD EDDDEITPDL LQETCWIVIRSYFDKK G*VIQQLDSFD*SIHMTALRIGEYAA PIDLQADAHHASGEKEKP |
| 471 | 5968 | A | 487 | 130 | 521 | KAKFRFTCF TSSFY N*DLDFKIYPSPI KVAEPS*LSGQCFSSLFFHQDLGFCF VLLFETESCSVTQVEHSGAISAHCN LRLPG*SNPVSVS LAAGTTGTHHY TQLIFVLVAEMGFCHVGQSGLELAS CR |
| 472 | 5969 | A | 488 | 32 | 452 | |
| 473 | 5970 | A | 489 | 38 | 525 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTS LGDAIKHLDDLKGTF AQLAS ELH\CDKLHVDPENFKLLG\NVLVT VLAIHF GQRIHP*RCRASWAEDG*L GVASALVLQDTTELTC P |
| 474 | 5971 | A | 490 | 818 | 947 | VCFLFLFF*DGVS LMLPRLECNGTIS AHRNLCFPGSSDSPVSA |
| 475 | 5972 | A | 491 | 17 | 416 | PPSSNPMGHFT*EDTATITSLWGT NAENAGGKTLLRLLGAYPWTQRLF DSFGNLSSASAIMGNPQGAHGLK VLTLL*DAVKHLDDL MGTFSHPTEL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PCYKLHLDSENKLLGYVLAIVMAIHFGKEVIPAV |
| 476 | 5973 | A | 492 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLGRLLVVYPWTQRFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFQAQLSELHCDKLHVDPENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 477 | 5974 | A | 493 | 34 | 548 | APSPDA\MGHFTTEEDKATITSLWGK\ VNVEDAGGETLGRLLVVYPWTQRFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFQAQL\ SELH\CDK\ LHVDPENFKLLG\NMLLVTRFGQSHFRAKNFTPEGCRASWQKQKMAEDGDLQWPVPCSSRIPLKPLGP |
| 478 | 5975 | A | 494 | 527 | 1022 | GWASAFWLWIKPGSPRGYRCNPHHVILPVSAGLELPLCSLLPSTDTCPASQTGSGRANRATPGCGRPAGVRKGRPACKRSKNFRAACGSGARSRPGHRTPGSSRPPGRQKRAPWASQARRPPA*SRPGGRGGAARPHPRRTGAPAGSARGAQRSERARPQPRDPA |
| 479 | 5976 | A | 495 | 2 | 379 | |
| 480 | 5977 | A | 496 | 3 | 723 | VPRVCLLLQQCLDGTDPGTGLPASDRPPISSPLATSGTIFSAISCFWDLPAFLWLAPSCOPTMSSQIRQNYSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEK\REGYERLLARMQNQ\RGGRALFQDIKKPAEDEWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKMGDHLTNLHRLGGPEAGLGEYLFERLTLKHD |
| 481 | 5978 | A | 497 | 1 | 196 | GTSVTKMEAFGLGSRGLWAGGPAPGQFYRITFTPDSFMDPASALYRGPITRTQNPMVTGTSVLGV*IEGGWVIA GHMLGFYVCLDRLRDFYRFRVNLSTVLDASGDFAE*HYL*QFYRITFTPDSFMDPASALYRGPITRTQNPMVTGTSVLGV |
| 482 | 5979 | A | 498 | 1 | 401 | GTRKWVTFISLLFLFSSAYSRGVFRDAHKSEVAHRFKDLG*ENFKALV VIAFAQYLQQCPFEDHVKL VNEVTEFAKTCVADESPDN*D*SLHTLFGDKLCTVAILPETYGEMADCCVQLEPERNECFLLQKD |
| 483 | 5980 | A | 499 | 47 | 411 | |
| 484 | 5981 | A | 500 | 316 | 493 | LLVGRALALPEGDRHDQHQQGLEQSILKLEKEIQDLENAELQISTKEEAIL*KLKAIER |
| 485 | 5982 | A | 501 | 27 | 526 | LSLTSRMEEAELVKGRLQAITDKRKIQEEISQRLKIEEDKLKHQHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSILRLEKEIQDLEKAEQISTKEEAILKKLKSIIERTTEDIIRSVKVEREERAESIEDIYANIPDLP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KSYIPSRLRKEIN |
| 486 | 5983 | A | 502 | 25 | 208 | VSRIEAVSGSHGFSIHKLLTVNVITY DCVSSWCLYVSFQQKDPLVLGQRQ LKSKPAGDLNT*GKVIKCKAAIAW KAGKPLCIEEVEVALPKAHEARIQV SRWFRLELSLA |
| 487 | 5984 | A | 503 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDSFGNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 488 | 5985 | A | 504 | 52 | 562 | APSPDAMGHFTV*EDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIKHLDDLKGTFQAQLS ELHCDKLHVDPENFKLLGNVLVTV LAIHFGKEFTP EVQASWQKMAED\ VTGVASALCFTKHLDFMCMMSFSQ R |
| 489 | 5986 | A | 505 | 801 | 927 | |
| 490 | 5987 | A | 506 | 659 | 837 | RKIKEAGHRGSQLYSQHFGRLRQE DCLSPGGQGCSEPR LHRCVPAWVT G*KKTL PKNKQ |
| 491 | 5988 | A | 507 | 3 | 203 | |
| 492 | 5989 | A | 508 | 23 | 678 | RPRVRMAEVQVLVLDGR\GHL\LGR LAA/LSVAKQVLLGRKVVVVRCEGI NISGNFYRNKLKYLAFLRKRMTN PSRGPYNFRAPSRIFWARTVRGMLP HKTKRGQAALDRLKVFDGMPPPY D/KAPLFL*QKKRMVVPAAALKVVR LKPTRKF\AYLGRLA\DEVGWKYQA VTAT\LEEKRKEKAK\HYRKKK*L\ MRLRKQ\AERNVRRIFANTPEVLKT HGLLV |
| 493 | 5990 | C | 509 | 275 | 370 | MPQGGACSPVLPGLVVSLLLTSY LVVVPQW* |
| 494 | 5991 | B | 510 | 1 | 1122 | MVFLSGNASDSSNCTQPPAPVNISK AILLGVLGGLILFGVLGNILVILSVA CHRHLHSVTHYYIVNLAVADLLLTS TVLPFSAIFEVLGYWAFGRVFCNIW AAVDVLCCTASIMGLCHSIDRYIGV SYPLRYPTIVTQRRGLMALLCVWA LSLVISIGPLFGWRQPAPEDETICQIN EETGYVLFSAALGSFYLPAILVMYC RVYVVAKRESRGLKSGLKTDKSDS EQVTLRIHRKNAPAGGSGMASAKT KTHFSVRLKFSREKKAATLGIVV GCFVLCWLPFFLVMPIGSFFPDFKPS ETVFKIVFWLGYLNSCINPIIYPCSSQ EFKKAQFQNVLRQCLRRKQSSKHAL GYTLHPPSQAVEGQHKDM* |
| 495 | 5992 | A | 511 | 928 | 1311 | AMIVPTAVQPGRQSKDPVSKEKKE KARKERWLGTVAHSCNPRTLGGQG GWIMRSRDRDHPGQQGETPSLLKM QKLAGRGGGHQSRLLGRLRQENGV NPGGGACSEPRWHCCTPAWATE*D |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; v=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SISNNNKK |
| 496 | 5993 | A | 512 | 23 | 288 | APSPDAMGHFAEEDKATITSLWGK VNVEDAGGETLGRLLVNPGLKL NSSLG*Q*FGGCILSPHHCLGKGRK CFFSIVEMLVILYFM |
| 497 | 5994 | A | 513 | 20 | 207 | LDAGTACAETMACTSRLYGLPRST WPNHPDAILPEGYFSSEI*SRPDCGL RVIYRGLTISSA |
| 498 | 5995 | A | 514 | 228 | 375 | CVALGAMRGMRRLPAGAPKMLMG V**ELDRLGYIAHPQLGKRARAGIV L |
| 499 | 5996 | A | 515 | 417 | 573 | ETPTGLRGGTCL*S*LPRRLRWENC LNPGGRCSEPRSHHCTPAWATEQ DS |
| 500 | 5997 | A | 516 | 173 | 420 | LLLANQLMSLQIRQNYSTDLEAAV NRLGNLDLQAYTYLYLGFYYDRD DEGLEGVSHFFRELAEDKRDRY*RL LTMQNQRGG |
| 501 | 5998 | A | 517 | 3 | 415 | HEGHQYAPNPDAMGHFTEEDKATI TSLWIKVNEENAG*ETLARLLAGYP WTQRIFDRFGNLFASDIMGNSPVQ AHGKNVLTSLLDATKHLDDLKGT AQLSELHCYKLHVDPENFHALANE LATALAMHFR**FTP |
| 502 | 5999 | A | 518 | 3 | 232 | |
| 503 | 6000 | A | 519 | 1 | 2361 | |
| 504 | 6001 | A | 520 | 4806 | 5788 | HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLOHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIDFVLV SNIILPKFNHLCTHTHTHTLTLFST YLKNDKDKTIMCKLSLIG*LAESLEF GGGENVDYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSLWLDLGT LSV |
| 505 | 6002 | A | 521 | 151 | 364 | VTHDCICYLQQTHF*PKDKNRLKLK RCKKQFHENSNOQRVEVALLISAQ RDLRSKIDTEGKSIQQRKKSSC |
| 506 | 6003 | A | 522 | 925 | 1168 | SQHFGPRWVDHLRSGIGDQPGQH GETPALLKIQKLARCGYMRL*SLRR LRRENHLNPGGGGCSETRLHHCIPA WATEQDS |
| 507 | 6004 | A | 523 | 142 | 329 | THSLFLLWSLSHHSPTVNTTLRNLG ALHRRHGKL*AAETLDVFNLTSSCS LLFNPFYRNFR |
| 508 | 6005 | A | 524 | 108 | 283 | KQNLILSPRLKCNGPISVN*NFNLP LTRSQA*ASREAGTTGTCYHA**IG* IFIIDG |
| 509 | 6006 | A | 525 | 1 | 345 | GTRAAPLRIQSDWAQALRKDEGEA WLSCHPPGKPSLYGSLTCHGIVLYG IP*ATSSHRFIANDPNIITSHSSRPTVF VPSSFSSILFFLAHPLSISLPFFSLPA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FPLNFLPLRS |
| 510 | 6007 | A | 526 | 3 | 276 | HEPRRPQYSSGRRAAWLSYSLFSAG CGASAPRPLVMSDSGSYGKSDVEH LYRNY*STRI*GYIQTSHI*SG*GM TTDSYYGINIFYKLQ |
| 511 | 6008 | A | 527 | 2297 | 2435 | LKLVSKKRVYNFILLLML*TYFLK DGLFECLWHLTCKKKKLQKNP |
| 512 | 6009 | A | 528 | 123 | 317 | QETKKEQNKENKQIK*RSTRKKHR QGTNKTKERGERQTPPVGNRQTPT LGIHARPRRRATTSPRA |
| 513 | 6010 | A | 529 | 787 | 1069 | FASHFGRLRQADPLRSGVQDQPGQ QGETPSLLKIQKFPRRDGGRL*SQLP RKLRQENCFNRGGGDCSEPRLCFPL PAWATERNVKGKERKEKK |
| 514 | 6011 | A | 530 | 110 | 369 | CWLSCCLEVRSCLYTFLSAYNFKCV LTI*HTFFVFFWSLCVYYFFIVLCCL VLVWCLSSLYYGIIVYYLYFCYSLFI VLGYGILAV |
| 515 | 6012 | A | 531 | 268 | 331 | QM*TAKCARCEGLGLITLCLDCIVA NTLLVPNGETSWTNTNHLTLQVW LKDGYIGWGLMALCTGIAPVLAGG KDCCGARRCGNR*QMLRYDFS*AL VVLGAIYWLS |
| 516 | 6013 | A | 532 | 807 | 1060 | SWHFGRLRWADYLRPGAGDQLSQ HGEISSLLKTQKLPGCGDTHL*SQLL GRLRQENHLNLGGGGCSEPRSHHC TSAWVTERDSV |
| 517 | 6014 | A | 533 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 518 | 6015 | A | 534 | 38 | 550 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF VDSFGNLSSA\SAIMGNPVKAHGK KVLTSLG\DAIKHLE*SQGAPFAQA *SELH\CDKPALDPGGTFKLPGENV AGLTVFGQSHFRAKEFHP*RLQAS WHKQKMAEDGDLELASALVPSRY H |
| 519 | 6016 | A | 535 | 2 | 348 | ARAGAGRLRRAASALRLLSPRLPVR ELSSLARLYPHRVDDHYENPTNAGS LD*TSKNVGTGLQLAPA*GDVVKL QTLVDEKVKNVDARFKTLGCGSAI AYSSLATEWVTGKTADE |
| 520 | 6017 | A | 536 | 385 | 536 | RMSAGALFIGYCIYFDHKRRSDPNF KNRL*DGRKKQKLAKERAGLSKLP D |
| 521 | 6018 | A | 537 | 123 | 705 | AAPTALRVRGPPLLRGPCRHRPRSA FVEKMVGRNSAIAAGVCGALFIGY\ CIYFDPQKTK*TPTFKNRLRERRKK QNLCQRRELGLSKLPDLKDAESCC RKFFL*RNTSLGEELLSFDG*/YEY*E RAVDHLDKLP\IAVCGQPPQQLLQV LQQTLP\PPPVFQMLLTKLPTISQRIV SAQSLAEDDVGMRNKCLH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 522 | 6019 | A | 538 | 1 | 430 | |
| 523 | 6020 | A | 539 | 42 | 373 | |
| 524 | 6021 | A | 540 | 1 | 430 | QQLQRLVHPDFFSQRSQTEKDFSEK HSTLVNDAYKTLLAPLSRGLYLV* SS/YGIEIPERTDYEMDRQFLIEIMEI NEKLAEAESEAAMKEIESIVKAKQK EFTDNVSSAFEQDDFEEAKEILTKM RYFSNIEEKIKLKKIPL |
| 525 | 6022 | A | 541 | 24 | 452 | APSPDAMG/HSLWGVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 526 | 6023 | A | 542 | 38 | 547 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIKHLDDLKGTFAQA *SELH\CDKAALLDPENFKLPGGNV AG*PVFGQSHFRAKEFHPWRLQGFP GISRRWQKMVTWSWPVPCSSRYH |
| 527 | 6024 | A | 543 | 328 | 495 | NLGANNCSLLGIGLLKGSMGRLW PKAFSAG*KQGLQNQRKHTALVKIE DVDA*GE |
| 528 | 6025 | A | 544 | 154 | 340 | PGLLKAIIWGIAYLRATYWTYVLA DLHPFADMLHAGYSITSEVEQPVLA VQLTYNPDES*WP |
| 529 | 6026 | A | 545 | 124 | 323 | EVKSVYLVYILSNRFF*CTYMHILV YYVYFIGLTI*LEEHSMLVYQNLVH YFLVFNVGIIYLLYL |
| 530 | 6027 | A | 546 | 314 | 445 | SPILLQFTVVLTRYLFTKIQFIYFFET ESCSIAQARV*WCDLG |
| 531 | 6028 | B | 547 | 1 | 1011 | MDLKFNNSRKYISITVPSKTQTMSP HIKSVDDVVVLGMNLSKFNKLTQF FICVAGVFVYLIYGYLQELIFSVEG FKSCGWYLTLVQFAFYISIFGLIELQL IQDKRRRIPGKTYMIIAFLTVGTMG LSNTSLGYLNYPTQVIFKCKKLIPV MLGGVFIQGKRYNVADVSAACMS LGLIWFTLADSTTAPNFNLRVLYSY SIGFVYILLGLTCTSGLGPVTFCAK NPVRTYGYAFLFSLTGYFGISFVLA LIKIFGALIAVTVTGRKAMTIVLSFI FFAKPFTFQYVWSGLLVVLGIFLNV YSKNMDKIRLPSLYDLINKSVEARK SRTLAQTV* |
| 532 | 6029 | A | 548 | 244 | 1408 | SRHNGMDLTQQAKDIQNITVQETN KNNSIESKJITMDLKFNNSRKYIS ITVPSKTQTMSPHIKSV*RVVVLGM NLSKFNKLTQFFICVAGVFVYLIY GYLQELIFSVEGFKSCGWYLTLVQ FAFYISIFGLIELQLIQDKRRRIPGKTY MIIAFLTVG\TMGLSNTSLGYLNYPT QVIFKCKKLIPVMLGGVFIQGKRYN VADVSAACMSLGLIWFTLADSTTA PNFNLTGVVLISLALCADA VIGNVQ EKAMKLHNASNSEMVLYSYSIGFV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | YILLGLTCTSGLGPAVTFCAKNPVR TYGYAFLFSLTGYFGISFVLALIKIF GALIAVTVTGTRKAMTIVLSFIFFAK PFTFQYVWSGLLVVLGIFLMFTAKI WDKIRLPSLV |
| 533 | 6030 | A | 549 | 66 | 346 | IQQLPTFFHIFSIFLIR*FFYMKGFR* LVLFYCPHVYA*SYFSLFFCSLTI* FISFSLYFTLFLFFFTFLFICVLAMFI FFELHLSYIP |
| 534 | 6031 | A | 550 | 21 | 337 | GPEAQCPDQPPPWLSFQGLPQGT WATHSAPCSPNLTSSWCPDSEPGR AGGRGRPPTLDHDAPTTPL*PSKP HPCIPQALPSSRTLRLYATPRQHAA TQCTP |
| 535 | 6032 | A | 551 | 526 | 771 | PPPLGVPGTLQFLRPRAAVLIGSKLL RPGRFCRWIFSPLLLVNISWLGTVV HACNPSTLGDQGGGRIT*G*EFETSLP TWRNS |
| 536 | 6033 | A | 552 | 305 | 569 | KKPLKGEKGGSLKTRPSFKKPD YLLKKSVMGFL*TNPEQFKKEIRNTIPLI KGASSSSSSKTNLGINLTKVVKDLN NENSRTLLRQS |
| 537 | 6034 | A | 553 | 90 | 339 | EVSALPDLPVMLAGPTP*PSFPRT SYFSAPPLLLPLSCSFLLPLPMPHSC PPSSSPSPSLLLLSITPSPAPSPFLLF P |
| 538 | 6035 | A | 554 | 1179 | 1408 | GYPVGKRRRLGERQGPQPPTLLPCD KEAERGEHIYTYFIYILYI*YIYNIYII YIYNIYIHIYIYIYIHTYIYI |
| 539 | 6036 | A | 555 | 722 | 991 | SQHFWRPRQVNHVSLGVQDQHGQ HSENPVSTKIYIYIQKLARCSDRCL* S*LLRRLRHENHLNLGGGGCSELKS CHCTPAWATE*DPVSK |
| 540 | 6037 | A | 556 | 1 | 362 | GTSRQVCREHSFQSVKLSAGARSW CFLSHWDPAGEVSLTDCSEIFLPFLG MAAVYHYFSINIFFKTSFFRLILY** SYFHLFLYYSILCLFILLFIIFYYC YILFISNLFTIIFLFL |
| 541 | 6038 | A | 557 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDSFGNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 542 | 6039 | A | 558 | 38 | 497 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIKHLDDLKGTFAQA *SELALVDKLACGILENFKAPGEML LVTRFWQSHFRQKNFTPEGCKASW AERWVW |
| 543 | 6040 | A | 559 | 1 | 414 | FETVSLLLLRLEHTGTISTHCNLR GSNDSAASAS*VAGTTSVCHHTGLI SVFSIETEFHHVGQTGLELLTSSDPL TSASPGAGIKGGSHCAQSPICFRGN NEMNYQATGIYSKSEIFFCLGYVTM SRCLTSQSGS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 544 | 6041 | A | 560 | 178 | 334 | NVCRLPVTNAESDAMINDAIRPINF TGFLTMFA*NLTGADPADVILAAFD VL |
| 545 | 6042 | A | 561 | 322 | 649 | |
| 546 | 6043 | A | 562 | 3 | 452 | |
| 547 | 6044 | A | 563 | 24 | 587 | GIPQTQREPTMVLSPADKTNVKAA WGKVGAHAGEYGAEALERMFSLF PTTKTYFPHFDSLHGSAQVKGHGK KVADALTNAVAHVDDMPNALSAL SDLHAHKLRVDPVNFKLLSHCLLV TLGAHLPAEFTPAVHA\SLDKFLAS VSTGL\TSKYPLSWSPRWPCFLAPW ASPQPLLPPAPVPPWSLK |
| 548 | 6045 | A | 564 | 3 | 474 | |
| 549 | 6046 | A | 565 | 1099 | 1243 | |
| 550 | 6047 | A | 566 | 425 | 943 | MGRSAPVEISYETMRFMTRNPTN ATLNKFTEELKKYGVTTLVRCDA TYDKAPVEKEGIVLDWPFDDGAP PPNQIVDDWLNLLKTK\FREGARVC CVA\HCVGRVGE GAPVL/VLALAL DWNVGMK\YEDAV\QFIRQKRRGA FNSKQL\LYLEEYRPMRLRFRDTN GHC\CVQ |
| 551 | 6048 | A | 567 | 1 | 441 | |
| 552 | 6049 | A | 568 | 1 | 890 | MSKSESPKEPEQLRKLFIGGLSFETT DESLRSHFEQWGTLTDCVVMRDPN TKRSRGFGFV TYATVEEVDAAMNA RPHKVDGRVVEPKRAVSREDSQRP DYFEQYGKIEVIEIMTDRGSGKKRG FAFVTFDDHDSVDKTVIQKYHTVN GHNCEVRKALSKQEMASASSSQRG RSGSGNFGGGRGGGFGGNDNFGRG GNFSGRGGFGGSHGGGGYGGSGDG YNGFGNDGSNFGGGGSGYNDFGNY NNQSSNFGPMKGGNFGGRSSGPYG GGGQYFAKPRNQ/GGYGGSSSSSY GSGRRF |
| 553 | 6050 | A | 569 | 579 | 2102 | SPKEPEQLRKLFIGGLSFETTDESLR SHFEQWGTLTDCVVRFRD KAVKQ PISLAYLGAVFSECL*K*LIAL*LELC WQRNVLL*F*KLTS*I*G*WETGRTF YKRLV*SFLLPYSKLL*QKLLRSDF VLHKLTLFSG\MRDPNTKRSRGFGF VTYATVEEVDAAMNARPHKVDGR VVEPKRAVSREVS GFFFFFLNLLG YVLL*T*DSGVF*TYQNFLFEYRLC* SKPMVFLLL\DSQRPGAHLT/V*KKI FVGGIKRRHLKEHHLRDYFEQYGK IEVIEIHDLTRGSGKKRGFAFVTFD DHDSVDKIVSKYQIVAFSGSTICM AF*TLIPCCIVVFLVQKYHTVNGH NCEVRKALSKQEMASASSSQRGML VA*LNLKGNFELLQYE*FNA*TSCL KV/ESGSGNFGGGRGGGFGGNDNF GRGGNFSGR/GYVWFIYM*F*LLTIF AMKILQYGNCIQNVTLSPSHT*NLK LFLTGGFGGSRGGGGYGGSGDGYN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GFGNDGKFFRNK |
| 554 | 6051 | A | 570 | 250 | 381 | |
| 555 | 6052 | A | 571 | 249 | 468 | PNQRLKWKS*LMGQGRG*KWKLL VLFYHKA*RMWPA\CCLDLGLGTG \CTC\CLLVYANWLHLLFLCLCPYP WLS |
| 556 | 6053 | A | 572 | 2 | 488 | QEPAHDLRMYGKIIFVLLLSEIVSIS ALSTTEVAMHTSTLLPSSHKRVTSS S\QTNGETGTTCPIVSLYPAPCSDNT HYFVCDGWYYWNDPLNFLLYSMT DKGMRMWPACCLILPRITSCTCCSL AYANWLHL\FL\CLCPYPWAILNS LFSWPSLITGILYF |
| 557 | 6054 | A | 573 | 7 | 412 | |
| 558 | 6055 | A | 574 | 3 | 479 | NWELLWLLVLCALLLLLVQLLRF LRADGDLTLLWAEWQGRPE/WEL TDMVVWVTGASSGIGEELAYQLSK LGVSLVLSARRVHELERVKRRCLE NGNLKEKDILVLPLDLTDTGSHEAA TKAVLQEFGRGFFNGLRTELATYPG IIVSNICPGPVQSN |
| 559 | 6056 | A | 575 | 1 | 321 | |
| 560 | 6057 | A | 576 | 2 | 1243 | GAASAEPGAPEPLLLPACSLGGAGA VRLWAGRRGGAAIPQGSATLVRA VFFPPSWACAAAMNWELLWLL\V LCDVLLLVLVQLL\RFLRADG\DLTL LWAEWQG/RDRPEWELTDMVVW VTGASSG/ILGEELAYQLSKLGVSL VLSARRVHELEKGEKERCL\ENGQF LKEKDITLFLPLDLPTLGSH*SRLT KAVLQEVLRIDILGSTMVGM\SQR SL\CMDTSLDVYRKL\ELNYLGTVS LTKC\VLPHMIERKQKIVTVNSILG IISVPLSIGYCASKHALRGFFNGLRT ELATYPGIIVSNICPGPVQSNIVENSL AGEVTKTIGNNGDQSHKMTTSCV RLMLISMANDLKEVWISEQPFLVT YLWQYMPTWAWWITNKMGGKKRIE NFKSGVDADSSYFKIFKTKHD |
| 561 | 6058 | A | 577 | 175 | 354 | |
| 562 | 6059 | A | 578 | 2018 | 2182 | |
| 563 | 6060 | A | 579 | 140 | 287 | MVKRNQCPSLPPN*KMRSQGSTCQ PHCQRWLPSTRSYTHPLKARPWSA S |
| 564 | 6061 | A | 580 | 357 | 760 | |
| 565 | 6062 | A | 581 | 182 | 459 | |
| 566 | 6063 | A | 582 | 1 | 382 | |
| 567 | 6064 | A | 583 | 3 | 406 | |
| 568 | 6065 | A | 584 | 173 | 415 | |
| 569 | 6066 | A | 585 | 2 | 424 | |
| 570 | 6067 | B | 586 | 108 | 395 | VGAHAGEYGAEALERMFLSFPTTR TYFPHFDLSHGFCPGLRGHGQEGGR RADQRRGARGTTCPTSLSALSDLHA HKLSSGTRFNFQAPKATGLLG* |
| 571 | 6068 | A | 587 | 379 | 579 | |
| 572 | 6069 | A | 588 | 2 | 366 | SLPASDRPPISSPLATSGTIFSAISCF WDLPAFLWLAPSCQPTMSSQIRQN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART |
| 573 | 6070 | B | 589 | 220 | 480 | MSSQIRQNYSTDVEAAVNSLVNLY LQASYTYLSLGFYFDRDDVALEGV SHFFRELAEEKREGYERLLKMQNQ AWRPRSLPGHQEAS* |
| 574 | 6071 | A | 590 | 142 | 383 | |
| 575 | 6072 | A | 591 | 1 | 308 | |
| 576 | 6073 | B | 592 | 195 | 326 | MMGVLDGVLMELODCALXLLKDV IATDKEDVAFKDLDVAILVV* |
| 577 | 6074 | A | 593 | 5 | 1199 | PDSLRLILHLFKLSPQFSIMSEPIRVL VTGAAGQIAYSLLYSIGNGSVFGKD QPIILVLLDITPMMGVLDGVLMELV RLCPSPPERCGNGSVFGKDQPIILVL LDITPMMGVLDGVLMELODCALPL LKDVIAITDKEDVAFKDLDVAILVGS MPRREGMERKDLLEY/ADV KIFKSQ GAALDKYA\QKSGKVIVGGNPANT DCLTASKPAPCIPKENFSCLTRLDH NRAKAESGLRLVVT AHDGQNGIHW GNHSSTQYPDVNHAKVKLQGKEV GVYEALKDDSWLKGEFVTTVQQR GAAVIKARKLSSAMSAKAICDHV RDIWFGTPEGEFVSMGVISDGNSYG VPDDL LYSFPVVIKNKTWKFVEGLP INDFSREKMDLTAKELTEEKESAFE FLSSA |
| 578 | 6075 | A | 594 | 46 | 298 | |
| 579 | 6076 | A | 595 | 982 | 1193 | |
| 580 | 6077 | A | 596 | 69 | 399 | VSNYPTVGCCIFLQIRARNPAFQPQT LMDFGSGTGSVTW*VTFFSPILVNF SSRKPYLHHSKINRLENQRENQVG NL*CFFHQIRQGRRRYMDWGQNLK EMSSKKRRMY |
| 581 | 6078 | A | 597 | 600 | 887 | |
| 582 | 6079 | A | 598 | 813 | 973 | |
| 583 | 6080 | A | 599 | 166 | 437 | ADHLKSGV*DQPGQHGEILSLLKLQ *FPGRGGAHL*SQLLGRLKQENHLN PGGGGCSEPR LCHWTPVRATVGDS VQKK*KSQDGPRAKLG |
| 584 | 6081 | A | 600 | 3 | 238 | SGDRDHPG*HSETLSLLKIQQVAGR GGGRL*SRLRLRLRQENGVSPPGGG ACSEPRSHHCTPAWETERDSVSKK KKKKL |
| 585 | 6082 | A | 601 | 4005 | 4345 | SQHFGRRPRADHLRSGVQDQPDQH GETPSLLGGRGGRITKSGDRDHPG* HGETPSLLKMQ/EKLAGRGGGRLW SLLGRLRQENGVSPPGGRACSEPRS CHCTPAWLTEQDSVSKK |
| 586 | 6083 | B | 602 | 1 | 9234 | MGAPTLPPAWQPFLKDHRISTFKN WPFLEGCAC TPERMAEAGFIHCPT NEPDLAQCFFCFKELEGWEPDDPI EEHKKHSSGCAFLSVKKQFEELTLG EFLKLDRE RAKNKIAKETNNKKKEF EETAKKVRRAIEQLAAMD* |
| 587 | 6084 | A | 603 | 1577 | 2233 | SGCLLSPPSVGRQNSPVELGGAGLS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; v-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RAGWAPQERGRAALLISPGPNVR GGPDWLPSVLQMRGLPLWDLGGRP DVGRMSPGGRPGSCWATQLRFHIS LAPLFSWAGRSGSRLNPSTLGGRGG PITRSGDRDHPG*HGETLSLLKIQKI SQACWR/CACSPSYGRLRQENGVP GGGACREQRS GHCTPAWATEQDSV SKKKKKKSGSTIRLKHILHKII |
| 588 | 6085 | A | 604 | 151 | 454 | FQKIGPGAVAHACNPSTLGGRSRRI TRSGGRDHPG*HSETPSLLKIQKLA GRGGGCL*SQLLWRLRQENGVPNG GGACSEPRSRHCTPAWVTERDSVS KKK |
| 589 | 6086 | A | 605 | 1362 | 1647 | |
| 590 | 6087 | A | 606 | 10289 | 10708 | SQHFGKLRQEDHLRSGVREQPGQH GKTPYLLKIQKLARRSGACL*SQLL RRLRQENRLNPGGVGCSEPR LHHC TTAWTLQ*DPVSKKLKKKYIERQR YHQHMKHPWSTKIQYVCMDG*HR SVEKQIIQTLCMFVFTHTY |
| 591 | 6088 | A | 607 | 709 | 980 | |
| 592 | 6089 | A | 609 | 234 | 381 | PPWTQFSLSCVCLL/CSRPA/VSAWR QARENESQAKGETAYETITSCENRS H |
| 593 | 6090 | A | 610 | 1 | 1755 | |
| 594 | 6091 | A | 611 | 1128 | 1321 | |
| 595 | 6092 | A | 612 | 650 | 800 | |
| 596 | 6093 | A | 613 | 149 | 475 | |
| 597 | 6094 | A | 614 | 1 | 801 | |
| 598 | 6095 | A | 615 | 1284 | 1386 | |
| 599 | 6096 | A | 616 | 20 | 3888 | |
| 600 | 6097 | A | 617 | 204 | 411 | |
| 601 | 6098 | A | 618 | 1 | 1468 | |
| 602 | 6099 | A | 619 | 48 | 178 | |
| 603 | 6100 | A | 620 | 79 | 1953 | LQVGTASSLLLSRVFGDRGYSPET RKCPKPINVRVTMDAELEFAIQPN TTGKQLFDQVVK TIRPSRQVWYFAG LHYVD\NKGFTWLKLDKKVSAQ EVRKKNPLQFKFR/APKFYPÆDVA\ EELIPGTFTQKLFFLQVEGRESLSDE DLLAPLETGRALWGSYACASPRLG DYNK/EKLHKSGVPSASERLIPQRV MDQHKLTRDQWEDRIQVWHAHR GMLKDNAMLEYLKIAQDLEMYGIN YFEIKNKKGTDLWLGVDALGLNIY EKDDKLTPKIGFPWSEIRNISFNDKK FVIKPIDKKAPDFVFYAPRLRINKRI LQLCMGNHELYMRRRKPD TIEVQQ MKAQAREEKHQKQLERQQLETEK KRRETVEREKEQMMREKEELMLRL QDYEEKTKKAERELSEQIQRALQLE EERKRAQEEAERLEADRMAALRAK EELERQAVDQIKSQEQLAAELA EYT AKIALLEEARRRKEDEVEEWQHRA KEAQDDL VKTKEELHLVMTAPPPP PPPVYEPVSYHVQESLQDEGA EPTG YSAELSSEGIRDDRNEEKRITEAEKN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ERVQRQLVTLSSSELSQARDENKRTH NDIIHNENMRQGRDKYKTLRQIRQ GNTKQRIDEFEAL |
| 604 | 6101 | A | 621 | 269 | 361 | |
| 605 | 6102 | A | 622 | 210 | 367 | ISQSGDCCSVWLSLQGPPKGCPKP/ PSPGLQPRATPPA*VQQRTHPMSC SN |
| 606 | 6103 | A | 623 | 1792 | 1935 | |
| 607 | 6104 | A | 624 | 9 | 326 | |
| 608 | 6105 | A | 625 | 250 | 381 | |
| 609 | 6106 | A | 626 | 155 | 457 | NQKELGNTPRYPLEASNWLQPVKD WPVTNQRLKWKS*LMGQGRG*KW KLLVLFYHKA*RMWPA\CCLDLGL GTG\CTC\CLLVYANWLHLLFLCLC PYPWLS |
| 610 | 6107 | A | 627 | 2 | 488 | QEPAHDLRMYGKIIFVLLLSEIVSIS ALSTTEVAMHTSTLLPSSHKRVTSS S\QTNGETGTTCPIVSLYPAPCSDNT HYFVCDGWYYWNDPLNFLLYSMT DKGMRMWPACCLILPRTSCTCCSL AYANWLHLALFL\CLCPYPWAILNS LFSWPSLITGILYF |
| 611 | 6108 | A | 628 | 2 | 364 | |
| 612 | 6109 | A | 629 | 946 | 1142 | LSGIIHYSFFTIRNIKALFSLC*VFQF GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIHFIA |
| 613 | 6110 | A | 630 | 946 | 1193 | LSGIIHYSFFTIRNIKALFSLC*VFQF GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIHFIA*SAFPVQGLLFRS WNL |
| 614 | 6111 | A | 631 | 946 | 1142 | LSGIIHYSFFTIRNIKALFSLC*VFQF GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIHFIA |
| 615 | 6112 | C | 632 | 294 | 710 | MVRSRQMCNTNMSVPTDGAVTTS QIPASEQETLVRQESDYSQPSTSSSI IYSSQEDVKEFEREETQDKEESVESS LPLNAIEPCVICQGRPKNGCIVHGKT GHLMACFTCAKKLKKRNKPCPVCR QPIQMIVLTYFP* |
| 616 | 6113 | C | 633 | 822 | 1149 | MLVLHICLLLTI RGFRAW SRGSLKT PQFPSRGLTTAEARRPGPRGSFHSPG QGTGRSYALIRGGTVLLAAKAAGS RSEGSRPPLGLGFLHLSDTQGHGTG PRSSQARAV* |
| 617 | 6114 | A | 634 | 5 | 76 | |
| 618 | 6115 | A | 635 | 269 | 354 | |
| 619 | 6116 | A | 636 | 184 | 299 | FFCTFSTDGVSPC*PGWSRSPDLVIH SPRPPKVLGLQA |
| 620 | 6117 | A | 637 | 3 | 307 | ESCSEAQAGVQGAQSWLTATSSFQ VHAILLPQPPK*LGLQVPATTPG*FF VFLVETGFHCVSQDGLKLQTS*SAH LGLPKCWDYRHEPLRPAKKQLFKN VP |
| 621 | 6118 | A | 638 | 2 | 131 | SKAALTGSGPGP/IPLCFVSAVLAPFI RPS*SLLAGRGLDGGQD |
| 622 | 6119 | A | 639 | 1 | 822 | |
| 623 | 6120 | A | 640 | 1258 | 1454 | LSGIIHYSFFTIRNIKALFSLC*VFQF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIHFIA |
| 624 | 6121 | A | 641 | 248 | 386 | SARLSLPKIWDYRREPLHPARSFFIY SSSSILY*S*LVSITALLF |
| 625 | 6122 | A | 642 | 132 | 243 | LGLQVPATAPG*IFFVFLVETGFHH VSQDGLDLLTS |
| 626 | 6123 | A | 643 | 397 | 954 | |
| 627 | 6124 | A | 644 | 1 | 1388 | |
| 628 | 6125 | A | 645 | 2285 | 2409 | |
| 629 | 6126 | A | 646 | 36 | 224 | |
| 630 | 6127 | A | 647 | 242 | 933 | YGESKDOWNQKDLLSALVLTTVNCL PTPIMAKSAEVKLAIFGRAGVGKSA LVVRFLTKRFIWEYDPTLESTYRHQ GNHSMMEVVSMGGY*DTAGQEDTI QREGHMRWGEGFVL\VYDIT*PRKF LKEVLALKEHLDEIKKPKNVTLILV GNKADLDHSRQVSTEEGEKLATEL ACAFYECSACTGEGNITEIFYELCRE VRRRRMVQGKTRRRSSTTHVKQTI NEMLTKISS |
| 631 | 6128 | A | 648 | 596 | 709 | |
| 632 | 6129 | A | 650 | 1 | 367 | |
| 633 | 6130 | A | 651 | 135 | 307 | |
| 634 | 6131 | A | 652 | 170 | 372 | |
| 635 | 6132 | A | 653 | 3 | 320 | |
| 636 | 6133 | A | 654 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 637 | 6134 | A | 655 | 52 | 518 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIHLDDLKGTFQAQLSE LHCDKLHVDPENLKLGNVLETAL AIQFRRKNSPL*GQASWQKMVTGV ASALSSRYH |
| 638 | 6135 | A | 656 | 123 | 219 | |
| 639 | 6136 | A | 661 | 413 | 545 | |
| 640 | 6137 | A | 662 | 4 | 350 | |
| 641 | 6138 | A | 663 | 1034 | 1091 | |
| 642 | 6139 | A | 664 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 643 | 6140 | A | 665 | 38 | 602 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHG KKVLTSLGDAIKHLDDLKGTFQA A*SELHL*QSCNVDPENFKAPGEM LLVTR/VLAIPFSAKEFTPEGCRASW AERWVTCSWPVALFLQDTTEAQLP MNAELFKDKAFILASNYK |
| 644 | 6141 | A | 666 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 645 | 6142 | A | 667 | 38 | 536 | APSPDA\MGHFTEEDKAT\TSLWCK VNVE\ DAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHG KKVLT\SLGDAIKHLDDLKG\TFAQ A*SEL\HC*QAGMWDPENFKLLGE MLLVTRFGQSHFRQKNFTPEVARL SWAERWVTWSWPSALVPSRYH |
| 646 | 6143 | A | 668 | 132 | 357 | |
| 647 | 6144 | A | 669 | 1 | 89 | |
| 648 | 6145 | A | 670 | 136 | 594 | LNRVAFLPGA AVILIGHLHTHTGPS GVCNVSMRGFSSPAGWPTGSHRG KERPAGRLMHRMGWSAVEWTG\ AQGIPCISTCPERTGGDAATRSRPP VLPPPPRPPQRRCRHLVSRAGTPRC ACAGTLTSKRGTHWRSTELLRRSP LRSSQ |
| 649 | 6146 | A | 671 | 400 | 696 | |
| 650 | 6147 | A | 672 | 120 | 352 | |
| 651 | 6148 | A | 673 | 276 | 401 | |
| 652 | 6149 | A | 674 | 139 | 470 | |
| 653 | 6150 | A | 675 | 136 | 1058 | GVVGAAASGAGSRKAGLAGVPGPP GRANRESPPGPVAMGRVIRGQRKG AG\SVFRAHV KHRKGAARLRAVDF AERHGYIKG\IVKDIIHDPGRGAPLA KV\VFRDSYRFFKKRTEL\FIAAEGNH TGQF\VYCGKKAQLNIGNVLPVGT\ MPEGTIVC/CALEEKP\GDRGK\LAR ASGNY\ATVISHNP\ETKKT\RVKLPF RVQRRLSPSANKSLWLVLVAGGWP ECDKPILKAGRAVPQI*RQKRNCW VPRVTGVWAMNPF EAFFLKGGNPPA HRQSPPIRRDAPAGRKVGLIAARR TGRLRGTKTVQEKEN |
| 654 | 6151 | A | 676 | 21 | 340 | |
| 655 | 6152 | A | 677 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 656 | 6153 | A | 678 | 38 | 529 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIK\HLDDLKGTFQA DVNLHC*QACMLDPENFQASWGN VL\VTRFWAIPFSGKEFHP*RCQAFL GRKMGDLELASALVPSRYH |
| 657 | 6154 | A | 679 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | EVQASWQKMVTGVASALSSRYH |
| 658 | 6155 | A | 680 | 3 | 545 | HSLFGTSEVINKLRSPDAMGHFTEE DKATITSLWGKVNVE\ DAGGETLGR LLVVYPWTQ\RFFDSFGNLSSASAIH GOPPKSRHMGKKVLTS\LGDAIKHL \DDLKGHLLPKPEVKLH\CDKAALL DPEELSSFLGEMLLGDPFLGNPIFGQ KNFTP\AEVARLSWAERWWTWSWPS ALVPSRYH |
| 659 | 6156 | A | 681 | 1 | 432 | |
| 660 | 6157 | A | 682 | 334 | 845 | AVRVRYVAFRYRAPRAVCLRLWSC RREVIHVPVRGKQGGKVRAKAKIS RSSPRGPCRFPVGPSCTELLRKIGNY AER/MSGAGAPV*LGGRCLKYLTAE IPEAWLANAAA*QORRPRIIPRHLAS SPIRNDEGS*TKLLGQKLTAQGGV LPNIQ\AVLLPKKDGESEGRRSK |
| 661 | 6158 | C | 683 | 392 | 445 | MQPAVQRVGNLSRYFPS* |
| 662 | 6159 | A | 684 | 183 | 481 | |
| 663 | 6160 | A | 685 | 253 | 385 | |
| 664 | 6161 | A | 686 | 256 | 374 | |
| 665 | 6162 | C | 687 | 354 | 416 | MKESPGGELPQTGKKPVFLF* |
| 666 | 6163 | A | 688 | 2 | 171 | |
| 667 | 6164 | A | 689 | 320 | 584 | TRLPFDRPRATGCHQVPSPERRSPIS QDRLTHVQLLFTWNPSP\LRPSKFSF EYLL\APRSCTCGGSHPGPKP*ASR LTAAALLLVAA |
| 668 | 6165 | A | 690 | 33 | 494 | |
| 669 | 6166 | A | 691 | 1 | 522 | PLKRSDGCNDGRPTRPPTRPDITVF TSNLKQTRMVHL\TPEEKSAVTALW GKVNVD\EGGKALGRLL\VVYPW\ TQRF\ESFGDLSTP\DA\VMGNPKV KAHSKKVLRGAF\SDGLAHL\DNLK GTFAHTEVSLHCDK\LVDP*RTFR LLGQRAW SVVAGPIHFWQKNFNPT SCRLA |
| 670 | 6167 | A | 693 | 241 | 1104 | |
| 671 | 6168 | A | 694 | 95 | 462 | |
| 672 | 6169 | A | 695 | 33 | 494 | |
| 673 | 6170 | A | 696 | 1 | 523 | PLKRSDGCNDGRPTRPPTRPDITVF TSIAHTDTMVHLTPVEKSAVTALW GKVNVD\EGGKALGRLL\VVYPW\ TQRF\ESFGDLSTP\DA\VMGNPKV KAHSKKVLRGAF\SDGLAHL\DNLK GTFAHTEVSLHCDK\LVHRSGLKNFR LLGQRAW SVVAGPIHFWQKNFNPT SCRLA |
| 674 | 6171 | A | 697 | 318 | 515 | |
| 675 | 6172 | A | 699 | 2 | 648 | |
| 676 | 6173 | A | 700 | 137 | 507 | |
| 677 | 6174 | A | 701 | 118 | 375 | VAVVQIIFLPVFIAEKYKDLVPDnsk TADNATKNAEPLINLDVNNPDFKA GVMALANLLQIQRHDDYL VMLK\A IRLVQERLTQD |
| 678 | 6175 | A | 702 | 1 | 969 | AATVLTITIGEAPSRSDSAPARPLAA SPVPAPPAPPRFFSPGRGPVDQSEKR WTMFRKLTSLDYHNPAGFNCKD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ETEFRNFIVWLEDQKIRHYKIEDRG\NLRNIHSSDWP\FFEKYFKRC*TCPFKIQDRQESYLTGFFGLAVRLEYGDNAEKYKDLVPD\NSKTA*QLQLKIAEPLINLDVNNP\DFKAGVVGFG*TWLQIQRH\DG\LP\GQMLKANS\GF\WVQERLDHQGCQFA*GQIKQKRGLPVALDKHILGFD\TGDAVLNEAAQILRLHIEELRELQTKINEAIVAVQAIADPKTDHRLGKSLEDEHLRTSASHLL |
| 679 | 6176 | A | 703 | 105 | 1591 | |
| 680 | 6177 | A | 704 | 110 | 431 | |
| 681 | 6178 | A | 705 | 171 | 1577 | GGNRATIQAGQCGNQIGAKFWGR*SVNEHGIRPHRHP\THGDS\DPAAWT RNPPVYYNESHKVGK\YVPR\AILG GI*EPGEPWDSVR\SGSFLGPPKGEKI FPPFRPDNFVFGQSGAGNN\WAKRP LAQEGAEL\VD\SLDV\GTEGRQRS CD\CLQG\FFA*PTSLGRGGT\GSGMG TLLYQQGFEKEYPD\RIMN\TF\SVVP\ SPKCLDTVVQPYKATLSVHQLVEN TDETYCIDNEALYD\ICFRTLKL\TTP TYGDLNHLVSATMSGVTTCLRFPG QLNADLRKLAVNMVFPRLHFFMP GFAPLTSRGSQQYRALTVPELTQQV FDAKNMMAACDPRHGRYLTVA\AV FRGRMSMKEVDEQMLNVQNKNSS YFVEWIPNNVKTA\VC\DIPPRGLKM AVTFIGNSTAIQELFKRISEQFTAMF RRKAFLHWYTGE\GMD\EMEFT\EAES NMNDLVSEYQQYQDATAEEEEEDFG EEAEAEA |
| 682 | 6179 | A | 706 | 1 | 558 | |
| 683 | 6180 | A | 707 | 1306 | 1459 | LASMCMCWIESHFCPPGPTGGSRRG PP/HLWLPGRSSGRSQRRLAESTEAP R |
| 684 | 6181 | A | 708 | 1073 | 1324 | |
| 685 | 6182 | A | 709 | 1 | 797 | |
| 686 | 6183 | A | 710 | 1 | 3210 | MVKGSIQQEELTILNIYAPNTGALRF IKQVLRDLQRDLDSHTIIMGDFHTP LSTLDRSTRQKVNKDIQELNSALHQ EDLIDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEITNC LSDHSAIKLELRIKNLTQNRSTTWK LNNLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTFKAVCRGKF IALNAHKRKQERSKIDTLTSQ\KEL EKQEQT\HSKASRRQEITKIRAE\KEI ETQKTLQ\NINESRSWFFERINKIDRP LARLIKKKREKNQIDA\KNDKGDIT TDPTEIQTTIREYYK\HLYANKLENL EEMDKFLNTYTLPTLNQEEVESLNR PITGAEIVAINSLPTKKSPGPDGFTA EFYQRYKEELVPFLLKPFQSIEKEGI LPNSFYEASIIIPKPRD\TTK\KENFR PISLMNIDAKILNKILAKRIQQHIKN LIHHDQVGFIPGMQGWFNIRKSINVI QHINRAKDKNHMIISIDAEKAFDKI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QQPFMLKTLNKLDDMIVYLENPIVS AQNLLKLISNFSKVSGYKINIQKSQA FLYTNNRQTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFK\ENHKPLL EIKEDTNKWKNIPCSWVGRINIVKM AILPKVIYR/FNAIPIKLPMFFTELE KTTLKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSERTPHIYNLY IFDKREKNKQWKGDSL FNKWCWE NWLAICRKLKLDPFLTPYTKINSRW IKDLNVRPKTIKLEENLGFTIQDIG MGKDFISKTPKAMATKAKIDKWDL IKLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSPSLAIREMQIKTTMRYH LTPVRMAIHKSGNNRCWRGCGEIG TLLHCWWDCCLVQPLWKA VWRFL RDLELEIPFDP AIPLLGIYPKDYKSC CYKDTCTRRKQLDCAEPVEPRKVG DGEWSLTKWTRPGSRALPWPPEQA KPYPPTLPTLAQDF |
| 687 | 6184 | A | 711 | 1 | 2666 | MVKGSIQQEELTILNIYAPNTGAPRF IKQVLSDLQRDLDSHTLIMEDFNT LSTLDRSTRQKVNKNTQELNSALH QADLIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEIITN YLSDHSAIKLELRIKNLTQSRSTTW KLNNLLLNDYWVHNEMKAEIKMF FETNENKDTTYQNLWDAFKA VCRG KFIALNAYKRKQERSKIDTLTSQK ELEKQEQTHSKASRRQEITKIRAE KEIETQKTLQKINESRSWFFERINKI DRPLARLIKKKREKNQIDTIKNDKG DITDPTEIQT TIRESYKHL YANKLE NLEEMDTFLDTYTLPRLNQEEVESL NRPITGSEIVAIINSLPTKKSPGPDGF TAEFY/PESYL*QTHRQYHTEWAKT ASIPFENWHKTGMPSLTTPIQHSVG SSGQGNQPGEGNKGYSIRKRGSSQIV PVCRRHDCLSRKPHRLSPKSP*ADK QLQQSLRIQNQCTKITSILIHQQQTN REPNE*TIHNCFKENKIPRNPTYK GCEGPLQGELOTTA QGNKRGHKQ MEEHSMMLMGRKNQYRENGHTAQQ NLQIQCHPHQATNDFLHRIGKNYFK VHMEPKKSPHRQVNPKEQSWRH HTT*LQTIQGYSNQNSMVL VPKQR YRSMEQNRALRNNAAYLQLSDL*Q T*EKQAMGKGFPI**MVLGKLASH M*KAETGSLPYTL YKNQFKMD*RF KR*T*NHKNPRRKPRHYH*GHRRG QGLHVQNTKSNGNKSQN*QMGSN* TKELLHSKRNYHQSEQATYNMGEN FRNLLI*QRANIQNLO*QTQNLQEK NKQPHQKVGEQHEQTLLKRRHLCS QKTHEEMLIITGHQRNANQNHYEIS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SHTS*NGNH*KVRKQQRQNS |
| 688 | 6185 | A | 712 | 1 | 4371 | |
| 689 | 6186 | A | 713 | 1 | 1849 | MVKGSIQQEELTILNTYAPNTGAPRF IKQVLSDLQRDLDSHTFIMGDFNTP LSTLDRSRREQEVNKDTQELNSALH QADLIDIYRTLHPKSTEYTFFSATHH TYSKIDHIVGSKAVLSKCKRTEITN YLSDHSAIKLELRIKKLTQNRSTTW KLNNLLNDYWVHNEMKAEINMF FETNENKDDTTYQNLWDTFKA/EIQA TIREYYK\HLYTNKLENLEEMDKFL DTYTLPRLNQEKVESLNRPTGSEIV AINSPLTKKSPGPDGFTAIFYQRYK EELVPFLKLFQSIEKEGILPNSFYEA SIILIPKGRDTTKKENFRPISLMNID AKILNKILANRIQQHIKKLIHHDQVG FIPGMQGWFNICKSINVQHINRTKD KNHMIISIDAEKAFDKIQQPFRLKTL NKLGVGDGTYLKIIIRAIYDKPTANIL NGQKLEAFPLKTGTRQGCPLSPLLF NIVLEVLARAIQKEKEIRDVKDLFK ENYKPLLKEIKEDTNKWKNIPCSW VGRINIMKMVILPKDSTWAEVLVG DRRSGRLTEMLVIFLVFQSFHSFLN TLMSLPSIFSSWPCFCSSQLVSLRT CRSVCLSSAAGVSRVASLGNQKKR DLGSENIL |
| 690 | 6187 | A | 714 | 1 | 1825 | MVKGSIQQEELTILNTYAAHTGAPR LIKQVLSDLQRDLDSHTIIMGDFNTP LSTLDRSTRQKVNKDTQELKSALH QADLTDIYRTLHHKSTEYTFFSAPH HIYSKIDHILGSKALLSKCKRTEITN YLSDHSAIKLELWIKNLTQNHSTTW ELNNLLNDYWVHNEMKAEIKMFF ETNENKDDTYHNLWDTFKA VCRG KFIPLNAHKRKQERSKIDTLTSQLKE LEKQEQTHSKASRRQETKIRAEK EIETQKTLQKINESRSWFFERINKID RLARLIKKKREKNQIDAIKNDKGD ITTDPTIEIQTIREYCKHLYANKLEN LEEMDKFLDTYTLPRLNQEEVESLN RPITGAIEIVAINSLPTKKSPGPDGFT AKFYQRYKEELVPFLKLFQSIEKE GILPNSFYEASIILIPKGRDTTKKEN FRPISLMNIDAKILNKKLAKRIQQHI KKLIHHDQVGFIPGMQGWFNIRKSI NVIQHINRAKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLGIKYLGIHLT RDVKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPKNILI TLQLLLVLPELSTLIPLWLPALAGQ |
| 691 | 6188 | A | 715 | 1 | 3552 | |
| 692 | 6189 | B | 716 | 1 | 3786 | MVKGSIQQEELTILNTYAPNTGAPRF IKQVLSDLQRDLDSHTLIMGDFNTP LSTLDRSMRQKVNKDTQELNSALH QVDLIDIYRTLHHKSTEYRFFSAPH HTYSKIDHILGSKALLSKCKRTEIT NYLSGHSIAIKLELKIKNLTQNRSTT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WKLNNLLNDYWIHNEMKAEIKM FFETNENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKAGRKKEITKIRAQ LKEIETQKTLKKLMNPGAEIQTIRE YYKHLIYAKKLENLEEMDKFLDTYT LPRLNQEEVESLNRPIITGAEIVAINS LPTKKSRTTRWIHSRILPEEASILIPKP GRDTTKKENFRPISLMNIDAKILNKI LAKRIQQHIKKLIHHDQVGFIPGMQ GWFNIHKSINVIQHINRAKDKNHHIS IDAEKAFDKIQQPFMLKTLNKLIGD GTYFKIIRAIYDKPTANILNGQKLE AFPLKTGTRQGCPLSPLLFNIVLEVL ARAIRQEKEIKGIQLGKEEVQLSLFA DEMIVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTRDV KDLFKENCKPLLNEIKEDTNKWKN PCSWVGRINIMKMAILPKVIYRFNAI PTKPPMTFFTELEKTTLKFIWNQKR ARIAKSILSQKNKAGGITLPDFKLYY KATVTKTAWYQYQNRDLQDQNR TEPSEITPHIYSYLIFDKPEKNKQWG KDSL FNKWCWENWLPICRKLKLD FLTPYTKINSRWIKDLNVRPKTIKTL KENLGITIQDIGMGKDFMSKTPKAM ATKDKIDKWDLIKLKSFC TAKETTI RVNRQPTKWEKIFATYSSDKGLISRI YNELKQIYKKKTNNPINKWVKDMN RHFSKEDIYAAKKHMKKCSSSLAIR EMQIKTTMRYHLTPLRMAIKKSGN NSASPTARNKTARNQRTKMIAVTA PRNRAPLELELILYRQNRQSKTHILE TNNTSAELLVPFEEDYLIEIRTVSDG GDGSSSEEIRIPKMSMIDHILPKSIPE ELQNGEGFGYIIMFRPVGSTTWSKE KVSSVESSRFVYRNESIPLSPFEVK VGVYNNEGEGSLSTVTIVYSGEDD GYVFLWMVEPQLAPRGTSLSQSFSA SEMEVSWNAIAWNRNTGRVLGYE VLYWTDSDSKESMIGKIRVSGNVTT KNITGLKANTIYFASVRAYN TAGTG PSSPPVNVTTKKSRYLITTAYLEVPE I* |
| 693 | 6190 | A | 717 | 2 | 3155 | |
| 694 | 6191 | B | 718 | 1 | 3414 | MVKGSIQQEELTILNIYAPNTGAPRF IKQVLSDLQRDLDSHTLIMGDFNPN LSTLDRSMRQKVNKDTQELNSALH QVDLIDIYRTLHHKSTEYRFFSAPH HTYSKIDHILGSKALLSKCKRTEIT NYLSGHSIAKLELKIKNLTQNRSTT WKLNNLLNDYWIHNEMKAEIKM FFETNENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKAGRKKEITKIRAQ LKEIETQKTLKKLMNPGAEIQTIRE YYKHLIYAKKLENLEEMDKFLDTYT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LPRLNQEEVESLNRPITGAEIVAINS LPTKKSRTTRWIHSRILPEVQGGTEK EGILPNSFYEASIIIPKPGRDTTKKE NFRPISLMNIDAKILNKILAKRIQQHI KKLIIHHDQVGFIPGMQGWFNHKS NVIQHINRAKDKNHIIISIDAEKAFD KIQQPFMLKTLNKLGDGTYFKIIRA IYDKPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLAIRAEKE IKGIQLGKQEVQLSLFADEMIVYLE NPIVSAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKENCK PLLNEIKEDTNKWKNIPCSWVGRIN IMKMAILPKVIYRFNAIPTKPPMTFF TELEKTTLKFIWNQKRARIAKSILSQ KNAAGGITLPDFKLYYKATVTKTA WYWYQNRDLQDWNRTPESEITPHI YSYLIFDKPEKNKQWGKDSL FNKW CWENWLPICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLKENLGITIQ DIGMGKDFMSKTPKAMATKDKIDK WDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIY KKKTNPNPINKWVKDMNRHFSKEDI YAAKKHMKKCSSSLAIREMQIKTT MRYHLTPLRMAIKKSGNNSASPTA RNKTARNQRTKMIAVTAPRNRAPL ELELILYRQNRQSKTHILETNNTSAE LLVPFEEDYLIEIRTVSDGGDGSSE EIRIPKMSTGGEEGMAAVFKNKCRC SWSRVVIAHSSSGNQMGTNPEQD PGQHAIPLEGTLTHTRTHSDWDHLD TAMN* |
| 695 | 6192 | A | 719 | 1 | 5127 | |
| 696 | 6193 | A | 720 | 965 | 9275 | |
| 697 | 6194 | A | 721 | 3 | 376 | |
| 698 | 6195 | A | 722 | 1 | 380 | |
| 699 | 6196 | A | 723 | 104 | 462 | |
| 700 | 6197 | A | 724 | 762 | 902 | |
| 701 | 6198 | A | 725 | 78 | 747 | LRRGRSRETNEEPPPPTVQVQGGPGP QREEKQKTKMAKFVIRPATAADCS DILRLIKELAEYEMEEQVILTEKDL LAEDGFGAEHPFYHCLVAEVPKEHW TSEG\HSIV\GFAMYYFTY\DPWIGQ VICILEDFFVMSDYRGSGIGSEILK\NLSQ\VAMRCRCSSMHFLG*PEWN EPS\NFYKRRGASIDLSS*RRGWRL FQGSCKGVIWLKNGPTEGVEGVAC C |
| 702 | 6199 | A | 726 | 149 | 460 | |
| 703 | 6200 | A | 727 | 1 | 501 | |
| 704 | 6201 | A | 728 | 1 | 391 | SPLNKVQLNELNEREVQLGVANK VSWHSEYKDSA WIFLGGLPYDLTK GDIICVFSQ\QRSTIVA VDNFNIGIKIK GRTIRVDHVSNYRAPKDSEEIDVT RQLQEKGC GARTPSPSLSESSEDEK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PTKKP |
| 705 | 6202 | A | 729 | 18 | 240 | |
| 706 | 6203 | A | 730 | 254 | 1223 | SPLTRVKLINELNEREVQLGVADKV FWHSEYKDSA WIFLGGLPYGLTNEG DIICVFSQYGEIVNINLVRD\KKTGK SKGFCFLCYEDQQRSTILAVDNFNGI KIKGRTIRVDHVS\NYRAPKDSIED DVTRQLQEKSGSGARPPSPTLSESSE DEKPTKKHKKDKK\EKKKKKKEKE KADREVQAEQPSSSSPRRKTVKEKD DTGPKKHSSKNSERAQKSEPREGQ KLPKSRTAYSGGAEDLERELKKEKP KHEHKSSSRREAREEKTRIRDGRS SDAHSSWYNGRSEGRSYRSRSRSR DKSHRHKRARRSRERESSNPSDRW RH |
| 707 | 6204 | A | 731 | 2143 | 2346 | |
| 708 | 6205 | A | 732 | 2016 | 2206 | |
| 709 | 6206 | A | 733 | 90 | 401 | |
| 710 | 6207 | A | 734 | 276 | 488 | |
| 711 | 6208 | A | 735 | 186 | 537 | IWFPLRRRKARQEEKSGLGAPRSPS HNYPGYPGLGCLGKTNTS*TYILDQS NIGKRVAAILN*ILGGRKLRLEKSL SCQPKVEELYERVAW/IP*KPGCLLL VSVKVRNVFDWCTWVY |
| 712 | 6209 | A | 736 | 3 | 318 | |
| 713 | 6210 | A | 737 | 1 | 280 | REPTMVLSPADKTNVKAAWGKVG AHAGEYGAEALERMFLSFPTTKTP VNFKLLSHCLLV/TLAAHLPAEFTPA VHASLDKFLGSVSTVLTISKYR |
| 714 | 6211 | B | 738 | 34 | 264 | MVLSPADKTNVYFPHFDLSHGSAQ VKGHGKKVADALTNAVRTVDDMP NALSALSDLHAHKLRVDPVNFKLL STACW* |
| 715 | 6212 | A | 739 | 3 | 190 | EPTMVLSPADKTNVKAAWGKVGA H/AGEYGAEALERMFLSFPTTKIQIP LSWSLGGHASCPLG |
| 716 | 6213 | B | 740 | 12 | 298 | MVLSPADKTNVKAAWDLLPALRPE PRLCQVKGHGKKVADALTNAVAH VDDMPNALSALSDLHAHKLRVDP VNFKLLSHCLLVDPGPAHFPAEF TPAVHASLDKSTKTYFPHFDLSHGS AQVKGHGKKVADALTNAVAHVDD MPNALSALSDLHAHKLSVDPGNFK LPSTLPAAGDPC |
| 717 | 6214 | A | 741 | 2 | 392 | QTQREPTMVLSPADKTNVKAAWG KVGAH/AGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVA DALTNVA/AHVGGPVNFKLLSHCLL VTLAAHLPAEFTPAVNASLDKFLV SVSTVLTISKYR |
| 718 | 6215 | A | 742 | 623 | 1235 | SNLVELSNTLSWSSGGKVGHAHAGE YGAEALERMFLSFPTTKTYFPHFDL SHGSAQVKGHGKKVADALTNAVA HVDDMPNALSALSDLHAHKLRVDP VNFKLLSHCLLVDPGPAHFPAEF TPAVHASLDKSTKTYFPHFDLSHGS AQVKGHGKKVADALTNAVAHVDD MPNALSALSDLHAHKLSVDPGNFK LPSTLPAAGDPC |
| 719 | 6216 | A | 743 | 117 | 403 | |
| 720 | 6217 | C | 744 | 62 | 370 | MKSMRKQAPIITAFILTSRSGKNWIP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KLSASVNASLKIPVQCLEILPTTHCS SRDLIFQKFNLLMNQYLIYLGMLSV DTEEDTQLASLFPGEKHSSVSFVCP* |
| 721 | 6218 | A | 745 | 3 | 1242 | AAPQAGLSPVAIAAAIQLHLHSTQC SSPNTCCLPRRTRATIYYSRWSYHP LGSVP*SP*PFQEAS/ALTLPPACSFY GPLT*FQPKP*GSFPLSQ*MEYTIGL YT*TFHCPGTSRRQIPSSYLNCKDAF LPLL/SNPPQCRPFTGVGLVDVLTGF ETNNKYEIKNSFGQRVYFAAEDTD CCTRNC CGPSRPFTLRIIDNMGQEV TLERPLRCS SCCCPCCLQEIKSLDEQ CVVGKISKYWTGILREAFDADNFG IQFPLDL DVKMKA VMIGACFLIDRN CSPAMEQSWMENYFDEMTEIGFRR SVITNFSELKEHVLTHCKEANKNLD KMLDEWLTRKNSVEKTLNELMEV KTINEKLTIGKISKYWSGFVNDVFT NADNFGIHVPADLDVTVKAAMIGA CFLFAFRLGSELHN |
| 722 | 6219 | A | 747 | 129 | 1235 | EGCAAAVPDSLEAQKRKPSPGPSL DLVSLGSGNSGSQRTVLIMDKQNS QMNASHPETNLPVGYPPQYPPTAFQ GPPGYSGYPGPQVSYP PPPAGHSGP GPAGFPVPNQPVYNQPVYNQPVGA AGVPWMPAPQPPLNCPGLEYSQI DQILIHQQIELLEVLTGFETNNKYEI KNSFGQRVYFAAEDTDCCTRNC CG PSRPFTLR IIDNMGQEVITLERPLRCS SCCPCCLQEIEIQAPPGVPIGYVIQ TWHPCLPKFTIQNEKREDVLKISGP CVVCSCCGDVDFEIKSLDEQCVVG KISKHWTGILREAFDADNFGIQFP LDLDV KMKA VMIGACFLIDFMFF ESTGQPGNKNSGVWVVGFS |
| 723 | 6220 | A | 748 | 647 | 797 | |
| 724 | 6221 | A | 749 | 2 | 424 | |
| 725 | 6222 | A | 750 | 2 | 460 | ARATHREPTMVLSPADKTNVKA WGKVG AHAGEYGAEALERMLLSF PTTPTYFPHFDLNHGSAHVKGHGK NVDDALTNAVTHVYYPNSLYALS DLHPHNL RMDPVNFMLLSHCLL*T LVVHLPAELTPAVHASLNNVLESER TELTSSTS |
| 726 | 6223 | A | 751 | 1 | 456 | RPRRPQREPTMVLSPADKTNVKA WGKVG AHAGEYGAEALE/RMFL/SF PTTKTYFPHFDLSHGSSQVKGHGKK VADALTNAVGHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLVT LAAHLPAEFTPAVHAFLDKFLASVS TVLTSKYR |
| 727 | 6224 | A | 752 | 1 | 594 | PRLFWSPQTQREPTMVLSPADKTN VKA AWGKVG AHAGEYGAEALER MFLSFPTTKTYFPHFDLSHGFAQVK GATGKKVDDVALTKRRGAPLDDMP NALVRPLKR PCTTHKA FGVEPGSTS KLLSHLPCLGEPWAAHLPRPSFNP WRLQRLPWGQSFLGFLVEEPLLEPS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KIPVKA WKPSVGHCFAPWGFPPAP SSLS |
| 728 | 6225 | A | 753 | 2 | 386 | |
| 729 | 6226 | A | 754 | 33 | 476 | |
| 730 | 6227 | A | 755 | 5 | 417 | |
| 731 | 6228 | A | 756 | 1 | 412 | |
| 732 | 6229 | A | 757 | 2 | 446 | |
| 733 | 6230 | A | 758 | 3 | 713 | |
| 734 | 6231 | A | 759 | 87 | 236 | |
| 735 | 6232 | A | 760 | 181 | 322 | |
| 736 | 6233 | A | 761 | 213 | 427 | |
| 737 | 6234 | A | 762 | 213 | 422 | |
| 738 | 6235 | A | 763 | 1 | 732 | |
| 739 | 6236 | A | 764 | 31 | 1074 | TLILSGFTVKQVYAIDQIFSSLRLTIT IKMFCGDYVQGTIFPAPNFPIMDA QMLGGALQGFDCDKDMLINILTQR CNAQRMMIAEAYQSMYGRDLIGD MREQLSDHFQDVMAGLMYPPPLY DAHELWHAMKGVGTDENCLIEILA SRTNGEIFQMREAYCLQYSNNLQE DIYSETSGHFRDTLMNLVQGTREEG YSDPAMAAQDAMVLWEACQKKTG GHKTM LQMILCNKSYQQLRLVFQE FQNISGQDMVD AINECYDGYFQELL VAIVLCVRDKPAYFAYRLYSAIHDF GFHNKTVIRIL IARSEIDLLTIRKRYK ERYGK\SLFHDIRNF\ASGHYKKSTG LPIC |
| 740 | 6237 | A | 765 | 613 | 926 | |
| 741 | 6238 | C | 766 | 79 | 405 | MIGGTPQMFFISGAKGQWSPSLQPP PRAHRSSPWAPSSKSTSGGTAALGS LGSKDYFPRTGDGVVELRRSDQRR AHLPGCPTVLR TLLPQQRGDRDLQ QLRHHELRL* |
| 742 | 6239 | A | 767 | 1 | 321 | |
| 743 | 6240 | A | 768 | 110 | 431 | |
| 744 | 6241 | B | 769 | 756 | 1533 | MREIVHIQAGQCGNQIGAKFWEPW KASSIELSQCRNSPSKVFRSKEHDGL PVTPTTR* |
| 745 | 6242 | A | 770 | 20 | 453 | GIPGSTISLFCSEKKLREVERIVKAN DREYNEKFQYADNRIHTSKYNILTF LPINLFEQFORVANAYFLCLLILQLI PEISL TWFTTIVPLVLVITMTAVKD ATDDVILQNEKWMNVKVGDIKLEN NQFVAADLLLLSSSEPH |
| 746 | 6243 | A | 771 | 1 | 1014 | |
| 747 | 6244 | A | 772 | 128 | 2654 | LVQDHKAGEHQVGAMARLGNC SL TWAALIILLPGSLEECGHISVSAPIV HLGDPITASCIKQNC SHLDPEPQIL WRLGAELQPGGRQQRLSDGTQESII TLPHLNHTQAFLSCCLNWGNSLQIL DQVELRAGYPPAIPHNLSCLMNLTT SSLICQWEPGPETHLPTSFTLKSFKS RGNCQTQGDSILDCVPKDGQSHCCI PRKHLLLYQNMGIWVQAENALGTS MSPQLCLDPMDVVKLEPPMLRTMD PSPEAAPQAGCLQLCWEPWQPGL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HINQKCELRHKPQRGEASWALVGP LPLEALQYELCGLLPATAYTLQIRCI RWPLPGHWSDWSPSLELRITTERAP TVRLDTWWRQRQLDPRTVQLFWK PVPLEEDSGRIQGYVVSWRPSGQAG AILPLCNTTELSCFHLPSAQEVAL VAYNSAGTSRPTPVVFSESRGPALT RLHAMARDPHSLWVGWEPPNPWP QGYVIEWWGLGPPSASNSNKTWRME QNGRATGFLLENIRPFQLYEIIIVTP LYQDTMGPSQHVVAYSQEMAPSH APELHLKHIGKTWAQLEWVPEPPEL GKSPLTHYTIFWTNAQNQSFSAILN ASSRGFVLHGLEPASLYHIHLMAAS QAGATNSTVLTLMILTPEGSELHIIL GLFGLLLLLTCLCGTAWLCCVAPTG RIPSGQVSQTQLTAAWAPGCPQSW RSCPDPRDSDGWGRHLK*AVLSPHI LVCRMPSSCPALARHPSPPSSQCWRR MKRSRCPGSPITAQRPVASPLWSRP MCSRGTEQFPPSPNPSLAPAIRSFM GSCWAAPQAQGGGTISAVTPLSPS WRASPPAPSPMRTSGSRPAPWGPW |
| 748 | 6245 | A | 773 | 123 | 2486 | |
| 749 | 6246 | A | 774 | 128 | 2573 | LVQDCHKAGEHQVGAMARLGNCSL TWAALIIILLPGSLEECGHISVSAPIV HLGDPITASCIKQNCSHLDPEPQIL WRLGAELQPGGRQQLSDGTQESII TLPHLNHTQAFLSCCLNWGNSLQIL DQVELRAGYPPAIPHNLSCLMNLTT SSLICQWEPGPETHLPTSFTLKSFKS RGNCQTQGDSDILDCVPKDGQSHCCI PRKHLLLYQNMGIWVQAENALGTS MSPQLCLDPMDVVKLEPPMLRTMD PSPEAAPQAGCLQLCWEPWQPGL HINQKCELRHKPQRGEASWALVGP LPLEALQYELCGLLPATAYTLQIRCI RWPLPGHWSDWSPSLELRITTERAP TVRLDTWWRQRQLDPRTVQLFWK PVPLEEDSGRIQGYVVSWRPSGQAG AILPLCNTTELSCFHLPSAQEVAL VAYNSAGTSRPTPVVFSESRGPALT RLHAMARDPHSLWVGWEPPNPWP QGYVIEWWGLGPPSASNSNKTWRME QNGRATGFLLENIRPFQLYEIIIVTP LYQDTMGPSQHVVAYSQEMAPSH APELHLKHIGKTWAQLEWVPEPPEL GKSPLTHYTIFWTNAQNQSFSAILN ASSRGFVLHGLEPASLYHIHLMAAS QAGATNSTVLTLMILTPEGSELHIIL GLFGLLLLLTCLCGTAWLCCVAPTG RIPSGQVSQTQLTAAWAPGCPQSW RRMPSSCPALARHPSPPSSQCWRRM KRSRCPGSPITAQRPVASPLWSRPM CSRGTEQFPPSPNPSLAPAIRSFMG SCWAAPQAQGGGTISAVTPLSPSW RASPPAPSPMRTSGSRPAPWGPW |
| 750 | 6247 | A | 775 | 151 | 273 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 751 | 6248 | A | 776 | 785 | 920 | |
| 752 | 6249 | A | 777 | 332 | 473 | |
| 753 | 6250 | A | 778 | 264 | 387 | |
| 754 | 6251 | A | 779 | 257 | 354 | |
| 755 | 6252 | A | 780 | 101 | 290 | |
| 756 | 6253 | A | 781 | 21 | 215 | |
| 757 | 6254 | A | 782 | 158 | 955 | KMTSSSEQEEDEKNNQSATPRQTGP ATTMNSKGQYPTQPTYVPVQPPGNP VYPQTLHLPQAPPYTDAPPAYSELY RPSFVHPGAATVPTMSAAFPGLASL YLPMAQSVAVGPLAGSTIPMAYYP VGPIYPPGSTVLGGKGGYDAGARF GAGATAGNIPPPPGCPPNAAQLA VMQGANVLVTQVRKGNFFMGGSDG GYTHLVRNQGHLCAREKTSHTLQH FSQCNCFSHINLKLQFRHMLLGCLS GAQTRHFSNLIRNHVMVAVPP |
| 758 | 6255 | A | 783 | 167 | 342 | |
| 759 | 6256 | A | 784 | 368 | 525 | |
| 760 | 6257 | A | 785 | 311 | 487 | |
| 761 | 6258 | A | 786 | 148 | 298 | |
| 762 | 6259 | A | 787 | 164 | 314 | |
| 763 | 6260 | A | 788 | 232 | 382 | |
| 764 | 6261 | A | 789 | 2 | 390 | |
| 765 | 6262 | A | 790 | 3 | 376 | AQKAGLGTIFIMTCSPLLLTLLIHCT GSWAQPVLTQPPSVSAAPGQKVTIS CSGSGSNIGNNYVSWYQQLPDPLFH AHK*LLPGSRDSGLEAR*QPRQGGG GDHHTLQTKQQQVRGQQLPEPDA |
| 766 | 6263 | A | 791 | 2 | 353 | |
| 767 | 6264 | A | 792 | 2 | 382 | |
| 768 | 6265 | A | 793 | 3 | 654 | |
| 769 | 6266 | A | 794 | 9 | 885 | |
| 770 | 6267 | A | 795 | 1 | 412 | |
| 771 | 6268 | A | 796 | 2 | 616 | WPIEIDIQCGGIPRDNLHHDLLPSP HPSHCPPTRPAVSAEGRTRDQSSSM TCSPLLLTLLIHCTGPWAQSVLTQPP SVSATPGQRTVISCGRSRSNIGDNYV SWYKQLPGTAPQLLIYDNNKRTSGI PDRFSGSKSGTSA TLGITGLQTGDE ADYYCGTWD TILSAGVFGGWTKLT VLGQPKAAPSVTLFPPSSEELQANK AT |
| 772 | 6269 | A | 797 | 489 | 715 | |
| 773 | 6270 | A | 798 | 20 | 371 | |
| 774 | 6271 | A | 799 | 181 | 382 | |
| 775 | 6272 | A | 800 | 353 | 479 | |
| 776 | 6273 | A | 801 | 3 | 368 | HEAASSSSASPFQTKIEKMVDLTQV MDDEVFMAFASYATIILSKMMLMS TATAFYILTRKVFANPQHCVTFGKG ENAKKYLRTDDRVRVRRHLNDL ENIIPFLGIGLLYSLSGADPSTAI |
| 777 | 6274 | A | 802 | 246 | 363 | |
| 778 | 6275 | B | 804 | 55 | 366 | MGHFTTEEDKATITSLWGKVNVEDA GGETLGRLLVVYPWTQRFFDSFGN LSSASAIMGNPKVKAHGKKVLTSL GDAIKHLDDLKGTFAQLPHRLVIVA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LSSSVK* |
| 779 | 6276 | A | 805 | 129 | 409 | |
| 780 | 6277 | A | 806 | 24 | 253 | |
| 781 | 6278 | A | 807 | 32 | 433 | |
| 782 | 6279 | A | 808 | 15 | 468 | |
| 783 | 6280 | A | 809 | 25 | 1404 | APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSA\SAIMGNPVKVKAHGK KVLTSGLDAIKHL\DDLKGTFAQLE *TCTCDKL\H\VDPENFKLLG\NVLV TVL\AIHF\GKEFTPE\VQSFLGRKMV TGVASALSFPDYH |
| 784 | 6281 | A | 810 | 113 | 387 | |
| 785 | 6282 | A | 811 | 1330 | 1465 | SECCGLSRPGHWPFI*WLPSL/CLI DVPT*QRKGGLVRNWVLP*NLWE LLP/ALAGSGEGHLKNMTGSKLSRM PNRISDSESE/GVNTARIHGEMFWR GDNWACTCCRGARSLAADSADPA TGLTSFPLASASSSATRASIPKRCLN SWFSTTRP |
| 786 | 6283 | B | 812 | 17 | 718 | MVVVAAAPNPADGTPKVLLLSGQP ASAAGAPAGQALPLMVPARGASP EAASGGLPQARKRQRLTHLSPEVPS LPRKLKNRVAAQTARDRKKARMSE LEQQVNQKLLLENQLLREKTHGLV VENQELRQRLGMDALVAEDFCLLQ SDILLGILDNLDPMFFKCPSPPEPAS LEELPEVYPEGPSSLPASLSLSVGTS SAKLEAINELIRFDHIYTKPLVLEIPS DTG* |
| 787 | 6284 | A | 813 | 464 | 714 | |
| 788 | 6285 | A | 814 | 349 | 581 | |
| 789 | 6286 | A | 815 | 223 | 513 | DHEEPQAREGDQSVHRPHAERTGQ PGMWRHPRLDECQPQELL/TKHSTS PSQEKEVHTPHP/RPLESCWASLNR DPQHSSPTPGKTSKSRENKEISQ |
| 790 | 6287 | A | 816 | 384 | 464 | PLPQLLRFAQPKPEAHLTPARPQPK RTCHGLTCRRGVSPGWRRDGPRT HRSAGATRRPIQETASPVPQPEAAPP HRARGSGKMRDGKPGAGNTERRD PQSRTVGLNKKNSTPHQSPQPPADV *TSAGG |
| 791 | 6288 | A | 817 | 1 | 255 | IVMGHSMPLPHF*IWSPPPGRAAARL APLSGAGHSGPRLAPWT*AGQLQT QSLVRP*PELGKSELSAPSLVIGSW MDM*PKPGQ |
| 792 | 6289 | B | 818 | 191 | 1072 | MWRSCRLRLRXRGTPSPESAGGWPQ RFYESGANHPVSSPGLRPADRKEEV LFRMFISIHTGEALAIAVATEWDSQQ DTIKYYTMHLTTLCNTSLDNPTQRN KDQLIRAAVKFLDTDTICYRVEEPE TLVELQRNEWDPIIEWAEKRYGVEI SSSTSIMGPSIPAKTREVLVSHLAS NTWALQGIDGSRPCCCSRLEEEYQI PEVGGNIEWAHDYELQELRARTAA GTLFIHLCSESTTVKHKLLKE* |
| 793 | 6290 | A | 819 | 1518 | 1891 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 794 | 6291 | A | 820 | 217 | 491 | |
| 795 | 6292 | A | 821 | 1789 | 2411 | KTYWRKKVEKVVVSNR\VTSPC\C IVTSTYGWTANMGENH*KLQALKE TTSTMG/YMASQRKHRGIKPLTISI IEYLKAKRPEGLIRTDKS\VKDL\VIL LY\ETALLSSGFQSWKIPRHH*AQVS YRMIKL\GLGIDEDGPYLLDDTSA\A VNLKELPPLEGDDDTFTHGKEVGLI LLGLRGWTLPSVLYNSSDNIFFQG CFPLFLVNI |
| 796 | 6293 | A | 822 | 592 | 1122 | |
| 797 | 6294 | A | 823 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 798 | 6295 | A | 824 | 38 | 531 | APSPDA\MGHFTEEDKATIT\SLWGK VNVE\ DAGGETLGRLLVVYPWTQR FFD\SFGNLSSASAIMGNPKVKAH GKKVLTSLGRCHKSTWDDLKG\TF AQA*SELHL*QSCNVDPENFKLLG\ NVLVTRFGQSHFRQKNFTPEGCRAS WAE/MMGDLQLASALVPSRYH |
| 799 | 6296 | A | 825 | 1 | 278 | |
| 800 | 6297 | A | 826 | 80 | 591 | RGCKREGLSMSSLIRR VISTAKAPG A\IGPPTVQAVLVDRTHLHFRDQIG HGPLPSWTS LCPGGVAGRSLNKLL KNMGEIPESLPGCDF\TNVVKTTCS GLDINDLQLLFNEILQTVFSRSNFPA RAAYPSWLLLPQKGSRIEIA\VAIQ GPLTTAFILSGDPCCVVWDC |
| 801 | 6298 | A | 827 | 1 | 396 | |
| 802 | 6299 | A | 828 | 1 | 346 | |
| 803 | 6300 | A | 829 | 3 | 720 | RGIPASRWARKAVVLLCASDLLLLL LLLPPAG\SGRAEGSPGTP\DEFTP\PP RKKKKDIRDSNDADMARLLEH\WE KHDD\NEEGDLPEHKRPSAPVDFSKI DPG\KPESILKMTKKGKTLMMFVT VSGSPTEKETEEITSLWQG\SLFNAN YDVQRFIVGSDRAIFMLRDGSYAW EIKDFLVGQDRCADVTLEGQVYPG KGGGSKEKNKTKQDKGKKKKEGD LKSRSSKEENRAGNKREDL |
| 804 | 6301 | A | 830 | 349 | 567 | |
| 805 | 6302 | A | 831 | 1098 | 1684 | |
| 806 | 6303 | A | 832 | 2 | 441 | PCRNSRVENFVSMWVCSTLWRVRT P\PGSG/GLLPASGCHGPAASSYSA SAEPARVRALVYGHGHPAKVVET VIPGHTWQLRNVA*PTLRR*FERNT HSSLDDMNISVWLCA*\LKNLELAA VRGSDVRVKMLAAPINPSDINMIQG |
| 807 | 6304 | A | 833 | 3 | 421 | ASMWVCSTLWRVRTP\PGSG/GLL PASGCHGPAASSYSASAEPARVRAL VYGHGHPAKVVEGITRELFQRF WIFLQLITAVISSASTVLKNLELAAV RGSDVRVKMLAAPINPSDINMIQGN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YGFLPELPAVGGNEGV |
| 808 | 6305 | A | 834 | 2 | 611 | ILQLGRGRAVRVCSTLWRVRTPPG SGG/GLLPASGCHGPAASSYSASAEP ARVRALVYGHGDPKAVVELKNL ELAAVRGSDVRVKMLAAPINPSDIN MIQGNYGLLPELPAVGGNEGVAQV GAEGSNVTGLKPGNWVVPANAGL RTWRNRG*VHPKEALIQVPSDIPQ SAATLGVPCTAYRMLMDFEQLQP GDSVIQNAS |
| 809 | 6306 | A | 835 | 159 | 312 | |
| 810 | 6307 | A | 836 | 637 | 974 | |
| 811 | 6308 | A | 837 | 240 | 419 | |
| 812 | 6309 | A | 838 | 20 | 283 | |
| 813 | 6310 | A | 839 | 508 | 715 | IPGNFEP SRLGRG*KTQACSPSLLWE FWLTQYLPALGAGHILKNFTTFPVI SCVSKLSTLFGGKMPEN |
| 814 | 6311 | A | 840 | 3 | 362 | |
| 815 | 6312 | A | 841 | 7 | 479 | GAIMGVDIAINKDRRVRRKEPKSQD IYLRLLVKLYRFLARRTNSTFNQVV LKRLFMSRTNRPPLSLSRMIRKMKL PGRENKTA VVVGTITDDVRVQEV KLKVCALRVTSRARSRLRAGGKIL TFDQLALD/SPYVRSGRGRKFERARG RRASRGYKN |
| 816 | 6313 | A | 842 | 2 | 723 | CAVNSAEQORGAIMVSGHLFITKDRK VR\RKPEPKSQDIYLRLLVKLYRFLA RRTNSTFNQVVLKRLFMSPHQPGP PLSLSRMIPED*SFPGPGRRAVV VG\TITD\DVVRVQEV\PKTERVCCTC AVDQAGAPQAAIL\RAGGQDSFTFR PSLALGTSPKGLVGTCSWLFRRFRQ RGPRRWYPAIFGKGPQGTAPAATP KPYVRSGRGRKFERARGRRASRGY KKLTLDPTLLLKKFLPKKK |
| 817 | 6314 | A | 843 | 1221 | 2238 | EPLIVCVCFCLCPPLFFSFLGSAEK AVLEQFGFPLTGTEARCYTNHALSY DQAKRVP\RWVLAHIFQKAR*\MG DADRKHCKFKPDPNIPTTFSAFEN YVGSGWSRGHMAPAGNNKFSSKA MAETFYLSNIVPQDFDNNSGYWNRI EMYCRELTERFEDVWVVSGLTLP QTRGDGKKIVSYQVIGEDNVAVPS HLYKVILARRSSVSTEPLALGAFVV PNEAIGFQPQLTEFQVSLQDLEKLS VLVFFPHLDRTSDIRNICSVDTCALL DFQEFTLYLSTRKIEGARSVLRLEKI MENLKNAEIEPDDYFMSRYEKKLE ELKAKEQSGTQIRKPS |
| 818 | 6315 | A | 844 | 1 | 306 | |
| 819 | 6316 | A | 845 | 216 | 339 | |
| 820 | 6317 | A | 846 | 425 | 553 | |
| 821 | 6318 | A | 847 | 190 | 334 | |
| 822 | 6319 | A | 848 | 241 | 435 | |
| 823 | 6320 | C | 849 | 280 | 450 | MLEKNWCPSLQVPIILNWAQPCGKI LTECCTLGYSLIQGDFTFIRKHAR TRLVKR* |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 824 | 6321 | A | 850 | 1 | 301 | |
| 825 | 6322 | A | 851 | 2 | 3484 | |
| 826 | 6323 | B | 852 | 225 | 326 | MAFKDTGKTPVEPEGAIHRIRITLTS RKRKSFEK* |
| 827 | 6324 | A | 853 | 348 | 515 | AFKDTGKTPVEPELAIHRIRITLTS\ RNVKSLEK\VSFAVMRGGGGIGRK ATSFTR |
| 828 | 6325 | A | 854 | 42 | 529 | SARSLHDSPHVRSRRGKTSVRKPA RNRPLAFKDTGKTPVEPEVAIHRI RITPNKAANVK\SLEKVVCLTLIRRA QKEKNFQS*KGPVS/RLPYPRFLRIH FQGKTPCGLKVFKDVGVRFPWRRI HK\RLADLHSPS\EIVKQITFHQYLSP GVEVEVHHLQML |
| 829 | 6326 | A | 855 | 14 | 345 | |
| 830 | 6327 | A | 856 | 1 | 396 | |
| 831 | 6328 | A | 857 | 3 | 718 | RGIPASRWARKAVVLLCASDLLLLL LLLPPAG\SGRAEGSPGTP\DEFTPPP RKKKKDIRDSNDADMARLLEHWE KHDD\EEGDLPEHKRPSAPVDFSKI DPSKPESILKMTKKGKTLMMFVTV SGSPTEKETEEITSLWQGS\LFNANY DVQRFIVGSDRAIFMLRDGSYAWEI KDFLVGQDRCADVTLEGQVYPGKG GGSKEKNKTKQDKGKKKKEGDLK SRSSKEENRAGNKREDL |
| 832 | 6329 | A | 858 | 80 | 349 | |
| 833 | 6330 | A | 859 | 504 | 738 | |
| 834 | 6331 | A | 860 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDFSFGNLSSA SAIMGNPVKVAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 835 | 6332 | A | 861 | 38 | 608 | APSPDAMGHFTEEDKATITSLWGK\ VNVEDAGGETLGRLLVVYPWTQR FFD\SFGNLSSASAIMGNPKVKAH GKKVLTSLGDAIKHLDDLKGTFAQ L\SELHCDKLHVDPENFKLLGEML LVTVLAIIPFRAKEFTPEGCRASWQ KQKMAEDGDLQWPSGPVPPDTTEA SWPMNSEAFKDKAFILASNYK |
| 836 | 6333 | A | 863 | 727 | 1089 | |
| 837 | 6334 | A | 864 | 432 | 742 | |
| 838 | 6335 | A | 865 | 184 | 352 | |
| 839 | 6336 | A | 866 | 204 | 394 | |
| 840 | 6337 | A | 867 | 1 | 2286 | MDLLGRVGS DWALQSSCLTDPELW GWEGTPRFLAAAAQGFGGPVLKAQ ACSLGAGIAPTELPRPVRWSLLFLA VRSNYQALWPQSPAGLPLVPQPETP RGANIPSPVVHAGDDRGWHMTV EQKFGLFSAEIKEADPLAASEASQP KPCPPEVTPHYIWDVRACSPTKAV GCSTWGARTVPGVGVAEPKAFGKL GQSAQNPSSAVSAGPRFLVQRFEIA KYCSDQVEIFSSLLQRSMSLNIGRA KGS MNRHVAAIGPRFKLLTLGLSLL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; /-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HADVVPNATIRNVLREKIYSTAFDY FSCPPKFPTQGEKRLREDISIMIKFW TAMFSDKKYLTASQLVPPADIGDLL EQLVEENTGSLSGPAKDFYQREFDF FNKITNVSAIHKPYPKGDERKKACLS ALSEVTVQPGCSLPSNPEAIVLDVD YKSGTPMQSAAKAPYLAKFKVKRC GVSELEKEGLRCRSDSEDECSTQEA DGQKISWQAAIFKLGDDCRQDMLA LQIIDLFKNIFQLVGLDLFVFPYRVV ATAPGCGVIECIPDCTSRDQLGRQT DFGMYDYFTRQYGDESTLAFQQR YNFIRSMAYSLLLFLLQIKDRHNG NIMLDKKGHHHIDFGFMFESSPGGN LGWEPDIKLTDEMVMIMGGKMEA TPFKWFMEMCVRGYLA VRPCLGST GDRVQQIESCLGDVQDVAGEAYM DVVVSLVTIMLDTGLPCFRG/QIKFL KHRFSPNMTEREANFIMKVIQSCF LSNRSRTYNMIQYYQNDIPY |
| 841 | 6338 | A | 868 | 3 | 164 | |
| 842 | 6339 | A | 869 | 1 | 5340 | |
| 843 | 6340 | A | 870 | 649 | 1028 | |
| 844 | 6341 | B | 871 | 1 | 5823 | MCPVDFHGFQLDERRRDAVIALGI FLIESDLQHKDCVVPYLLRLLKGLP KVYWVEESTARKGRGALPVAESFS FCLVTLLSDVAYRDP SLRDEILEVLL QVLHVLLGMCQALEIQDKEYLCKY AIPCLIGISRAFGRYSNMEESLLSKL FPKIPPHSLRVLEELEGVRRRSFNDF RSILPSNLLTVCQEGTLKRKTSSVSS ISQVSPERGMPPPSSPGGSAFHYFEA SCLPDGTALEPEYYFSTISSSFSVSPL FNGVTYKEFNIPLEMLRELLNLVKK IVEEAVLKSLDAIVASVMEANPSAD LYYTSFSDPLYLT MFKMLRDTLYY MKDLPTS FVKEIHDFVLEQFNTSQG ELQKILHDADRIHNELSPLKLRCQA SAACVDLMVWAVKDEQGAENLCI KLSEKLQSKTSSKVIAHLPLLICCL QGLGRLCERFPVVVH SVTPSLRDFL VIPSPVLVKLYKYHSQYHTVAGNDI KISVTNEHSESTLNVMSGKKSQPSM YEQLRDIAIDNICRCLKAGLTVPVI VEAFLASLSNRLYISQESDKDAHLIP DHTIRALGHIAVALRDT PKVMEPIL QILQQKFCQPPSPLDVL IIDQLGCLVI TGNQYIYQEVWNL FQQISVKASSV VYSATKDYKDHGYRHCSLAVINAL ANIAANIQDEHLVDELLMNLLLEFV QLGLEGKRASERASEKGPALKASSS AGNLGVLPVIAVLTRRLPPIKEAKP RLQKLFRDFWLYSVLMGFAVEGSG LWPEEWYEGVCEIATKSPLLTFPSK EPLRSVLQYNSAMKNDTVTPAELSE LRSTIINLLDPPPEVSALINKLDFAM STYLLSVYRLEYMRVLRSTD PDRFQ VMFCYFEDKA IQKDKSGMMQCVIA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VADKVFDNFLMMADKAKTKENE EELERHAQFLLVNFNHHKRIRRA DKYLSGLVDKFPHELLWSGTVLKT LDILQTLSSLSADIHKDQPYDIPD APYRITVPDTYEARESIVKDFAA GMILQEAMKWAPTGTKSHLQEYLN KHQNWVSGLSQHTGLAMATESILH FAGYNKQNTTLGATQLSERPACVK KDYSNFMASLNLNRNYAGEVYGM RFSGTTGQMSDLNKMVQDLHSA LDRSHPOHYTQAMFKLTAMLISSK DCDPQLLHHLWCWGLRMFNEHGM ETALACWEWLLAGKDGVEVPFMR EMAGAWHMTVEQKFGFSAEIKEA DPLAASEASQPKPCPEVTPHYIWD FLVQRFEIAKYCSSDQVEIFSSLLQ SMSLNIGGAKGSMNRHVAAIGPRF KLLTLGLSLLHADVVPNATIRNVLR EKIYSTAFDYFSCPPKFPTQGEKRL EDISIMIKFWTAMFSDKKYLTASQL VPPDNQDTRSNLDITVGSRQQATQG WINTYPLSSGMSTISKSGMSKKTN RGSQHLKYYMKRRTLLLSLLATEIE RLITWYNPLSAPELELDQAGENSVA NWRSKYISLSEKQWKDNVNLAWSI SPYLAVQLPARFKNTEAIGNEVTRL VRDPGAVSDVPEAIKFLVTWHTID ADAPELSHVLCWAPTDPTGLSYFS SMYPPHPLTAQYGVKVLRSFPDAI LFYIPQIVQALRYDKMGYVREYILW AASKSQLLAHQFIWNMKTNIYLDE EGHQKDPDIGDLLDQLVEEITGSLS GPAKDFYQREFDFFNKITNVSAIKP YPKGDERKKACLSALSEVKVQPGC YLPSNPEAIVLDIDYKSGTPMQSAA KAPYLAKFKVKRCGVSELEKEGLR CRSDSEDECSTQEADGQKISWQAAI FKVGDDCRQDMLALQIIDLFKNIFQ LVGLDLFVFPYRVVATAPGCGAIEC IPDCTSRDQLGRQTDGMYDYFTR QYGDESTLAFQQARYNFIRSMAY SLLLFLQSKDRHNGNIMLDKKGHI IHIDFGFMFESSPGGNLGWEPRHQA DG* |
| 845 | 6342 | A | 872 | 1 | 337 | |
| 846 | 6343 | A | 873 | 1 | 337 | |
| 847 | 6344 | A | 874 | 838 | 929 | |
| 848 | 6345 | A | 875 | 21 | 338 | |
| 849 | 6346 | A | 876 | 2 | 424 | |
| 850 | 6347 | A | 877 | 3 | 452 | |
| 851 | 6348 | A | 878 | 3 | 604 | PTLLVPTDSERTHPWLLSPADKTN VKA\AWGKVGAGHAGEYGAEALER MFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMP NALSALSDLHAHKL\RVGPGSTFKL LK/HTCLAGEPWAAHLP\AEFQPLA VATSSLGTFKPGLLVEAPLLTFQIPV KAGSLGWPLFFCPLGLPPSPSPFLH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PYPRGL |
| 852 | 6349 | A | 879 | 2 | 416 | EGKPRTSGAEHRSCRGKASMSPNF KLQCHFILIFLTALRGESRYLELREA ADYDPFLLFSANLKRELAGEQPYRR ALRCLDMLSLOQQFTFTDDRPQLH CAGFFISEPÆESLPFHYDQ*SIDGK AGNFLKVL MGRIL |
| 853 | 6350 | A | 880 | 1 | 187 | |
| 854 | 6351 | A | 881 | 2 | 1099 | PRVRGRVGEVGRKAQDLRSRQHS SCRGKASMSPNFKLQCHFILIFLTAL RGESRYLELREAADYDPFLLFSANL KRDVAGEQPYRRALRCLDMLSLOQ QFTFTADRPQLHCAAFFISEPEEFIT HYDQVSI GLSKGGDF/LWKVFDGWI LKGEKFPASSQDHPLPSAERYIDFC ESGLSRRSIRSSQNVAMIFFRVHEP GNGISHLTIKTDPNLFSFAMFISSEFQ MGKFNLG*FPHQHRNCSFSIYPVVI KISDLYPGGHVNGSFS*RKSS\AGCE GIGDFVELLGGTGLDPSKMTPLADL CYPFHGPAQMKVGC DNTVVRMVS SGKHVNRVD FLRIVQLEAVTSWEN PNG\NSIGEFCL SGL |
| 855 | 6352 | A | 882 | 2 | 645 | HGIQAHGQIPSYKTIGGRDDSFHTFF SETGAGKHVPRLLL* NWKPTVMDE VRTGTYCQLFHLEQFITARKIAANN YARGHYTIGKEIIDLVLDRIKRLAD QCTGLQGFLVFHSFGGGTGS GFTSL LMERLSVDY GKKSKLEFSIYPAPQV STAVVEPYN SILTHTTLEHSDCAF MEEGEFSEAREDMAALEKDYEEVG VDSVEGE GEEEGEEY |
| 856 | 6353 | A | 883 | 90 | 1657 | EATTSPRLRLRHQLGSREAATMRECI SIHVGQAGVQIGNACWEL YCLEHGI QPDGQMPK*PKPLGEGDDSFNTFFS ETGAGKHVPRAVFVDLEPTVIDEVR TGTYRQLFHPEQLITGKEDAANNY ARGNYTIGKEIIDLVLDRIKRLADQ CTG\LOGFLVFHS\FGGGTGS GFTS\ LLMERLSVDYWQESPSLEFSIYPAA PRFPQPVVEP\YN\SILPTQHPPWEHS DCA\FM\VDNEAIYDICRRNLDIERP TYTNLNLRL\SIQIVSSITASLRFDGAL NVDLTAEFQTNLGPYPPIHFPLATY APCHLC*RKPTHEQLFCSQRSPKCF AFEPTNPDG*NGDPRHG*IHWLAC LLLP/RGDVVPKRCQMLPIAHPSKP KRS\IQVDWCP\TGFK\GINYQPP TVVPGGDLA\KVTREAVCMLS KHH SPFAEAWARPGPTSFDLM LCQACPF VHWYLGÆGMEEGEFSK\ARKDMA AL\RKDYEEVG\VDSVKGÆGEEEGK GILIIHSLFGPCSMSCSQNF SFLTDR R |
| 857 | 6354 | B | 884 | 46 | 386 | XIRHESGSRSHSHCSTLSSIGDVAKK LGEMWNNTAADDKQPYEKKA AKL KEKYEKDIAAYRAKGKPDAAKKG VVKAEKSKKKKEEEDEEDEEDEE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | EEEDXEDDDEEEDDDDE* |
| 858 | 6355 | A | 885 | 263 | 484 | |
| 859 | 6356 | A | 886 | 146 | 826 | TWGKGDPPKKPRGKMSSYAFFVQTC RGGVHKKKHPDASVNFS/ESFSKKCS ERWKTMSA*R/EKGKFEDMAKA/D KARYAEREMKTYIPPQRGRQKRKFK DSQLHPRGPPS\AFFPLLALAYRPKI K\GEHP\GLSIGDVAKKLGRDVGIN TAAD\DKQPYEKKA\AKLKEYEKD IAAYRAKGKPDAAKKGVVKAES KKKKEEEEDEEEG\DEEDEEEEEEDE EDEEDEEEDER |
| 860 | 6357 | A | 887 | 1 | 456 | RPRRPQREPTMVLSPADKTNVKA WGKVGAHAGEYGAEAL/RMFL/SF PTTKTYFPHFDLSHGSSQVKGHGKK VADALTNVGHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHAFLDKFLASVS TVLTSKYR |
| 861 | 6358 | A | 888 | 2 | 435 | QTQREPTMVLSPADKTNVKA WGKVGAH/AGEYGAEALERMFLSF PTTKTYFPHFDLSHGSAQVKGHGKK VADALTNV/EHVDDMPNALSALS DLHAHKLRVDPVNFQAPKATGLLV DGPAPHFPGRVSPLRLQGFLGTF LGC |
| 862 | 6359 | A | 889 | 9 | 390 | NSARATDSERTHHGARLLPDKTNV KA\AWGKVGAHAGEYGAEALERM FLSFPTTK\TYFPHFDLSHG\SAQV KGPTAKKVAERADQTPWRNVDDMP KRRCPP*SDLHAHKLRVDPVQLSS S*SHLPCW |
| 863 | 6360 | A | 890 | 2 | 413 | |
| 864 | 6361 | A | 891 | 2 | 6281 | |
| 865 | 6362 | B | 892 | 79 | 200 | XGDYPLGDLTPTTMEEATSGVNESE MAVASGHLNSTGVLE* |
| 866 | 6363 | B | 893 | 209 | 502 | MLLMYNSSDHDVYHMAVEMQRD VLEQIQQLATQLIMQTSSEGISAKS LRGRDSTRKQDASEKDSVPMGSPA FFSLSLWDTSGFGWILNKIIPMTLS* |
| 867 | 6364 | A | 894 | 283 | 340 | |
| 868 | 6365 | B | 895 | 1649 | 1741 | MSFAMTLKKKLEEEAEVKKRATD AAYQARQAVKTPPRRLPTVMVRSPI DSASPGGDYPLGDLTPTTMEEATSG VTPGTLPSTPVTSPFGIPDTLP PGSAPLEAPMTPVTDDSPQKKMLGQKATP PPSPLLSELLKKGSLLPTSPRLVNES EMAVASGHLNSTGVLLLEVGGVLP MIHGGEIQQTPNTVAASPAASESVSQ ATIVMMPALPAPSSAPAVSTTESVA PVSQPDNCVPMEAVGDPHTVTVSM DSSEISMIINSIKEECFRSGVAEAPVG SKAPSIDGKEELDLAEKMDIAVSYT AVEAALSFCENDDPQSLPGPWEHP IQQERDKPVPLPAPEMTVKQERLDF EETENKGIHELVDIREPSAEIKVEPA EPEPVISGAEIVAGVVPATSMPEPPEL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RSQDLDEELGSTAAGEILEADVAIG KGDETPLTNVKTEASPESMLSPSHG SNPIEDPLEAETQHKFEMSDSLKEES GTIFGSQIKDAPGEDEEEDGVSEAA SLEEPKEEDQGEGYLSEMDNEPPVS ESDDGFSIHNATLQSHTLADSIPSSP ASSQFSVCSEDQEA IQAQKIWKKA MLVWRAAANHRYANVFLQPGTR* |
| 869 | 6366 | A | 896 | 3 | 2926 | PGSTISSGTGKHKLLSTGPTEPWSIR EKLCLASSVMRSGDQNWVSVSRAI KPFAEPGRPPDWFSQKHCASQYSEL LETTETPK*VQSQRKRGEKGEVVE TVEDVIVRKLTAERVEELKKVIKET QERYRRLKRDAELIQAGHMDSRL DELCNDIATKKKLEEEAEVKRKA TDAAYQARQAVKTPPRRLPTVMVR SPIDSASPGGDYPLGDLTPTTMEEA TSGVTPGTLPTSTPVTSTFPGIPDTLPPG SAPLEAPMTPVTDDSPQKKMLGQK ATPPPSPLLSELLKKGSLLPTSPRLV NESEMAVASGHLNSTGVLLLEVGGV LPMIHGGEIQQTPNTVAASPAASGA PTLSRLLEAGPTQFTTPLASFTNVA SKPPVKLVPPPVEFFSQATIVMMPA LPAPSSAPAVSTTESVAPESQPDNC VPMEAVGDPHTVTVSMDSSEISMII NSIKEKCFRSGVTEAPVGSKAPSIDG KEELYLAEKMEIAVSYTGEELDFET VGDIHAIIDKVDDHPEVLDVAAVE AALSFCENDDPQSLPGPWEHPQQ ERDKPVPLPAPE\MTVKQERLDFEE TENKGIHELVDIREPSAEIKVEPAEP EPVISGAEIVAGVVPATS\MEPPELR SQDLDEELGSTAAGEIVEADVAIGK GDETPLTNVKTEASPESMLSPSHGS NPIEDPLEAETQHKFEMSDSLKEES GTIFGSQIKDAPGEDEEEDGVSEAA SL*EPKEEDQGEGYLSEMDNEPPVS ESDDGFSIHNATLQSHTLADSIPSSP ASSQFSVCSEDQEA IQAQKIWKKA MLVWRAAANHRYANVFLQPVTD DIAPGYHSIVQRPMDLSTIKKNIENG LIRSTAEFQRDIMLMFQNAV MYNSS DHDVYHMAVEMQRDVLEQIQQLA ATQLIMQTS\ESGINAKSLRGRDS\T RKQDASEKDSVP\MGSPAFLLSLFD GGTQGTPLCPLKPDMMKKVKPQS YPL |
| 870 | 6367 | A | 897 | 150 | 425 | VYHFLVALKIPPSLMVFPCCPSPFPS/ PPRLPPHPVLFPLPPSPSPSNP*VLGS PRGLSPPLL*GPPAPPKPACFCSFP RDPGKLRWALRG |
| 871 | 6368 | A | 898 | 65 | 259 | |
| 872 | 6369 | A | 899 | 273 | 962 | KRERAVSLGQSGLPVAVRAGPQGGG CTWGADALGGTGACGACSLRSSTP HFLGQSERVPH*QGG\TGIFHHPEHG S*AKK/DPVRPPCA*QGKGVAFLLPA EA*VSGDQGGPGAVLSP/GRDCPFPS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PGP/PGNPQPLAARQGPAPGNSGSL WPWQEPPVDWPSEGTP/GPLLRRQQL QSQPKNATGRERHPPQT/AKFPSPCP NTVL*IPEIK*NPWGEQQSRPALGST QDQRICNNH |
| 873 | 6370 | A | 900 | 1 | 253 | KRKVSLCHPGWSAGAPSRLTATSSS LVKRFSCLSFPSSWDYRCAPHLAN L/CRG/RGFTMLARLVLS*PQMIYQ SRPPKVLGLQV |
| 874 | 6371 | A | 901 | 327 | 638 | LGLQGSTIFHKTLKKDLLQLEKQLN VNRDPGESNNSHNSQIKSFPIYHFF FFGLLRN*PTNTLDRFVFGFENTHLS VL/QRKTISFNLVCWSHTPSINVCAI YQ |
| 875 | 6372 | A | 902 | 834 | 1187 | RKYETCLSALEIFT*SCSAVGII*FFC LFLGDEVLLCCPGLFTGCHHRWNY SLKLLGSKRSFCLSLSSWNYRHAP PSLGF*KNFKKNFE\KDLAML\PLGV FNSYP*VILLWASSNG |
| 876 | 6373 | C | 903 | 150 | 364 | MSILPLQSYINMNAGNLYGQMHNH FPYIVKQKKQVCRTVCTVSLVYHK MCVYMCVCECLXXXXXXXXXXXXX X* |
| 877 | 6374 | A | 904 | 29 | 372 | SYENNHSYAGWSGSRKRFTLFLQIY /CRYITPLYILLYVFEQ*VYYPFKVT* I*MQEIYMDRCITIF/LYIVKQKKQV CRNSVYSITCLPQNVCGICVYVSVYI HTYIYIYTHHH |
| 878 | 6375 | A | 905 | 1 | 815 | MGNLGQVRRSLWDYLLGLTHPRG LTTSQPGRSGLSPPAPPQQSFCMCQ NVTPGIMALGMSAVYFQVSGTKEQ PVPGHPMQSILLELWGFQVHHCV GNRPDFMEHSKDLTSLLDHSCH WHGRSHSSKEYLELHRENFLILRS AFPTGLLRAWPRDGISQYLLVELKN NMFRFLVAGSAEGAAGPPCPGPRK VAKKKPHLKQAPKNAGPRRWDEG R*GFPSQKQKEEQKKLGGA*KRKA RGGRGWPWTGGIKKSGQKSKLFPW CLRRW |
| 879 | 6376 | A | 910 | 140 | 512 | PARGESRLDPSQWGEPAECAKEPT AVPRGPGLRNRTALTGTQKPPQSRE GARCIIIGGSAPSTPPSSARRRWPGG HS*AGRPGRSSRQEPGCCIDRAPGP GLPPPASQPPGAAPLRCPTAVGPS |
| 880 | 6377 | A | 911 | 68 | 675 | RSTRTVHIPLLSCAQLPGQTP*PLSP WWFFCTPSSQGPPEPREDQPGCAPG PQEAPKPAGNLPPTDSSARAASETG RVLPS/PPTLIFCNLPRRG/FVSV AHL WLMSPFIRL*EATPGPGGQSGDLGG LILHPGQPGHGGQQRGAAGALQR GP/DTSPTPCSRAAAAGMPTA*TLTP *RILPRTAPSPTTPGEQLPRPGNSGR DG |
| 881 | 6378 | A | 912 | 3 | 3492 | GGTVPQGLRTHGTGRGDTVGGDGE PPPQDRTLHLPQPPHPLPAPGQGA PAGRGGGAAQP/AGSPTAPCGPGTS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GFAEDSREERGHRLPGEPEVPQP*R LHPG/PPGC/MPDVDFS NFS GESSDF DGLAGTSRN/RQAPGNPRSHGDIQA DRVPGWGHROPAGGAEPGKGAEG GAAA AVPAAAGAPGPRDPCRGA PAGG*PQPHEA*G*RTL P*GAEAEG RDAQPLAAL*QCAAGEGAGRLTLP QPAGGAVSTEAGAAASQHGFL* A GIARAVPEDSQRPGVRG*GAEPPEG GE*ETALADFQPGGEGHSGAEPGRG AGEPTGAGGAHPLAAGAGRGCREA ARAGQTLRAAELHGPCVPLCPVLG REGTDPAAVPEE*DGLPTLQGE GEC AAGPGVRAAEGARPGVLREGQCSE GDFPEPGGEG LPPQAGVRADGPGL RAAHTASPAAGRASGCAQAG/RPGP GSPVHGRSSGWCGCMPSAPETTAT APRQLHRVSALVGPECHVQPRAGG QLPLQQPRAPQPAVPVQAGGRGLR GRTL VFQQLPGDPGGRPGSPAGS*G RRPTPGL*APRHGRPSAAGKQPAAS LPWKA*CLGECTSRSSPGLQRRPHA AEASPQDPEPGHHAGVPPGGCIAGA DQRHRREPHGHLHPPGHPGLGGGP DGLAPGHPCDGD*LRSLRALVQGSP GGHDPGGGRGASQEGGRLLLPVCE GQHGR L*EATPGPGGQSGDLGGLIL HPGQPGHGGQGQ RGAAGALQ RGP AR/PPTPCSRAAAAGMPTA*TLTP*R ILPRTAPSPTTPGLSSSS*PSSRT*LSS AP*PASHL/PGGPQ/IAGPHRQY GQS QGQPSAFVL*QGPVGPQQDGG LQH VLLGRELPHPGALYPGAAPSTRPAP ACAPRAQGGWEDPERETVPPPRV*E VPGRVLEPGGV*GLEPAGGDIIPGGR GVRGPLLGEPA\SCGVPHGKEHPCP PGRPAGQCLHPAQDGHLP HRHPRL CQREDGKEAQEGPTAVGHLRGAAP GGCEAGGGRPGPGALS IQPGS*RL ERPGRPAQLCPPGHRRRAEEGATPT SSKN*PQARGRASPPSNASVTEELT QGRGWALPPSNASVTEELTQARGR ASPPSNASVTEELTQARGRASPC LH LRRLSKDKLLPRNTTGSKLITSGSL LPISWKPAWGTGT |
| 882 | 6379 | A | 913 | 232 | 485 | TRLRLTPKVCPYRWSHFDRKFLSRV LMRRSAQKSRDRILNVFHELNL/NS VLDMRPMEF*GLRAAS*PQGERRGS LAFIREFHHT |
| 883 | 6380 | A | 914 | 2 | 1163 | |
| 884 | 6381 | A | 915 | 771 | 1597 | GACHLRLTPKVCPYRWSHFDRKFP SARVL\MRRSAQKSS/RDRILNVFHE L\NLKDAISYVAEVAEPLALPGRGC SRLGHWLIQFWT*GQWSFRVSGLLP D/TQGERRGSLAFIRSPSTDNVVNV DFTPRSSTVEASVSYLLYVAMVMQ LPWGRAQPRELRVTDRAVVAPGLG VAWKRGEVQKEGVGVSSHKPSYIR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PWPDSLSAGRKVKGRGSSGLGARP DVFAPGPQQPVMVPMPLLLLRPW APQLTASSHRRSTLPDVQMLGSPSL TARALERDQ |
| 885 | 6382 | A | 916 | 3 | 471 | DSWLWWLRQRLQQIGGISGSTSTSS MLSRA VCGTSRQLAPVLGYLGSRQ KHS LPDLPYDYG ALEPHINAQIMQL HHSKHHAAYVNNLNVTEEKYQEA LAKGELLEAIKRDFGSFDKVKEK\L TAASVGGKGSCWGGLGFNKERGH LQIAAWPNQDP |
| 886 | 6383 | A | 917 | 54 | 873 | GPRAAQERHSLWWLRQRLQQIG GISGSTSTSSMLSRA VCGTSRQLAP VLGYLGSRQKHS LPDLPYDYGAL EPHINAADHASLHHSKHHA/APYVN NLNVTEEKYQGGLWPRGDVYSPR* ALQPCT*KFNGGGWHINHSIFWTN PQAPNGGGETQRGSLLGSHQNVDF GSFDKFK\EKLTAA SVGCPKAPGW GWLGFQ*GNRGH/LYQIAACPKSGI PLQGTG/LLFPLLIDVWEHALLPS SIKNVRPDYLKAIWNVINWENVTE RYMACKK |
| 887 | 6384 | A | 918 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMG NPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 888 | 6385 | A | 919 | 41 | 601 | APSPRRPWGHFTEEDQGLLSTSLWG KVKCGKNAGRKKPLGKAPLVVL/H PWDPKRSFEQALGNPVPLPSA\IMG NPPKSRAHGK\KVL\SLGEMPIKHP G*SSKGTFAQA*SELH\CDK\LVHDP ENFKLLG\NVLVTVL\AIPFSAKEFT PGGCRASWAERWVTWSWPVPCSS RIPLSSLAHDCRAFOG |
| 889 | 6386 | A | 920 | 14682 | 14931 | EIGPGPRPLPSPLP*ATSTSVLAASGR PERTRHAGIKIVLEDIFTLWRQVET KVRAKIRKMKVTTKVNRHDKINGK RKTAKEQSPLLQESLFATGDVSHNL LRALDVGLLANLSALAELDISNNKI STLEEGIFANLNLSEINLSGNPFEC DCGLAWLPRWAEEQQVRVVQPEA ATCAGPGSLAGQPLLGIPLLDSCG EEYVACL PDNSSGTVA AVSFSA AHE GLLQPEACSAFCFSTGQGLAALSEQ GWCLCGSAQPSSASFACSLCSGPP PPPAPT CRGPTLLQHVF PASPGATLL AAFHIAAPLPVTATRWDFGDGSPEV DAAGPAASHRYVLPGRYHVM AVL ALGAGSALLGTDVQVEAAPAALEL VCPSSVQSDESLDLSIQNRVSGGLE AAYSIVALGEEPARAVHPLCPSDTEI FSGNGHCYRLVVEKAAWLQAQEQ CRAWAGATLAMVDSPA VQRFLVS RVTRSLDMWIGFSTVQGV EGPAP QGEAFSLESCQNWLPGEHPATAEH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | CVRLGPTGWCNTDLCALHSYVCE LRPGGPVQDAENLLVGAPSGDLQG PLMPLARQYGLSAPHEPVEVMVFP GLRLSREAFLLTAEFGTQELRRPAQ LRLQVYRLLSTAGTPENGSEPESSRP DNRTQLAPACMPGGRWCPGANICL PLDASCHPRPAPMAARQGPGLLGA PYALWREFLFSVPAGPPAQYSVTLH GQDVLMLPGDLVGLQHDAGPGALP HCSPAPGHPGPQAPYLSANASSWLP HLPALQEGTWACPAALRLLAATE QLTVLLGLRPNPGLRLPGRYEVRAE VGNGVSRHNLSCSFDVVSVPVAGLR VIYPAPRDGRLYVPTNGSASVLQVD SGASATATARWPGGSVSARFENAC PALVATFVPGCPWETNDTLFSVVAL PWLGEGEHVMDEVVENSASRANLS LRVTAEEPICGLRATPSPEARVLQG VPVRYSPVVEAGSDMVFRWTINDK QSLTFQNVFNVYQSAAVFKLSLT ASNHVSNVTNYNITVERMNRMQ GLRVSTVPAVLSPNATLALTAGVLV DSAVEVAFLWTFGDGEQALHQFQP PYNESFPVPDPSVAQVLVEHNVHT YAAPGEYVLTVLASNAFENRTQQV PVSVRASLPSEAVGVSDGVLVAGRP VTFYPHLLPSPGGVLYTWDFGDGSP VLTQSQAANHTYPSRGIYHVRLEV NNTVSGAAAQADVRVFEELRGLSV DMSLAVEQGAPVVVSAAVQTGDNI TWTFDMGDGTVLSGPEATVEHVYL RAQNCTVTVGAASPAGHLARSLHV LVFVLEVLRLVEPAACIPTQPDARLT AYTGNPARYLFDWTFGDGSSNTT MRGCPTVTHNFTSRGTFPLALVLSS RVNRARYFTSICVEPEVGNVTLQPE RQFVQLGDEARLVACAWPPFPYRY TWDFGTEEAVPARVGGPEVTFIYRD PGSYLVTVTASNISAANDSALVEV QEPMLVTSIKVNGSLGLELHYLWD LGDGRLEGPEVTHAYNSTGDFTV RVAGCNEVSRSEAWLNVTVKRRVR GLIVNASCTVPLNGSMSFSTSLEA GSDVRYSWVLCDRCTPISGAENEV GSAQDSIFVYVLQLIEGLQVVGGR YFPTNHTVQLQAVVRDGTNIYSWT AWRDRGPALAGSGKGFSLTAEAG TYHVQLRATNMLGSAWADCTVDF VEPVGWLMVAASPNPAAVNTSVTL SAELAGGSGVVYTWSEGLSWET PEPFTTHSFPTPGLHLVTMTAGNPL GSANATVEVDVQVPVSGLSIRASEP GGSFVAAGSSVPFWGQLATGTNVS WCWAVPGGSSKRGPHTMVFPDA GTFNIRLNASNAVSWVSATYNLTV EEPVGLVLWASSKVVPAGQLVHF QILLAAGSAVTFRQVGGASPEVLP GPRFSHSFPRIGDHVVSQSKNHVS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WAQAQVRIVVLEAVSGLQVPNCCE PGIAMGTERNFTARVQRGSRVAYA WYFSLQKVRGDSLFI LSGRDVITYP WPRGCWRSSSENRTL VLEVQDAVQ YVALRSGPCFTNRLAQFEAATSPSP RRVAYHWDFGDGSPGQDTPDKPRA EHSYLRPGDYRVQVNASNLVSFFV AQATVTVQVLACREPEVDVVLPLQ VLMRRSQRNCLDAYVDLRDCVTY QTEYRWEVYRTASCQRP GCPARVA LPGVDVSRPQLVLPRLALPVGHYCF VFVVSFGDTP LARSIQANVTVAPER LVPITEGGSYRVWSDTQDLVLDGSE SYDPNLEDGDQTPLSFQWACVAST QREAGGCALNFGPRGSSTVTIPRER LAAGVEYTFSLTVWKAGRKEEATN QTCWWRPRALPSLFLMQILCNTTA CFSFASFQ TCHSSTYSLQATYALVT KATQSPSNTNRSSWLQYTRTHTPVS SALCMPFRRPGWKVANRMSILGGG WHDAEDAGAPLVYALLQRC CQG HCKEFCVYKSSLSGYGAVLPPGFRP HFEVGLAVVVQDQLGA AVVALNR SLAITLPEPNGSAMGLTVWLHRLTA SVLPGLLRQADPQH VIEYSLALVTV LNEGPSREL VCRSCLKQTLHKLEA MMRILQAETTAGTVTPTAIGDSILNI TGDLIHLASSDV RAPQRSELGAESP LRMVASQAYNLTSALMRILTRSRV LNEEPAFSRAPANLSDVVQLVFLVD SNPFLFGYISNYTVSTKVASMAFQT QAGAQUIERLASERAITVKVPNNSD WAARGHRSSANSV VVQPQASVGA VVTLDSSNPVAVLHLQLNYTLLDG RYLSEEPEPYLA VYLHSEPRPNERN CSASRRIRPESLQ GADHRPYTFFISP GTRDPVGSYRLNLSSHFRWSALEVS VGLYTSLCQYFSEEDV VWRTEGLL PLEETSPRQAVCLTRHLTAFGASLF MPPSHVRFVFPEPTADVNYTVMLTC AVCLVTYMVMAAILHKLDQLDASR GCAIPFCGQRGRFKYEILVKTGWGR GSGTTAHVGIMLYGVDSRSGHRHL DGDRAFHRNSLDIFQIATPHSLGSV WKIRVWHDNKGLSPA WFLQHIIVR DLQTARSTFFLVNDWLSVETEANG GLVEKEVLAASHAALLRFRRLVA ELQRGFFDKHIWLSIWDRPPRSCFT RIQRATCCVLLICLFLGANAVWYG AVGDSAYSTGHVSRLSPLSVDIVA VGLVSSVVVYPVYLAILFLFRMSRS KVLIDISCLDSSVLDSSFLTFSGLHA EVRALLGVLGWAGGPAAL AQLGL QTLCTSQQAFAGQVKSDLFLDDSK RSGPVPVPFPFPPCPKPPPLSWLPQG ALKGPGHAGIKIVLEDIFTLWRQVE TKVRAKIRKMKVTTKVNRHDKING KRKTAKEQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 890 | 6387 | B | 921 | 1 | 714 | MVKLSIVLTPRFLSHDQGQLTKELQ QHVKSVTCPCEYLRKVINTLADHR HRGTDGFGGSPWLLIITVFLRSYKFAI SLCTSYLCVSFLKTIFPSQNGHDGST DVQQRARRSNRRRQEGIKIVLEDIF TLWRQVETKVRACKMKVTTKV NRHDKINGKRKTAKEHLRKLMSKE REHGEKERQVSEAEENGKLDMKEI HTYISPLLQESLFATGSEWRQRSIVI LQDCPTGPTSQKLK* |
| 891 | 6388 | B | 922 | 1 | 387 | MRVRWLLFWLLFWLLGFISHQST CVINTLADHRHRGTDGFGGSPWLLI TVFLRSYKFAISLCTSYLCVSFLKTIF PSQNGHDGSTDVQQRARRSNCRQ EGIKIVLEDIFTLWRQVETKVRACK KMK* |
| 892 | 6389 | A | 923 | 277 | 489 | |
| 893 | 6390 | A | 924 | 465 | 634 | |
| 894 | 6391 | A | 925 | 1 | 4652 | MGSTGVYKVTPRSCHRFEQAFYTY DTSSPSILTLTAIRHHVLGTITTDKM MDVTVTIKSSIDSEPALVLGPKSV QELRREQQLAEIEARRQEREKNGNE EGEERMTKPPVQEMVDELQGPFSY DFSYWARVLCFVGTGPAKLKYINY FRSGEKITVTPSSKELLYPPSMEA VSGESCPGKLEIHGKAGLFLEGQIH PELEGVEIVISEKGASSPLITVFTDDK GAYSVGPLHSDLEYTVTSQKEGYV LTAVEGTIGDFKAYALAGVTLHSQ DVLMLPGDLVGLQHDAGPGALLHC SPAPGHPGPQAPYLSANASSWLPHL PAQLEGTWACPACALRLAATEQL TVLLGLRPNPGLRLPGRYEVRAEVG NGVSRHNLSCSFDVVSFVAGLRVIY PAPRDGRLYVPTNGSASVLQVDSG ASATATARWPGGSVSARFENACPA LVATFVPSCPWETNDTLFSVVALP WLGEGEHVMDDVVENSASRANLS LRVTAEEPICGLRATPSPEARVLQ VPVLLAGSSGYLVGFKFLESHGSD SGSANSFHLISRNEFKTLPDLTRV PRYSPVVEAGSDMVFRWTINDKQS LTFQNVVFNVYQSAAVFKLSLTAS NHVSNVTVNYNITVERMNRMQGL RVSTVPAVLSPNATLALTAGVLVDS AVEVAFLWTFGDGEQALHQFPQPY NESFPVPDPSVAQVLVEHNVTHY AAPAALGGGAVLTRQPSVLLHLC VPHVAWEPGTLKAGPQVSTVLT ASNAFENRTQQVPVSVCASLPSVSV CASLTGACWYPRVLIRSGRVPIVSL ECVSCKAQAVYEVSRSYVYLEGR CLNCSSGSKRGGYTFTLTVLGRSGE EEGCASIPLSPNRPPLGGSCRLFPLG AVHALTTKVHFECMGWHDADAG APLVYALLQRCRQGHCEEFCVYK GSLSGYGAVLPPGFRPQFEVGLAVV VQDQLGAAVVALNRSIAITLPEPNG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SAMGLTVWLHGLTASVLPGLLRQA DPQLVIEYSLALVTVLNEYERALDV AAEPKHERQRRRAQIRKNITETLVSL RVHTVDDIQQIAAALAQC MRKLPE QDIAQGSYIALPLTLLVLLAGYNHD KLIPLLLQLTSRLQGVGALGQAASD NSGPEDAKRQAKKQKTRRTLATSIN TSREPSTDDQLPAHNQTMPQRHAR RSAPPRAYDRKTRQEENPHQTRSH AAAKRRERPPHDLQKQATTRLIPAG PRRDGTSPRRTQPPPNTRRPAAAG HLARFRAAPGARGARPPTARRGR EELDPAHIYAAAPGLTPPRAGRTPP TPERRDRNTRRRRTREEGEGEFRPV SFLKTIFPSQNGHDGSTDVQQRARR SNCRRQEGIKIVLEDIFTLWRQVET KVRAKIRKMKVTTKVNRHDKINGK RKTAKEHLRKL SMKEREHGEKERQ VSEAEENGKLD MN*IHFYMEMFQR AQALRRRAEDYYRCKITPSARKPLC NRVSLLVFLAFGHSLPGQDMDTFFS LRLCASSPAEGDGREEGCLQAFTVP SLLVTVLRKNTFIPTQWGPHLIF |
| 895 | 6392 | A | 926 | 3 | 156 | EMFQRAQ/ALRRRAEDYYRCKITPS ARKLLCNRCTYNLVLP GSEKKYYS HA |
| 896 | 6393 | A | 927 | 183 | 1518 | ASTQSAVGLVSSVVVYPVYLAILFL FWMSRSKVAGSPSPTPAGQQVLDID SCLDSSVLDSSFLTFSGLHAEVINTL ADHQHRGTDFGGSPSVLIITVSLRSY KFAISLCTSYLVWINTLADHRHRT DFGGSPWLLIITVFLRSYKFAISLCT TYLCVSLKTIFPSQNGHDGSTDVQ QRARRSNCRRQEGIKIVLÆDIFTLW RQVETKVRAKIRKMKVTTKATRLT KIKERRKTAQDHWRL SMKEREHG EKERQVSEAEENGKLD MKEIHTYM EMFQRAQALRRRAEDYYRCKITLF QRKPLCNRVMAAVEHRHSSGLPY WPYLP AETLKNRMGHQPPPTQQH SIIDNSLSLKT PSECLLTPLPPSALPS ADDNLKTPAECCLLYPLPPSADDNLK TPPECLLTPLPPSAPPSADDNLKTPP ECVCSLPFHPQRMISRN |
| 897 | 6394 | A | 928 | 123 | 1040 | WRWFTIGTFRILLMFCCLGYEWLSG /GCTTWHSAWV*GSSCHPAIICFLCF VAKSDP*RNPGLRKERTPRSQQGQ SWFGEDQKSGLSILWADIVHRGT\DI FGGSPWLLIITVFLRSYKFAISLCTSY LCVSLKTIFPSQNGHDGSTDVQQR AR\RSNRRRQEGLSICMHTKKRVS SFAGIKIVLEDIFTLWRQVETKVR KIRKMKVTTKVNRHDKINGKKKTA KEHLRKLGMKEREHEEKERQVSE AEENGKLD MKEIHTYMEMFQRAQ ALRRRAEDY*QHDKITPSARKAFFA NRVQQWRQW |
| 898 | 6395 | A | 929 | 39 | 525 | TKFVLGTFQILFTASF SHPSWWPLA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LENPHDSNLSGLFPLIDLDFSP*VLS CWASHTMENCS*LRSKRQITLWCS RMAELVYCLSWKCSHLKRHDFPM GKYQTPTCIDKGNMLYLSKLLGIES QCLGAEMGIPIKAMQSFTTSGRPKN EHSRNFVIIWKVLI |
| 899 | 6396 | A | 930 | 1030 | 1384 | LIALRKMGRNAQAQICITSDG*NPS PLKTESTLKT\TQFSLYPWGEKFERT PSLMGQKNFRTVCQLSQMGAIGFQ/ HIQEW DGERKST\TKN*KDGEISW LECMNN\VTCTPDSMKK |
| 900 | 6397 | A | 931 | 1 | 225 | |
| 901 | 6398 | A | 932 | 2 | 167 | |
| 902 | 6399 | A | 933 | 1 | 3339 | PASVHPSVRPTVQRKGLQAGRTSTR GTEARRGAKSAADPCGPGQGTVA AMQSCARAWGLRLGRGVGGGRRL AGGSGPCWAPSRDSSSGGDSAA AGASRLLERLLPRHDDFARRHIGPG DKDQREMLQTLGLASIDELIEKTV ANIRLKRPLKMEDPVCENEILATLH AISSKNQIWRSYIGMGYYNCSVPQT ILRNLENSGWITQYTPYQPEVSQG RLESLLNYQTMVCDITGLDMANAS LLDEGTAAAEALQLCYRHNKRRKF L\VDPR\CHPQTIAVVQTRAKYTGV TELKLPCEMDFSGKDVSGVLFQYP DTEGKVEDFTELVERAHQSGSLAC CATDLLALCILRPPGEFGVDIALGSS QRFVPLGYGGPHAAFFAVRESLV RMMPGRMVGVTRDATGK\EVY\RL AP*KPREQHRRDKATSNICTAQA LANMAA\MFANYHGSHGLGHIA\RV VHNATLILSEGLKRAGHQLQHDLF FDTLKIQC GCSVKEVLGRAAQ RQIN FRLFEDGTLGISLDET VNEKD LDDL LWIFGCESSAELVAESMGEECRGIP GSVFKRTSPFLTHQVFNSYHSETNIV RYMKKLENKDISLVHSMIPLGSCTM KLNSSSELAPITWKEFANIHPFVPLD QAQGYQQLFRELEKDLCELTGHDQ VCFQPNSGAQGEYAGLATIRAYLN QKGEHR TVCLIPKSAHG TNPASAH MAGMKIQPVEVDKYGNIDAVHLK AMVDKHKENLAAIMITYPSTNGVF EENISDVCDLIHQHGGQVYLDGAN MNAQVGICRPGDFGSDVSHLNLHK TFCIPHGGGGPGMGPIGVKKHLAPF LPNHPVISLKRNEACPVGTVSAAP WGSSSILPISWAYIKMMGGKGLKQ ATETAILNANYMAKRLETHYRILFR GARGYVGHEFILDTRPFKKSANIEA VDVAKRLQDYGFHAPTMSWPVAG TLMVEPTESEDKAELDRFCDAMISI RQEIADIEEG\RIDP\RVNPLKNVLH TPLTCVTSSHWD RPYSREVA AFPLP FVKPENKFWPTIA\RIDDIYGDQHL\ VCTCPPMEVYESPFS\EQKRAVFLV LCSLSFKGIDFDGLSPEAFDKQERFH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LPTPSLK |
| 903 | 6400 | A | 934 | 2 | 287 | |
| 904 | 6401 | A | 935 | 36 | 427 | |
| 905 | 6402 | A | 936 | 247 | 1183 | CCWESPVDPPQLRQISGIALFCSFKE PPLLGLVHPNTKLRQGRKGCLKIN LLGPES\MAHIGGCCDVYWGQQMGR VVKLENG*NRRLPGFGSGPLAKPE DDEPCVWGDPLGIRGRGPKWGLLF VGRHLTRGLF*R*NPWETVKVKKLL SSETPI*GGRNMSF\VNDLTVTPGW KEDLISPMPKQQNGQRRKLPAFWV MGGHKMTGRLLLEV*YCDPGK*KFY WTQLRFPNGVQPVS*QKTLSLVAET SMARIRRVYVSGPDERR\ADLFVEN MPGFDPNIRPSSSGGYWVGMSTIRP *PGSSMLDFLSERPWD |
| 906 | 6403 | A | 937 | 179 | 516 | VFSVLRAEDKICELLFCLKIKLFSAS FLVFRNQLPRKNDYFSEPPSENPPP ETGESVCLQLKSGAHLRCRVCGCLG PKTCSRCHKAYYCSKEHQTLDWRL GHKQACAQPGG |
| 907 | 6404 | A | 938 | 41 | 274 | KRGTERKTHFGGCSIQFSDIASGKNI LPGLCFLTHKR\WFCSL*RQGWVSR WSHE*GCTRCWRLGKFLWVADRFL GSG |
| 908 | 6405 | A | 939 | 3 | 1111 | CAPRQPAPRMAAAGARPVELGFAE SAPAWRLRSE\QFPSKVGGRPALWG AAGLPGPQALACELCGRPLSFLLOV YAPLAPGR\PD\A\FH\RCIFLCCREQP \CCAGLARFLGIRLPRKNDYFSEPP SENPPPETGESVCLQLKSGAHLRCR VCG\C*GPKTCSRCHKAILLAAREH QTLADWEIGDIRQACAQPDHLADHI NFQDHNFPFFQEF\EIVETEDEIMP* GVWKKEDYSRDY*GALG*STLKGR TWISMAAKHE\SRED\KFFQKF*NRL ALGTEQDS*YAGRG\APIWISGENIP QEKDIPDCPCGAKKILEFQVMPQLL NYLKADRLGKSIDWGILAAFTCAES CSLGTGYTEEFVWKQDVTDTIP |
| 909 | 6406 | A | 941 | 3458 | 4042 | AGMIRRPSPWPSIRPPAVFTNSCTS LQEPSGGTGRVQVPSIYQAS\STQIC VKGPD*GRNGKGNLSFGKAGIFHFP WCPKCPRPSSSPISMGLLSPEVDSVE R\PTFRFPLAPIYKECV*NGAG/AQ APDPRQKRGWPCHWNLMGVGRMP RVSPHLPEAWGPKHPDDRYTKGTA ICPRNHLPCDPRISAIGQPQG |
| 910 | 6407 | A | 942 | 226 | 401 | TSGDHWNI\AVAPHENSDDL\LVQGH DYKYRYFGLIVCVL*QAI\VTPEEPQS IVPRLRTR |
| 911 | 6408 | C | 943 | 211 | 282 | MFYPFFNPRYFSVGF\IAMNRHTD* |
| 912 | 6409 | A | 944 | 1390 | 1698 | HLFPHIKAGR*YGRPCREGILQ*KE* ETTGRHTCVLQGL\FQEVVQVRN VFLHEALQLVKFAMQIFEVLLKFP EPIVKHDL\QNT\EC\FFRHMEKEHS SKK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 913 | 6410 | A | 945 | 27 | 412 | IAEGNWCVYMPDIIWVFPPQAEAEEDCHSDTVRADDDEENESPAETDLQAQLQMF\RAQWMFELAPGVSSSNLENRPCRAARGSLQKTSADTKGKQEQAKEEKLSHIDIVTNYIFFFWHMEIFTGHSK |
| 914 | 6411 | A | 946 | 24 | 1489 | GGSSAAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRSGPLPREDGCRTPGPQLLPLHGA\LLRPR TLLSSAAEDKARSRH\PD\TQHPSSGGRCKGGTESPSSAAGRPASMAEAE\EDCHSDTVRADDDEENESPAETDVQALIP\MIQAQWKLEPAPRVSSSNLENRPCRAARGSLQKTSADTKGKQEQAKEEKARELFLQAVEEEQNGALYEAIKFYRRAMQLVPD\EFKITF\TRSPDGDGVGNSYIEDNDDDSKMADLLSYFQQQLTFQESVLKLCQ\PELESSQIHISVLPMEVL MYIFRWVGSSDLDTSLAEQLSLVCQRIPNILCPETPENMPVLALL*KFWGR\SC\IKLVSVTSPGRE DVF*ERPRV\RF\DG\VYISKTTYIRQGEQSLDGFYRA\WHQVEYYRYIRFFPDGHVMMMLTTPEEPQSIVPRLR\TREYQGLDAIPTGVTIRLSPRHRTIRTQSIWLLITKEKRKEKPL |
| 915 | 6412 | A | 947 | 17 | 499 | DRVLLCN/PRLECNGMITAHCSKP KPPGSK*SSCFSLPSSWDY\KHEPPYRANLKNFFVETGSLYVAQAGFELLDSSNPPCFSLPKCWDYRPP*ATTPS/FKND SHFNFLNRF/SHFVVF*VLRNLNLCNNIP*GLKVGEIQSPKAETKLGVERGGKNYIRFSK |
| 916 | 6413 | A | 948 | 9 | 296 | RPSHQCRLLPPRASLGLSELCPEDQ QSYIP*LGHHAECR*S/TSGGSCPLSVSSQASRAS/GPTSLTTAAPTSPRTGASALTEQYWSNRFLNHFAE |
| 917 | 6414 | C | 949 | 114 | 383 | MQMVGWVGGLGGIKQDKVLLSSE GPRSRDGGGTWRPTLKTSTVRXXXXXXXXXXXXXXXXXXXXXXXXX SALL* |
| 918 | 6415 | A | 950 | 1896 | 2251 | IGTPLCRMEDPFLEEAVPWSSVSSQASRASWPTSLTTAAPTSPRTGASALTEVGRPKT*DHKISSVSTK/TSSHCPGPEHTTSAVPVSRASSCPVTVTTKLSKHPLQLARRVGFTLLY |
| 919 | 6416 | A | 951 | 141 | 439 | |
| 920 | 6417 | A | 952 | 278 | 1177 | RHPLAFFKASRAGPQRPLDGTLGPEDSRASSPMIQNSRPSLLQPQDVGDVTETLMLHPVIKAFLCGSISGTCSTLLQPLDLLKTHLQTLQPSDHGSRRVGMLAVLFKGV\RTERLLDLWKGMSPSIVR\VSLGVGIYFGHSLLF*SSISWRRPIPQTAEVNHAGGSGSRVAGVCMSPITVIKTRYESGKYGY\KSIYALRSIYHSEGH\RG\LCGLTATILRDAPLSGIYLMFYNQTKNIVPHDQVDA TLIPITNFSCGDICWYSGPHWVTSTC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 921 | 6418 | A | 953 | 109 | 376 | GMFIQNSYGRLLFHLKVSMDWPST SLTRAKSHLGQQFPTSRTSQEENWS P*RGSRTPPTPHLPCQNLRPSMPT/F *QVNFKQFRGAFLSG*KSSVAIRTIQ QSNMALMGTYAL |
| 922 | 6419 | C | 955 | 123 | 329 | MISRAPLPQLSELHCDKLHVDPENX KLLGNVLVTVLAIHFGKEFTPEVQA SWQKMVTAVASALSSRYH* |
| 923 | 6420 | A | 956 | 41 | 565 | APSPRRPWGHFTEED\KATNTSLWG K\VNVE\ DAGG/EKTPGKGPLVVLPP WTPEVPLTSFGNLSASAAHHGQTP KVQGTMAKKVLTSLGDA\TKHL\ D DSQGAPFAQA*SELALVDKPAMWD PENFKASWGNVLVTRFGQSHFRA KNFTPEGCRVSLGRKMGDLELASA LVPSRYH |
| 924 | 6421 | A | 957 | 1 | 1000 | STRAPSPGPFSSKLAGAYKSWCRR DPRTHSAGAAQAARSVPICPAPT ASATMSHHWGYGKHNGPEHWHK DFPIAKGERQSPVDIDHTAKYDPS LKPLSVSYDQATSLRILNN\GHAF\N VEFDDS\QDKAVLKGGPL\DG\TYRL ISVFTFHWGSF*WDKVSEAYCGIKK KYAAELTLGHWNTKYGDFGKAVQ EPDGLAVLGIFLVGSAKPGLOKVV DVLDSIKTKGKSADFTNFDPRGLLP ESLDYWTYPGSLTTPPLECVTWI VLNFPFSVSS\EQVFEIP*TLTFNGG GVNPEELMVDNWRPA\QPLKNR\QI KASFQIRWSHSLYSK |
| 925 | 6422 | A | 958 | 3 | 402 | EELTMAGIFV*PTIPIVSL/SLFCH*V LTLNSGISPAGSPVLIFSTPEPKR*TS QGESRFHTFYLLKKLGLNR*I*HPSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSQ NRFLKPLQHSLLPPLKPLTYAPNL |
| 926 | 6423 | A | 959 | 1666 | 2187 | NFPSSASPPPTDSFL\GLSSEAPSEHR SPSCALDPIFFQTLW**SFSFSSLNFI NMLKFVPLNKT KPPLTLAFPYLKQL ASLPIQSCFFF*DKILLCHLGWSAVA QL*LTATSTSWAQVMFPRSWAYRH APPHT/LASCFYFCRDR/SLTIFPRLV SNSWAQVILPPRPPKMLGIQA |
| 927 | 6424 | A | 960 | 3 | 695 | TQLLRPAVFVGSAAAGIRRLWSA SSGHWCAPAAGRAHAPVPRLVRL GAASTAAPQDAQTGPQPMPRADCI MRHLPYFCRGQVVRGFGRLQASL GIP\TANFPEQVVDNLPAISTGIYY GWASVGS\GDVHKMVMSIGWNPY YKNTKKSMETHIMHTFKEDFYGEIL NGAIGDYLRPDDNFDSLQSLISAIQG DFEEAKK*LDLPEHLKLKEDNFFQ VSKSKIMNGH |
| 928 | 6425 | A | 961 | 60 | 569 | STDLEELPTLGWF*KQELIILSCPFVS LTYRERLPANFFKFQFRNVEYSSGR NKTFLCYVVEAQGGQVQASRG YLEDEHAAAHAEAEAFFNTILPAFDP ALRYNVTWYVSSSPCAACADRIKT LSKTKNLRLLILVGRLFMWEEPEIQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AALKKLKEAGCKLRIMNLV |
| 929 | 6426 | A | 962 | 62 | 858 | QLRWDSGARAWPRPACLSPLPQRL LSHSPSMAQKEEAAVATEAASQNG EDLENLDDPQKLKELIPLPFEIVTG ERLPANFFKFQFRNVEYSS\GRTKTL \LCYVV*STGARGGKVQASWGYLE DE\HAACPLQKESFSFNTILPAFRPK PLAVTNVT/WGYVSSSPCAACADR\ IVKTLSTKNLRLLLVGRLFMWEE PEIQAALKKLKEA\GCKLRIMKPQD FRILSWE\NFVEQEEGESKAFQPWE DIQENFLYYEKLADILK |
| 930 | 6427 | A | 963 | 409 | 747 | VILQAQGSMPGP*SLRAFPAESERC QKQERLEPEEGRTCAAGLRGGPRR WWPLSSWTGDLRPSARN*ILPAA PMMEERKDPAPAQPPWTS\TLPQFV SPEVLCSPPIENSHT |
| 931 | 6428 | A | 964 | 1092 | 2338 | RCYCSI*PCFHLFQLSFQILDPPVLGT TFL |
| 932 | 6429 | A | 965 | 146 | 180 | |
| 933 | 6430 | A | 966 | 2 | 921 | |
| 934 | 6431 | A | 967 | 1 | 621 | |
| 935 | 6432 | A | 968 | 2 | 152 | |
| 936 | 6433 | A | 969 | 157 | 1203 | NNSGVMPEMPEDMEQEEVNIP**G GFWVTGCHWGFLGRAVHKEFQQN NL/WHAVGCGFRRARPKFEQVNL\ DSNAVHHIHDFFQPHVIVHCAAERR PDVVENQPDAAASQLNVDASG\NLG KGKAAAVWEHFSILHLGSGFCILM GTNPPYREEDIPASLNLYGQTKL DGRKGCPWRNHLGAAVLRIPILYG EVEKLEKKCCCELLMFE*KCQFQQQ SQAQWIIHWQARGSPPHMSKDVA PLCARQ\LAEKRLDPASIKGTFHWS GNEQMTKYEGMCQLPDA\FNLPS SHL/RDPITDSPVLGAQRPRNAQLD CSKLETLGIGQRTPFRIKESLWPF LIDKRWRQTVFH |
| 937 | 6434 | A | 970 | 1 | 508 | NSNRQNGPPKKGERERASN/C/YPG APAAQAE/APLVPLSRQNKSTVETS NLKMLISFPKTLRGPQEGWWHQG INPGSGAATLGPGS/SPQRQS/IAAS CSMARRTFFAVSSNSFFLLL/CFLCM GSSSGSQSSSLKQKKHWAKSGSFS VGQWMKPASAIRSGVQRSPRRAS S |
| 938 | 6435 | A | 971 | 21 | 351 | VVSITKAPAYREVS VHNSCLRSNEG GKQPSHTKCLCNSNLLTTQFKTKPI E/CWPEKTYMGSSSGSQSSSLKQK KHWA KSGSFSVGQWMKPASAIRSG VQRSPRRASS |
| 939 | 6436 | A | 972 | 1 | 1011 | |
| 940 | 6437 | A | 973 | 2 | 94 | |
| 941 | 6438 | A | 974 | 661 | 2244 | QYFKNPVGSTAVFEMDRLFISSGTA EMTSRGF\QRS\CNNPP\CSSMTGRR ANQIHHLTPDFS\LRELL\PPK\KAGT WADCVSPPCGERDRCEGWADRHR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | A\CSSPAKSPTASSQVI*KGFKATAF FSRGRSGQHVAPRLHLGLSNHTAV GKREYLARRFLSLYSVSSSTRSFTPF PQ*LRMAFVLSF*IVVCAIL*INNSN KIRKPCC*TVEEPGTLSPFSHHTQV MHLPKKKKTKKHNNKKTVL*GGT GVTDKPEAAQIQQAPGKVPPODCD SLNNMRSRHHCGRLCHANKAVSS SKRDTAFLPHFSPGKPGNQNSKNE PPKKRERERSSSH/YPAAAPAAQAEA PLVPLSRQNRSTVETSNLKMLISFPK TLLRGPQEGWWHQGINPGSGAATL GPGSSGQRPQSMMAASCSMARRTFF AVSSNSFFLLLVSFALFLALS\SSF KKFNQRVNSS\NCFD/TERKAQPG RNCFLCSSMGSSSGSQPSSSLKQKK HWA KSGSFSVGQWMKPASAIRLRG CRRSPRRASS |
| 942 | 6439 | C | 975 | 597 | 683 | MWFHVCLLVVIFFYFLVHMKYLKC KFLG* |
| 943 | 6440 | A | 976 | 224 | 290 | MPPIPMPIAPVPFPFGPGFPP/VYFPV PLPLP/LLFPF*PLFPF*PEVSAKPVTL WSRKRQRSKGEKEGRGRGTGK |
| 944 | 6441 | A | 977 | 3 | 1815 | HFVPVSPEAAAAESTACGV TAKML SVRVAAVVVRALPRRAG\LSRNA LGSSFIAARNFHASNTHLQKTGTAE MSSILE\ERILG\ADTSVDLE*NLGVS *SIGDGIAPRTWG*RVNQAEMVVEF SSRLKGYVL*TLEPDNVGVVVFVN DKLIKEGDIVK\RTGAIVDVPVGE LLGRVVDALG\NAIDGKGPIGFQRR VGEVGL\KAPGIIPRISVREPMQTGI KAVDSLVPIGRGQRELIIGDRQTGK TSIAIDTIINQKRFNDGSDEKKLYC IYVAIGQKRSTVAQL\VKRLTRCKM PWKYTIVVS\ATASDAAPLQYLAPY SGCSMGEYFRDNGKHA\LIYDDLI QNKAVA*PVKMSLLLRPPGREAY PGDV FYLHSRLLERA AKMND AFGG GSLTALQV\IETQAGDVSATIQT DV NSI\TLPEQIFLET EWFNKGVRPAIN VGLSVSRAGSPPTNPGAMKPGSQV PWKLELASSIREVACFLPPVSVSD\L DAATSTNLLESVA VPS*LEFAESQG PVFSPWLIEGTSCLLSYAGCKGDIFD KLEPSKITKL RNAFLSHVVSQH QDL VGALCRADGKISEQS\DAKLKEIVT\N FLAGFEA |
| 945 | 6442 | A | 978 | 532 | 878 | SYHFGRPRQADHLRSGVQDQPGQH EETPSLLKRQK\LAGHGGIYL*PQLL GWL RQENCLNLGGGGCSELGLHHC IPAWATEQDCLKKQNETKKESYS** GTSC\IAFLFILKSDQK |
| 946 | 6443 | C | 979 | 36 | 236 | MGPTIPDXSXFWRKPITWMP TWE GTSNVGPQLSSSKSLHSXRGH PAPI PTGQAGPRDSGPGASP* |
| 947 | 6444 | C | 980 | 26 | 160 | MRFQSTGLGAPHCALNKC VSCLN X XXXXXXFLLRGPKLNPFKGG* |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 948 | 6445 | A | 981 | 1 | 523 | FFPKGFFLGYPRVFPFPFLNPGPGQ I*FSPP*K/RKLRAP*KKASSSSSVK TGNTFIESTVGCAPCALEPHHSAP/ PQQPAPSGPGPPGEPG*ERLCASHK AFISHKQSH*SPQ*PCQAGVTLSRLQ TTNSPRPVPVRRGCGGLEPRP*VS/PS QPTACSENSQGSQPSPKRTLS |
| 949 | 6446 | A | 982 | 145 | 1315 | CLPPPGLGPAPSLSSSCWGPPMPRT IRGIPPGSICRLCFCPAAGLLSLVAL QRPASSPTRHSALLCLRWA*PTSPS LPQSLGSRAQLHSPLP*QAGSPCHA HTCGHLGPPVV*VPLPCPRSHSHSS CLFPAGSQCP*QAPAGVSISCQASSS ASSCGPGPQGYGQTPGPIPETPRDR\ PCHPTPPKSKLQARGPWRAWVG*R TADGSCGKKP*/CGPTIPDPKSSPLA GLSSPFPWFWAETHHPGMP*RGKR DPRKCGNPQPPSPKLKSPPTAHGD HPAP*FPTGKGWTPKDSWTPGPPP* SRRPRPLN*WTAA*PWGQNPWAWT PAHPRKKP*RPRGSCLSLSVSACGK WAPSPTSQGCCEGRCDVPAKQQGL AHPTVLLNKCVCVSLN |
| 950 | 6447 | A | 983 | 1 | 682 | PPLFFQAAGKMADIQTERAYQKIQP TTFQNOQGRGSCCGETGKAEKLPRIY YKEHSGGLGLQRHPKEAY*GPPTLTK KCPFTGKCVHFEGGILSGVVTKM KMQRITIVIRRDYLYH\YIR\KYNRLP RKRHKNMV\HLSPCFQGTSRFG\DI VTGGAKCRPSEARQWRFNVLKGH QGLARHQRSSFQKFLRLGHRGRSPT MEIRLVPASPGKKKKKSFVPTGGAV DSIGGRGV |
| 951 | 6448 | A | 984 | 1 | 465 | |
| 952 | 6449 | A | 985 | 1585 | 2239 | |
| 953 | 6450 | A | 986 | 9 | 2580 | SLPPKKCELRLHNCWGLFSPPARQ SGSVAAVVAASAVSGVSGPQSPPLT CASSSLRSPRPARTRPVAVCVSPTTP RLPPRSSLRADMSGDHLHND SQIEA DFRLMDSLKHKDKQKDENARAR GHKEEKDRVEESKHSNSEHKDSEKK HKEKEKTKHKDGSSEKHKDKHKD RDKEKRKEEKVRASGDAKIKKEKE NGFSSPPQIKDET*DDG\YFVPPKEDI KPLKRPRDEDDADNK/PHKKIKTED TKKEKKRKLEEEEDGKLKPKNKD KDKKVPEPDNKKKKPKKEEQKW KWWEEERYPEGIKWKFLHKGPFV APPYEPLPENVKFYDYGKVMKLSP KAEVATFFAKMLDHEYTTKEIFRK NFFKDWRKEMTNEEKNIITNLSKCD FTQMSQYFKAQTEARKQMSKEEKL KIKEENEKLLKEYGFCIMDNHKERI ANFKIEPPGLFRGRGNHPKMGMMLK RRIMPEDIINCSKDAKVPSPPPGHK WKEVRHDNKVTWLVSWTENIQGSI KYIMLNPSSRIKGEKDWQKYETAR RLKKCVDKIRNQYREDWKSKEMK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VRQRAVALYFIDKLALRAGNEKEE GETADTVGCCSLRVEHINLHPELDG QEYVVEFDLGLKDSIRYYNKVPVE KRVFKNLQLFMENKQPEDDLFDRL NTGILNKHLDLMEGLTAKVFRVT YNASITLQQQLKELTAPDENIPAKIL SYNRANRAVAILCNHQRAPPKTFEK SMMNLQTKIDAKKEQLADARRDL KSAKADAKVMKDAKTKKVVESK KKA VQRLEEQLMKLEVQATDREEN KQIALGTSKLNLYLDPRTVAWCKK WGVPIEKIYNKTQREKFAWGHLT WLDEDEYF |
| 954 | 6451 | C | 987 | 65 | 235 | MQFRVKYHICSTLLSLKTKICITCIIP SHLFPASTIPSWGCFHLYIHIAQKHV ING* |
| 955 | 6452 | A | 988 | 16 | 148 | SPAEQGCVCVCVCVCVCVCVCVCV CVCVCVCVCVCVCVCVCVCVCVQVG ACVCN/CVCVCVCVCVCVCVCVCV CVCVCVCVCRCRWVLACATCVL |
| 956 | 6453 | A | 989 | 287 | 504 | LPRNFKTIYLDSEMVLESSKRGVCV SVCVCVCVCVCCLCVCVCVCVCVCV /C*YLDLNHGKCTHPVSFSVRIFLA |
| 957 | 6454 | C | 991 | 201 | 488 | MGSRPRFCLFTTNTLCPDVTSSVC SPKTTXRRLLKXTFMPRCRKPQAVL TSSEMALAACSXFSRSPDDFTQYQV AELVWDSLQPLGQXRSHCSLR* |
| 958 | 6455 | B | 992 | 53 | 302 | MTSALTQGLERIPDQLGYLVLSEGA GLASSGDLENDEHAASAMSELVST ACGLRLHRGMNVHFKRLSVVFGEH TLLETRVLTEX* |
| 959 | 6456 | B | 993 | 277 | 573 | TSALTQGLERIPDQLGYLSSGDLEN DEQAASAISELVSTACGFRLLHRGMN VPFKRLSVVFGEHTLLVTVSGQRVF V* |
| 960 | 6457 | A | 994 | 134 | 1271 | NPGPVQVGVEGGQEEGPSSKKQAK TRQVCLASITEAPGPKIRFSEPLRPP AGCRHQMGSPSGSASSPQTPFCPG/ PPSPA VCV/PPKTTGGETHQTG A*RA HSMPCRSRKTAGCAEQLQRWHWL PAHHSPPGQMTPALHLHSVPGSRA GLGFAPAPGSAQKSSG*RCKS*EAC *RDGRPDTLHLQTQVSGLTWPQVF SFPSQVPSRPPPPYMLVNTDLPÉPPS APTLAPRLPWPSTSHLCYPKGPVLP LWPLPSDPASSPPFVSARPA/ALPAAP EHPPTDPSPAFSSPSLPFPSPLPPRAD RR*GWSAGPPGG/EPHRLGSRDAEP PAGPLAHASSLTIAVFGAGGAPYQI GSFRLQAPVTCLQPLRSSFCLRHW LAPPLA |
| 961 | 6458 | A | 995 | 1 | 422 | |
| 962 | 6459 | A | 996 | 3 | 760 | TSRGRVGTQAGEPRDLRPPPCPSSPL RV\AVV\CLEQPERGAWEAHNIPQP NGDSA VRSFG\TGTHVKLPGPAPD\ NPNVY\DFKTTYDQMYNDLLRKDK \ELFTQNGILHIAGRNKRKIP\GPERF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QNCKDLFDLILTCEERVYDRVGWK I*ISR\EQGDLSPVHVVNLDIQDNH EEATLG/ARFLICE\VCQCIQHTEDM\ ENEIDELLQEFEEKSGRTFL\HTV\CF ILFSFLDICF |
| 963 | 6460 | A | 997 | 425 | 591 | EYLKQWNVVFVDIKNHL/MHLHA HIHTQV*THTQTHTHRHTHTHTHTP CHCLVHTA |
| 964 | 6461 | C | 998 | 120 | 368 | MGTAHKPGYPQISTTVCTYVPDFAIL SPVLSFCRLIYLHTRMLQATELLQ ALQNSTTKGNRRERARDNSKMRH DGRAWRC* |
| 965 | 6462 | A | 999 | 2 | 393 | ARGKKPNLRAFLPLPRAWPEPQTL QQPRWP*TVQLPVPAGDKALALGR RKSGPGPGFVVLRTVPHALSHVRS FRSLLLPLSLTLCVSFSFCLSVFPSL PCSDGANPWQSQSWKQEDGSSSPW EVSA |
| 966 | 6463 | C | 1000 | 1247 | 1716 | MLRPLRRCFFSSSQTACSSDLNRSV GSSQARPQGSPPSFSASCRKCSSLVH KEGPQLLVVGQVPSFYGPSTCPFHT AAADSAWPCRSRASFKVLSHDFHR PLVLLAAQRLPPARFPLGRLGARSH TAGGAERAGVGAAQQLQRRPRWP GRRARAPR* |
| 967 | 6464 | A | 1001 | 3 | 630 | FCPRGQEFGEKNKLLSPRRPWGHFT EEDQGLLSTSLGQG*ILEDAGRKK PLGKAPLVV\YPMGPQGFL*TGFGQ PCPSCPLPIMGQPPKVQGHMAKK\V LTSLGEMPIKH\DDPQGHLCPSLSE LHCDK\LVDPENFKLLGKCAGD\V FGNPFRQRIHPWRLQASWQKMAED GDCKWPVPCPPDTTEASWPMNSEA FKDKAFILASNYK |
| 968 | 6465 | A | 1002 | 41 | 625 | APSPDAHGVISQRRTKATNTSLLGQ G*ILEDAGGRKPLGKAPLVVLPKW DPKRSFEQALGNPVPLPSA\IMGQPP KVQGHMAKEGA*PSLGEMPIKH\LD DPQRAPFAPA*SELH\CDK\LVDPEN NFKLLG\NVLVTVLAIHFGKEFTP/E RLQASWAEDG\D*SGQCPVLQIPLK PLGP*IQKLSKDKAFILASNYK |
| 969 | 6466 | A | 1003 | 106 | 1315 | KQSGRAPGKVVSRAFPGLNPCPGW K\LLTQ\VGAAQVLGRLGDGLGAALG PGNRTHIWLFRGLHGKSGTWWDE HLSEENVF\IKQLVSDDKAQLASK LWPLKDEPWPIHPWETGSFKV\GL FDLKAGHVGLLWTKDGQKHVVTL LQVQD\CHVLKYTSKENCNGKIGNP VC*EGKTVSRFRKATSILEFYRELG LPPK\QTVK\IFNITDAAIKPGTPLY AASLFVQGGQYVDVTAKT\GKGFQ SCSLKRWG\FKGQPAYRIGQTENPT GRPGA\VAT\GDIGRVWPGTKMPGK MGKHIHGQNMGLK\VWRINTKPPIN YVNGSVTWDIKNCLVKVKADSKLP AYKDLGKNLPFPYHIFLMGDGRGNL PERFCID*KPCCQPRWRPPINICPNIL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WDVGRTLTI FL |
| 970 | 6467 | A | 1004 | 218 | 530 | KFEGCLPPRDETRIPWARRCAYVV *SKEVSL*HCNTVTPG\GKPNKTRVI WGK\VTTRAHGKPVAMVRAQIPEG NLSCLRPFGHR\IRSDGCYPSRILNLT EKS N |
| 971 | 6468 | A | 1005 | 2 | 269 | FESEDEGEEFDDWEDDYDYPEEEQ LSGAGYR\ADKMFLRTREPALDGGF QMHYEKT PFDQLAFIEELFSLMVVN RLTEELGCDEIIDRE |
| 972 | 6469 | A | 1006 | 1 | 456 | AELSELYEESDLQMDVMPGEGDL PKWEEATGTRAAIPWVPPATGAQQ LEEEGPMEEVEEAQPMAAPEGKRSL ANGPNAGEQPGQSPGRRTSRAEDE AEEFDDWEDDYDF\PREEPVKGAR LRFLPPS*KTPPSFWENRNTPLWGG LKIFY |
| 973 | 6470 | A | 1007 | 563 | 771 | WSMVSLCSTAAVAPVCSRIPERTRR ATASVTHFCGDLG*SPVKPLSLGYR SNLGGPEEGREGGRKARRK |
| 974 | 6471 | A | 1008 | 300 | 391 | AVCTMSEMAELSELYEESDLQMD VMPGEGDLPQMEVSGSGSRELSLRPS RSGAQQLLEEEGPMEEVEEAQPMAAP EGKRSLANGPNAGEQPGQ\VAGAD F\SEDEGEEFDD\WEDDY\DYPRRR SQLQWCPVTRVSAALEEA\DKMFL\ RTREPALDGRVSRCHYEKTPFGSV SLLSEELFFT*LVCQSV*PEEL\GCDA WRG |
| 975 | 6472 | A | 1011 | 100 | 270 | LRSSAVTVLVSLIHSPSSF AHHPSVD T*PHCLESPPGFKAIFIRGRLFTEACF CRIA |
| 976 | 6473 | A | 1012 | 13 | 670 | RQRPKARASIP LHQPPQEACQPPAA ALTRPQPRP/PSALSHPAKPHSVSSA GSSYKNNPFASSISKHGVSSGSSSSG GTPVQSSVSGSLVPGIQPPSVGQATS RPVPSSAGKKMPGFPEVDSGSPSRR SK\GDSSGGTQGVAKLLTSPSLKPSA VSSVT\RLPPCQKERVGLCCWPAPL *WLHPTNPAAQSC LGP*ARTPRGLG AAGVSLAQRKSLSTYRA |
| 977 | 6474 | A | 1013 | 3 | 578 | GIPWWTHASEAVQTEIPVVGPREW QSC*PRR/RLKPSAVSSVTSSLSLK GASGTVLLAGSSLMASPYKSSSPKL SGAMSSNSLGIITPVPIPV\QCSPSAL TPLPKQGS PRMPSSQALPPGPST\RP WPQSSGWLALQPAPCSASPTRCGA HPYPAESAR*SPDGQCAHAHRVPLP SPPLGALPLPRVLVSLP |
| 978 | 6475 | C | 1014 | 426 | 653 | MVTWGGGSHQRRERKEGPGTRVFM GREALES PCSASHCRPLLGFELSNT NLLWLFCYYLRLLCKQTGNPSCK KYI* |
| 979 | 6476 | A | 1015 | 1286 | 2318 | RTVPFYPMHLMVMMKTEPKIGVCK NPIIIVESTKVFS LKELHCHVPREKL APT VST/PLGVLSISQGGQCRSPSCGS/ GPEFCPL*AHSLGMGRHWDHPGSL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LQPEGAPEQWGALRYSDQMPGDQ ADSPTGVPTALPPEPVNTVPPTTAQ RKPQPRAAPLTTV*RQSCKAQSTGQ SAPPEQQGPGSLHGRHIRSAEKRSA ENSRSSRRTTPSSRKGA VSVHPGRPA RSDS\PRPKWQALPLKRSQFPWYSR PFPVKLRSTWKRVRKIRTQVFHAL* FP*GSSNQTSRETPK*QKSPNAECSR AQTSHETPASSYSCTLLLATAACKHTI TVKVGGHSAQCFQNSNSAVQL |
| 980 | 6477 | A | 1016 | 315 | 480 | |
| 981 | 6478 | A | 1017 | 1 | 1845 | |
| 982 | 6479 | A | 1018 | 1 | 447 | |
| 983 | 6480 | A | 1019 | 218 | 544 | SGFSLSLRGSISFSL/CFKVGMCVTY PRCYC*S\VPV*KPLIKPGWVSELPKP MNWASCSRTLASFLLQAARSHPW PMKMETMEQSKLRSQPCPKPAAGAV DPRAVVHGT |
| 984 | 6481 | A | 1020 | 198 | 562 | LKCGKQWSDPITSPQTESQLLGSSQ QQLHQQRHLQGP*K*NRDSPLCFSL SSCPIPKTYTNRHILLP/SSSKSLCKF L*PA*ISPQKMGFSFLSQSVCKFSKL LCSASLIKLFKAFNSIQVTS |
| 985 | 6482 | A | 1021 | 72 | 270 | |
| 986 | 6483 | A | 1022 | 545 | 812 | |
| 987 | 6484 | A | 1023 | 477 | 750 | |
| 988 | 6485 | B | 1024 | 537 | 867 | XEQAAPCSALSLPMASCLRGHGEA RADPWSSTRPIDLKFKGPFTDVVTT NLKLRNPSDRKVCFKVKTTVPHRY CVRPQQWNLLTPGSTVTVSVMLQP FDYDPNEKSKHKFM* |
| 989 | 6486 | A | 1025 | 822 | 1750 | SSAEPSPSSPAPSQQTAAAGAPPLC AVSPMASASGAMAKHEQILVLDPP TDLKFKGDG*VFIRPEQYYTV*KWC KRSKRHGPFRPFTDVVTTNLKLRN PSDRKVCFKVKTTAPRRYCVRPNS GIIDPGSTVTVSVMLQPFDYDPNEK SKHKFMVQTIFAPPNTSDMEAVV/W KEAKPDELMDSKLRC\VFEMPEN DKLNDMEPSKAVPLNASKQD\GPM PKPHSVSL\NDTETRKLMEECKRLQ GEMMKLSEENRHLRDEGLRLRKV AHSDKPGSTSTASFRDNVTSPPLSL VVIAAIFIGFFLGKFIL |
| 990 | 6487 | A | 1026 | 184 | 282 | VIASQNIFVLSSVTGPKDRSGRQPLV FLKSPG*THPS*SVSRNLFS\FA*PGD FRKTKGCRPDLSFGPVTLLRTKIFW LAIT*D*CFLGYIKMGHIVEHCQQ |
| 991 | 6488 | A | 1027 | 445 | 992 | HCCGRNCLQRRWGWKRVRSLLAGI VFVSPFFKLELQKPLPSEQITIGLML LPFPHFFCCFVFCFLFVCLFF*DRV MLCHPGWSAVVRSQLTVTSASRVQ AIICLSLPSSWDYRHPPCLAFSR/DR GFTILARLVLELMTS*ATTPSLFCCFI ADSVQQYAPSLYILRNTNPRLLAK IFVA |
| 992 | 6489 | A | 1028 | 33 | 476 | HEDHAGPEPPRSYIPPYNATVVQKL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LDQGALLMGKTNLDEFAMGSGSTD GVFGPVKNPWSYSKYREKRKQNP HSENEEDSDWLITGGSSRGSA AAVSA FTCYAALGSDTGGSTRNPAAHCG V/GFKPSYGLVSRHGLIPLVNSMDV PG |
| 993 | 6490 | A | 1031 | 187 | 1611 | RAWERQERQRSGCSWLTRGVRRG GEGRTTRRKMASKEMFEDTVEERV INEEYKIWKKNTPFLYDLVMTHAL QWPSLTVQW/LSLKVTKEGK\DM LHWLGLGHTSD*SRILVVARVHI PNDDSQFDAISHCSDKGEFGGFGS VTGKIECEIKIN\HEGEVNRAR\YM PQNPSHPLLTKTPSCLMVLVFDYTK HPAKPDPSGECNPD\RLRGHHKEG YGLSWNSNLSGHLLSASDDHTVCL WDINAGPKEGKIVDAKAIFTGHS VEDVAWHLLHESLFG\SVADDQKL MDM/WDTRSQYHLPRPSSLGWD HTA\EVNCLSFNPYSEFILATGSA D KTV\ALWDLRLNLRLNLHTFESH KD\ EIFQ\VHWSPHNETIFGFKCTC RR\N VWDLSKIGKEQSPEDAENGPP ENLL IHEGHQVKISDFSWDPPMKPW VICS \VSEDN\IMQIWQNGLKIFYN DERVR CHDHPKLEGKGS |
| 994 | 6491 | A | 1032 | 3 | 551 | FLLAPVEVSEGSFAEIWGQITGVGLF LCLGESPACWERGLSKRDLM SVKA CGPKAHFCLGYKAGGLPGTQRGAT QALL*KFEGVYARRMKPDSNLGRR CAYVV*SKEVSL*HCNTVTPG\GKP NKT\RVIWGKSKLGAHGKQWAWF VPKFPKAIFPA*RPFGHR\IRSDGC YPSRILNLTEKSN |
| 995 | 6492 | A | 1034 | 20 | 867 | ALERRVRKSGDCCTDSGTMNIFDR K\ITFDALLKFSHITPSTQQA/HM KK VYASFA\LCYFGAAAGAYVNM VT HF\IQAGL\LSALG\SLILMIW LMATP HSHETEQRKLGTSLLGFC IPYRKLGLGPALGSFVIAVKRQAS LPTAFMGHSNGSFPAFTLSALLC /RRPRS\YLFLG\ GIL\MSALS LVAFCPLG\NVFFWIPF WVFQAN LYVGLVVMCG\FVLFD TQLINEK AEQGDQDYNL/WHC\IDLFL DF UTVFQKNSMKDPGP*MKKDKKK RRRNEVTIQPFPI |
| 996 | 6493 | A | 1035 | 153 | 546 | PAQETGRPRSKAHVASTWRAFPPE DQVLLAGAP/LWEDEAHFWAKCG VEAL\TTLEVTRPACLEGK\VHGS L\ ARAWKSDEGQTPK\VAKQGER RKK KTGSG*/RRPDSSYNRRFCQ TLLPTF GKKEGPQWPTS |
| 997 | 6494 | A | 1038 | 1 | 433 | |
| 998 | 6495 | A | 1039 | 101 | 1898 | SAAMIGGLFIYNHKGEVLISR VYRD DIGRNA\DAFRVNVIHARQ QVRSP VHQHLLRTSFFHV/IRRS NIWLGSSS PRQN/VSTVAMVFE FLYKMCDVMA AYFGKIS EENIKNNFVVHYMELLD |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | EILEFGYPQEFRD/SGALKTFITQQG IQGVQAS/AQKEGSSQFTSQVTGQIG WRREGIKYRRNELFLDVLESVNLL MSPQGGVLSAHVSGP/VWVMKNYL SGMPECKFGMNDKIVIEKQGKGTA/ G*NQARAGKQSIADDLHLSTQCVR LS/KFDSERSISFIPPDGEFELMRYRT TKDIILPFRVIPLVREVGRTKLEVKV VIKSNFKPSL/LGQKIEVRIQPPLNT SGVQVICMKGKAKYKAGENSFVW KIKRMAGM/KNTHIIEIGFLPNKEK KKGGCPPLFPRNFGFKFAPSGLKVG /YLK/VLNPCLNYSDDHVIKWVR*U GRISGIYENSACKATRQLAQLPQPPF LQQVQVPLLPQTTHQVSPSPPCFAC PSPLQPSPEVLGLGQSNITKWDRWK QPLGSPGQGSSEGS CSPHPVCSWP NAQALSSVTQSPGGFPFLPHPCGHS SGVGGLVAPHLRAPPKASEWIPGLS PYSALG |
| 999 | 6496 | A | 1040 | 255 | 662 | TGEGYAGTEATDITHPQLRNQQWV PRCKPFPICDLKIQPERNYLFFLR/QR VSLCHPGWSAVV*SRLTATSAPFGS SYSPAFSLPSSWDYRCAPPRPANFCI FSRD/RGFTMLARMVLIS*PVIHPP WPPKVLGLQA |
| 1000 | 6497 | A | 1041 | 2 | 297 | TLILPQHVNCPPGINAWNTITSYIDN QICQGGQKNLCNNTGDPEMCPENG CVPDGPGL/VLRDSGSHHSIRLHSA/ LGDPAKPSQDFMNYIGLTIDLRSI |
| 1001 | 6498 | B | 1042 | 1 | 786 | MAPHDPGSLTTLVPWAAALLLALG VERALALPEICTQCPGSVQNLSKVA FYCKTTRELMLHARCCLNQKGTIL GILPQHVNCPPGINAWNTITSYIDN QICQGGQKNLCNNTGDPEMCPENG CVPDGPGLLQCVCADGFHGYKCM RQGCLSAAPQALAGKWPPKNCHL PSFVDGQPQGGQKEPCNNYPSIYTFV PVCQGICGKMLKTELLHLKYWDIG PGNRNSYKFAAGNVKFAVTLENSL LIPQKAKRNYHMTQQFRS* |
| 1002 | 6499 | A | 1043 | 137 | 1021 | GRAEAGSLASQCVALASGSPVLLG GPAVLISLTLDPAPQDMHPMSRE RAKFVKSL/YCKTDTKS*CLHA/RC CLNQKGT/ILWGLDLQ/CSL/EDPG QNFSIRHITTVIDLQANPLTGDLAN TFARGFTQLQTLILPQHVNCPPGINA WNTITSYIDNQICQGGQKNLCNNT GDPRKCVPEKGILCYLNGPKVFWQ CVCADGFHGIQSVLPGLVPHCL MFLREFWEPTHSIRL/HSAVFGGPSA* KAKDFHGTIYIGSLPFDLKLINLELSLA PVRGALLPRKGIFRPVGFRLKG |
| 1003 | 6500 | B | 1044 | 203 | 308 | XRPLFAPVRARAVEAAGPGSGRAA EHSPTGTAGCA* |
| 1004 | 6501 | A | 1045 | 78 | 308 | |
| 1005 | 6502 | C | 1046 | 35 | 259 | MQFSTHRGQKYERTPDTSGARVIER PYLTVIIHNNLEGLRLKEKSGKPYKF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AFYVILRCHFTDNFTTAALFVTR* |
| 1006 | 6503 | A | 1047 | 162 | 1341 | PPFQLIMGEIKVSPDYNWFRGTVPL KKIIVDDDDSKIWSLYDAGPRSIRCP LIFLPPVKWNCKMSFSRQILALTWM GLTGLIAFAVIPVYCDHLEFCDGFR KLLDHLQLADKVHLFGRFFGKGLWP MRFTGIPLQIS*SPIPLILCNSLMDTS IFNQTWDCKQLLA*CPAFMLQKNSS LG\VFHPGPGGPYGWAGCHLDFHG* DRA*ESFGVQELNLAQGLTLELSK FLCGNLH*NSGTYL*TYGMCLDPG GGAFLKLKKKWKLYPNPGPKL HLKTGGNFPYLCRSAEGNLMVQIH LLQFHGTKYAAIDPSMVARPRSLRC RKAALASARRSSSVSSSPVNDLTP VCSLYSQWAFSTRSDRPFPFQVPSG LTRGPHWGLGKVGLDGHL |
| 1007 | 6504 | A | 1048 | 321 | 888 | VELSVHPPIPADPRSLLAGAMPWKL PISLPAEPPCSLSCCLLPATQHPLH PALPAVDGAKKNPVFSGRLPPPP/PT QRTSASGISALYA*DREV*AQISELW AMRG*VQKVGTVQISRAGQLAAV TSVGNMSVYPLALMTPPPPSPPLPP PPPPVGRWSVGLRDLSPA VPSSEV CLWRSVLCLIPGY |
| 1008 | 6505 | C | 1049 | 137 | 320 | MLKSSFTCFPTEKGPKFLEDNLKTK XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXLV* |
| 1009 | 6506 | A | 1050 | 231 | 477 | GVYFIFIGLVVFCFVLFDDGRFTVA QAGVQWCDLGS LQPPAPGSNDSP WPQLPE*LGITGACHHARLIFILLE TGFRPC |
| 1010 | 6507 | C | 1052 | 60 | 523 | MAEAGFIHCPTENEPDLAQCFCK ELEGWEPDDDPMQRKPTIRRNLR KLRRKCAVPSSSWLHGLRPLRXLP PRVAAPLPGFIPWCHQPSCGPLSNV LGKEINIFKLDVSTVLLFCLESGTRG VLPVQVRVLLVQLLALSLSPPFGGPF WRFE* |
| 1011 | 6508 | A | 1053 | 61 | 208 | IFETGQRKSQEQNWSYSVTQA/GVQ WCDLGSPQPRPPGLK*FSHLSYMG |
| 1012 | 6509 | A | 1054 | 198 | 1011 | QTHGLQQPSQHLP/TSTLRTVTAST/ SMRSRHHCHGR LCHANKAVSSSKR DTAFLPHFSPGKPGNQNSKNEPPK KRERERSSH CYPAAPAAQAEAPLVP LSRQNKSTVETSNLKM LSF PKTLR GPQEGWWHQGINPGSGAATLGPGS SERPQSIEASCSMARRTFFAVSSNSF FLLLVSFALFLALSLSFKNSPRVNS SNCFLTERKAQPDECFLCSSMGSSS GSQPSSSLKQKKHWAKSGSFSVGQ WMKPASAIRSGVQRSPPRRASS |
| 1013 | 6510 | A | 1055 | 1077 | 1457 | ARRPEPPHPAHRRG GTPAQGGAG SPGASSDTSLRLEAPPQSIACWRSCC NAASWWTRSRGTCSRQTQR*GWP* CWRAQRGCAPALAAPQPFLAAHHG QRSAAASTTPGLHAGLRRSRPPRP PRP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1014 | 6511 | A | 1056 | 2583 | 3580 | DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTSDSPT LASQSAGITGVNHHAWLFFFC/SD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRYPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHT/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLYFIYFHRDEGSLCCPGWS* TPELK |
| 1015 | 6512 | A | 1057 | 166 | 409 | WSDVVGTRHLSAASFNSHAFWNLE EELTLVKGQALPSRGLDCPGRPAPP AACPGPKWRACLWV*FPNQNPISPG RNFNLKT |
| 1016 | 6513 | A | 1058 | 10 | 604 | ARPPKKPTSPTATTTTR*GARPATPP PRRPTAPIRWCTPSTAPPRACI*AT AP*QPQAPHQQTAAALFWASPPPSH QAPWIPPFLPQPPS/LPPPPHSPRGP PGAQGGGAPAEKPWRPWTAR*D WTPPGAGLELGGSPGLWGHRRARE GGAGEGRGFEDRTGRFYKRIFVGR GDSKLPGRGSFRSFSKGFFLCF |
| 1017 | 6514 | B | 1059 | 167 | 355 | MASGSNWLSGVNVVLVMAYGSLV FVLLFIFVKRQIMRFAMKSRRGPHV PVGHNAPKRSHFILK* |
| 1018 | 6515 | A | 1060 | 67 | 458 | |
| 1019 | 6516 | A | 1061 | 164 | 528 | |
| 1020 | 6517 | A | 1062 | 203 | 364 | |
| 1021 | 6518 | A | 1063 | 103 | 1019 | GNGRGAPGDPCAVASAEPGLTSQD SGVNPNNNSARGREAMASGSNWLSG VNVPLVMAYGSL/DVCTAIYFCEEA NHALCNEISKGTSCPCGTQCPQGT* K*EIDIRLSRVQDIKYEPQL\AADD ARLLTTGKPRGNQSC\YNYLVIGM KALGLPFRTS\EIFHSEGRHSPFP* WGKNFRSYLL\DLRNTSTAFQGCTA KHLIDTLFGMAMET\ARYGDKGVF WPRMKYLRVQEALSELATAVKARI GELFSDIH/HVQAAKDLTQSPEVSPT TIQVTYLPSSQKSKRAKHFL\ELKSF K\DNYNLTLESTL |
| 1022 | 6519 | A | 1064 | 1027 | 1365 | PEVNRLYCLFKNKI*KALLSFQTYIC IYVLDVLIREKMFVKMCQVVVCVAC IYMCVCVCIIH*CVCVCIIYHTHTHT C/VCDW*AIQ**TCPHYFFLILDQCC PNCTFPLMVTML |
| 1023 | 6520 | A | 1065 | 675 | 819 | HRLDRAHP*RAEGNCLLPVYLSY/G PLIA*TGQGTSSPCLCSL/*PRSAIHT PSQPGDPRQPQTVHSGELNPRVYTK |
| 1024 | 6521 | A | 1066 | 3 | 603 | VDDFVQPARRRWEMLGVLPSVFLG LRRFVHPAKGMKQTRGDSFAFQSG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SPGVCFEGQEAEGSLSYGVGLIAAG FVLLSPPSQC/HDSLATQVLVCGVA LLWPSSGRAGTVQP*PAPENRSASP FCLPGHIQVPVFTVPRSAITHTPSS NLGTPRQPQTVPLRGAESPGQPCPM SLRKLPQARPLVLYTCSCHPAVDEC FR |
| 1025 | 6522 | B | 1067 | 46 | 1983 | MRPRKAFLLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DEEEDDLEVKEENGVLVLNDANFD NFVADKDTVLLIFYAPWCGHCKQF APEYEKIANILKDKDPPIPAKIDAT SASVLASRFDVSGYPTIKILKKGQA VDYEGSRTQEEIVAKVREVSQPDW TPPEVTLVLTKEFDEVVNDADIIL VEFYAPWCGHCKKLAPEYEKAAKE LSKRSPPIPLAKVDATAETDLAKRF DVSGYPTLKIFRKGRPYDYNPREK YGIVDYMIEQSGPPSKEILTLKQVQE FLKDGDDVIIIIGVFKGESDPAYQQY QDAANNLREDYKFHHTFSTEIAKFL KVSQGGQLVVMQPEKFQSKYEPRSH MMDVQGSTQDSAIDFVLKYALPL VGHKVSNDKRYTRRPLVVVYYS VDFSFDYRAATQFWRSKVLEVAKD FPEYTFIAIDEEDYAGEVKDLGLSE SGEDVNAAILDESGKKFAMEPEEFD SDTLREFVTAFKKGKLKPVISQPV PKNNKGPVKVVVGKTFDSIVMDPK KDVLEFYAPWCGHCKQLEPVYNS LAKKYKGQKGLVIKMDATANDV PSDRYKVEGFPTIYFAPSGDKKNPV KFEGGDRDLEHLSKFIEEHATKLSR TKEEL* |
| 1026 | 6523 | A | 1068 | 1 | 849 | |
| 1027 | 6524 | A | 1069 | 74 | 2705 | KKLDFFRSLPVFQADFSHWQLFRVL FLLHPLVISMDSWFLVLLGSGLIC VSANNATTVAPSVGITRLINSSTAEP VKEEAKTSNPTSSLTSLSVAPTFSFN ITLGPTYLTTVNSSDSNGTTRTAS TNSIGITISPNGTWLPDNQFTDARTE PWPGNSSTAATTPETFPSPGNSDSK DRRDETPIIA VMVALSSLLVIVFIIIV LYML/RGFKKYKQAGSHSNFRLS NGPH*GMWEPQSVPLLAARSPASTNR KYPTPGPWDKLEEEINRRMADDNK LFREEFDALPACPIQATCEAASKEE NKEK\NRYVNILPYDHSRVHLTPVE GVPDSYINASFISGYQEKNFIAA QGPKKETVNDFWRMWEQNTATIV MVTTLKERKECKCAQYWPDQGCW TYGNIRVSVEDVTVLVDYTVRKFCI QQVGDMTNRKPQRLITQFHFTSWP DFGVPFTPIGMLKFLKKVKACNPQY AGAIVVHCSAGVGRITSTFVVIDAM LDMHTEKVDVYGFESRIRTRQ* QMVQTDMMQYVFYQALLEHYLYG DTELEVTSLETHLQKMYNTIPRTNT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NGL*EEFKKLTSIK\QNDKMRTGNL PANMKKNRVLQIIP*EFTRVIIPVKR GEENTDYVNASFIDGYRQKDSYIAS QGPFS\HTMRDFWRMIWSGKSCSIV MLTELEERGQEKCAQYWPSDGLVS YGDITVELKKEEECESFTVRDLLVT NTRENKSRQIRQFHFHGWPEVGIPS DGKGMISII\AAVQKQQQQSGNHPI TVH\CSPGGKERTGTFCALSNVL\E RVKA\EGILDVF\QTV\KSLR*\QRPQI GSRQLEQY*VLAYKVVPGVILDAIP QINACLQSKAANKGPVDPGGLPFNI LVIFLFC |
| 1028 | 6525 | A | 1075 | 734 | 1151 | YRRGPGGLRWAEMSGDFPIPLPVR GIHPIPLRASQ/PVL*GGQQGMGTGP ISQ/PGETEFQTGLSACPKPHRVPGP SSCTTEKPSQRLHEQMVRGG*SSMG GAGNGVGMESGTVQGTSGSGWR PAGTGVGARNCWYLL |
| 1029 | 6526 | A | 1076 | 118 | 399 | |
| 1030 | 6527 | A | 1077 | 1 | 214 | LLMRVSLPSEVFFCVVFETESRFVT QAGVQWHDG*LPPPPFRK*FSCL SPPSSWDYRHVPPCLANFCIF |
| 1031 | 6528 | A | 1078 | 2 | 152 | ETESLYVTQAGV\QWHDGSLQPPP PRFK*FSCLSLPSLTTFDTSLKSME |
| 1032 | 6529 | A | 1079 | 2 | 426 | |
| 1033 | 6530 | A | 1080 | 1 | 1716 | |
| 1034 | 6531 | A | 1081 | 2 | 886 | VGGRGEALDGGGSGAPPSVSQTES RAGTMSAYPKSYNPFDDGEG\EG ARPAPWRDARDL\PDGPDAPADRQ QYLRQEVLRRAAATAASTSRSLAL MYESEKVGVDSSSEELARQRGVLEA HREDGGTRL\QDLKISQKHINSI*ER VLGGLVN/YTFKSKPVE\PPPE\QNG TLTSQPNRLKEAISTSKEQEAQYQ ASHPNLRKLDDTDPGPPEAWASAP GVLMLTPKNPHLRA\YHQKIDS\NL DELSMGLGRLKDIALGMQTEIEEQ DDILD\RLTTKVDKLDVNIKSTERK VRQL |
| 1035 | 6532 | A | 1082 | 1549 | 1712 | SNL*FFFFEMESRSVA\RL\ECSGVIS A\HCNLC\PGSSNSPT\SAS*VAGITG A\THHSRLLFVFLG\ETGF\HHVG\QA GL\DSLTLMIQPALASPKCLGLQAVS PPMPSPYSSSFFCPLNILTPHVLYPG LNPPSSFCSDL |
| 1036 | 6533 | A | 1083 | 2 | 336 | |
| 1037 | 6534 | A | 1084 | 218 | 1080 | PSSRMNHLPEDMENALTGSQSSIAS LRNIHSINPTQLMARVIESYEGREKK GIS\DVREDFCLFVTF\DLLFVTLW D**EFKC*MGGHLRNTFRRRR*LQY *LTISSIFLILFLPGQFFRF*KCLILAY A\VCRLRHWWGQ*RLTTAMTSALL LAKVILLKLSSQGAFGVYVLPFTSFIL AWIETWFL\DFKVLPQEAEEENR/L SLIVQDASERAAL\PGWSFWMGQF YSPPGIRRQDLEGLKEKQGQLRKP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LFRNYEYYFLFKCGKLTESHARGKK RQAVESPCRQ |
| 1038 | 6535 | A | 1085 | 3 | 400 | |
| 1039 | 6536 | B | 1086 | 333 | 436 | XTPVFSYGDEIGLDAAALPGQPHEG LLLRFPYAA* |
| 1040 | 6537 | A | 1087 | 127 | 2041 | RGVWGGHVPGGSREEWSGEDQGG KRRGDAVAENCAEAREAGESVLGP RVQVGVEPPSDRKLRRVAGSAGTM SQDTEVDMKEVELNELEPEKQPMN AASGAAMSLAGAENGLVKEIFPQ KKKGGGSAEDEAEAAAAAKFTGL SKEELLKVAGSPGWVTRWALLL FWLG\WL\GMLA\GA\VIIVRAPR\C RKL\PAQKWWHTG\AL\YRIGEPLRP FQGQRRGANLAGSLKGRLDY\SSSL KVKGLVLGPIHKNQKDDVAQTDLL Q\NDPNFGSKEDFRSL\HSVKTKNL RGILD\LT\PNYRG*ELRWFTSQVDT\ VATKVKDALEFWLQAGVDGFQVR DIENLKDASSILGLSWQN\ISP\KGFSE \DRLLIAGTNSSDLQQILSLLESNKD LLLTSSYLSDSGSTGEHTKSLVTQY LNATGNRWCSWSLSQAR\LLTSFL PAQL\RLYQ\MLFTL\PGTPVFQAT GNE\IGLGCSCPLLGPMPGGSQFML W\DEVPAFPDIPGGC*VANMDCGR GQSEADPGSL\LSL\RRRLNDQRSKE APPYCHG\DF\HAF\PLGPWTLSPH QLGTQNETFSG*CLNLGDVGLSVAG\ LQASDLPASAKPWPADLLSTQ PGREEG\SPLELERLKLPEHE\GL\LL RFPYAA |
| 1041 | 6538 | A | 1088 | 652 | 905 | HLLPPLTPTTTQWGRDLLSPISQM RKLRRHRKVKKKTRT/WPGVVDHPL\ NLSTLGGGAWRIA*GQEFETSLGNI ARPCLYKKKFK |
| 1042 | 6539 | A | 1089 | 3 | 591 | |
| 1043 | 6540 | A | 1090 | 266 | 1905 | LGGHTWGTAAAGVWSDWPGRSW AELTSENSAGLSPSWGSPQDEVPGA WPMLQGAVEPMQIDVDPQEDPQN APDVNYVVENPSLDLEEFASYSGL MRIERLQFIADHCPTLRVEALKMA LSFVQRTFNVDMEYEEIHRKLSEAT RSSLRELQNA\DAIPESGVEPPAL\D TAWV*\VTRKKALLKLEKLDTDLK NYKGN\SIKESIRRGHDDL\G\DHYL\D CGDLSNALK\CYF\RP\RDY\WTS\AKH VINMCLN\VIK\GQRFTLQ\NWSHVLS YVSKAESTPEIAEQ\RG\ERDSQTQAIL TKLKCAAGLAELAARKYKQAAC LLASFDHCD\PELLSPSNV\AIYGG FCALVTF\D\RQELQRNV\SSSSSFQV VLGSWEPQVRDIIFKFYESKYAS\C LRLDEMKNLLLD\MYLAPHVRTL YTQICN\RALIQYFSPYVSPDMHRM AAAFNTTGGPPWKNELIKFIL\EGLI SARVD\SHSKIL\YARD\VDQRR\TTF* ESLCLMG\KEFQRRAKAMMLRAA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VLRNQIHVSYPYPTQRKDARGELTPA NSQSRMSTNM |
| 1044 | 6541 | A | 1094 | 2 | 397 | SQDHVRGFLEKESAI VS RPLNPFTA KALSGTSPGDSDDVQPGPSVGPPSK DKDKVLPSFWIPSLTPEAKATKLEK PS/RLECVEKLIRKDMVDPVTGDKL TDRDIIVLQRGGTGFAGSGVKLQAE KSRPVMQA |
| 1045 | 6542 | B | 1095 | 30 | 310 | MTRHGKNCTAGAVYTYHEKKKDT AASGYGTQNI RLSRDA VKDFDCCSL PRSCCHAYEKQ RG TRREEQKELQR AASQDHVRGFLEKESAI* |
| 1046 | 6543 | A | 1096 | 29 | 449 | |
| 1047 | 6544 | A | 1097 | 2 | 1069 | IETRCTPRCRNSARGESLVRMTRHG R\NCTAGAVYTYHEKKKDTAASGY GTQNI RLSRDA VKDFDCCCLSLQP CHDPVVT PDG LYERE AILE \YIL\H QKK\ELARQM KL TRKAGGGTRPPK EQKELQR\AASQ\DHVRGFL\EKESA IVSRPLNPFTAK\ALSGTSPGDSDDV \QPGPSVGPPSKDKDKVLPSFWIPFA TPRAKATK\LEKPSRTVTCPHVKGS PLR\MSEPERPVHFHNR* NSS \VEPR GASITPQASAYVCA\VTR\DSLSKRQ PPVAVLRPSGAVVTLE CVE KLIRKD MVD DPVTG \DKLTDRDIIVLASGAVT GFAGSGVKLQAEKSRP\VMQALRC AGGPNKPGLGP |
| 1048 | 6545 | A | 1098 | 5 | 576 | SRVVEFAKMAENSGRAGKIIRDDSG VKGAVSHEQVIAGLQTTFG RN QRG LASQS/AAELGDWKLNEATALVIDT TGREV\DET TRK CYRMVWKEFLVEA NLSKEVACPAFGRTTKEQIQKII*DT *HSSFQAKGKELK*ISGKKHNI/RVL MGEDEKPSQPKENS\EGGLGLKAS\S AGVVWSPRDQGLC IFF LP |
| 1049 | 6546 | A | 1099 | 534 | 1004 | RMSAGALFIWGTANYFDRKKTEVT PNFQEPGFRERRKKQKLAQGEKLG FPKLPD\LKDAEAVQKFFL* RNT SL GEEL\LAQ\GEYEKG\VDH\LTKEPLP VCGQPTASLLQVL/QQANFFPPPV\F QMLLD*SSPTISQRI VSA QSLAEDD VGM RN KCLH |
| 1050 | 6547 | A | 1100 | 91 | 942 | GLLVGVGAAAVMPGIVELPTLEEL KVDEVKISSAVLKAA\AHHYGA\QC DKP\NKE\FMLCRWEEKDP\RRCLE\ EGKLVNK\CALDFFKA**NRHCAE/P LFLQEYWGLCIDYTRPSKLPSTVR KQAGKSFDEC\VL DKL \GWVRP*PG ENCQKVTKVK TDR PLPENPYH\SRP RPDPSP\EIRGEILQPA\THGS\RFYFW TKLKMGPVAHTRSCAQT TT DENAH AGLHPTDSGVLSGIHQHLTKKLTYD DLAVILYHFLSIKIFKGEAPPLQHYP QSHQTTLCSPPQNP |
| 1051 | 6548 | A | 1101 | 140 | 812 | GDFGDRAGAGRETEEIFHSSQQLKI RPWAGAGRAAEPKDWRIWGTGEW GSRQIPSPVPSPSRNP HFL PQAGAG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HFVQNPCKYPTPSPLQRSLEELPLSP TVFKLLHPDPPPCKAPLTLQPVAPK *I*ESPPLPPMLDPRDFPSPAPHPANE LKKRRGNPRQWFFLSEPRLSHLQN GTGWGWKGKDGRGRRTGMELGLI PEAPVPISGPPFIHSHSQPPCYTGL |
| 1052 | 6549 | A | 1102 | 228 | 860 | STAQGNLLTVFIQPRASMSGGKYV DSEGLYTVPIREQGNIYKPNNKA MADELSE\KQVYDAHTKEIDL VNP RPLNIFNG*PWSKIDFKDVIAEPEGT HRF*RAFGKASFHLSL*RKYWFLP LCWSALFGHPRWALI WGHFTSANS LLFLAHL/WAVVP\CIK\SFLI*GFQCI SR/VSYSILRSTTGLVTPLFEAVG\KI FQQLSASNQKEI |
| 1053 | 6550 | A | 1103 | 825 | 920 | |
| 1054 | 6551 | A | 1104 | 222 | 1244 | RWEKKMALLCYNRGCGQRFDPET NSDDACTYHPGV PVFHDALKGWSC CKRRTTDFSDFLSIGGCTKGRHNSE KAPEPVKPEVKTTGTCELCELKPK FQEHIISSPLSQ*KQLKRPSDEPMT NLGIKNIWPPLKQALDKLKLSSGNE ENKKEEDNDEIKIGTSCKNGGCSKT YQGLESL EECVYHSGVPIFHEGMK YWSCCRRKTSDFNTFLAQEGCTKG KHMWTKKDAGKKV VPCRHD LHQT GGEVTISVYAKNSLPELSRVEANST LLNVHIVFEGEKEFDQNVKLWGI DVKRSYVTMTATKIEITMRKA EPM QWASLELPAACKQEKQKDDTTD |
| 1055 | 6552 | A | 1105 | 87 | 313 | ISQERG*RRDKERLAQREIK/RRRER EK/ER*EERIDKKREAKREKR/ERER KIP EEEEEERKKGIFVFIWFNPMSVP H |
| 1056 | 6553 | A | 1106 | 37 | 404 | PQLSRCRSECMYVNPTVVM TSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPAPVPCALGRGGRER WAAASFLYAPDPRPAHEVEHV N AILFLLSDRSGMTTGSTLPVEGGFW AC |
| 1057 | 6554 | A | 1107 | 19 | 919 | AVWWNSELFLAGRRVLVTGAGK/G WAAGKGGQRPAAGRGGQGTPSLSP LPAGIGRGTVQALHATGARVVA\VS RTQADLDSL VRECPGIEPVCVDLGD WEATERALGSVGP\VDLLVNNAAV ALL\QPFL\EVTK EAF\DRVCP SASRS FE\VNLR AVIQVSQIVARGF/I*ARGV PGAIR/VNVSSQCSQRAVTNHSVYL LPTKGVPLDMLDQG*WAL\ELGPH KLSRCRSELNASKP/TTVGD*RSMG PGPPWSDPHK\AKIMLNRIPLGKFA EVEHVVNAILFLLSDRSGMTTGST LPVEGGFWAC |
| 1058 | 6555 | B | 1111 | 28 | 384 | MKA AVLTLAVLFLTGSQARHFWQ QDEPPQSPWDRVKDLATVYVDVLK DSGKDSVTSTFSKLREQLGPVTQEF WDNLEKETEGLRQEMSKDLEEVKA KVQPYLDDFQKKWQEEMELYRQK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | * |
| 1059 | 6556 | A | 1112 | 44 | 1009 | GGIREGGPPRPFRMKA AVLTLAVLF LTGSQARHFWQGG*SPPRAAWDR VK\DLATRVPWTVLKEQRTETYVS QFEGRLRGENS*TLKLL\DNWGQR* PSTFQPSCAKQLGPALTQEFWYNLE KETEGFRQEMSKDL\EEVKAKVQP/ YTLDDFQERSWQEE MEL YRQKV E PLARKNFQEG\ARPESLHELARRSL PLGEAVSRPRARPMWDALRT\HLAP YSDEMMPALGRAPLGALRENGGAR MGQYHA\QATEHLSTLSEKAKPALE DLRQGLLPVLESFKVSFLSALEEYT KKLNTQLRRPPPPYPVLRINVSKV EKKKKK |
| 1060 | 6557 | A | 1113 | 62 | 393 | IPAKQPTPTSLKTPTEECDQHENTAS SPSPMTPPCT/PSTNQPSPKLPVSHSP NP*KPPAPKLLREMDLTFPPHFPPSV APTMKPLSSATTPMPRRISLSGSHSR RWDPFVG |
| 1061 | 6558 | A | 1114 | 3 | 450 | QTQREPTMVLSPADKTNVKA AWG KVG AHAGEYGA EALER\MFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVA DALTNAVAHVDDMPNALSALS DLH AHKLRVDPVNFKLLSHCLLVTLAA HLP AEFTP AVHASLDKFLASVSTVL TSKYR |
| 1062 | 6559 | A | 1115 | 9 | 675 | NSARATDSERTHHGARLLPDKTNV KA\AWGKVG AHAGEYGA EALERM FLSFPT\TKTYFPHFDLSHG\SAQG* RAHGK\KVA\DALTNAVAHVDD\DM PQTALSALSGPATAHKLRVDPVQL SSS*SHLPCWWTLGRPTSPSEFNPW RLHAFPGTKFPGLLVEAPLLEPSKLP LKLGSLRVGHAFAPLGLPPRALLP FPGTRNPVGLLNKILNWGGKKKKK KKIF |
| 1063 | 6560 | B | 1116 | 61 | 348 | ESALTQLLKAGGSLKKFLFHPGDTV PSTARIGYEQLALGVIAAGAGAI VH EKHPGKLAGYISSLLTLG FATAMA AVVLCVNSFIWQTEPFLYIDT* |
| 1064 | 6561 | A | 1117 | 2 | 256 | CLSCAFWAGSVVIAAGAGAI VHEK HPGKLAGYISSLLTLTG FATAMAAV VLCVNSFIWQTEPFLYIDTVCDRSD PVFPTTAIVL |
| 1065 | 6562 | A | 1118 | 3 | 270 | AVVLCVNSFIWQT/EPFLYIDTVCDR S/DALFLAVCVLKVIVSLVSLGVGL RNLCGQSSQPLNEEGSEKRL LGENS VPPSPSREQTSTAIVL |
| 1066 | 6563 | A | 1119 | 1 | 642 | |
| 1067 | 6564 | A | 1120 | 46 | 998 | AIVPSWDLDDKDTISLLSPVLCIFPSPS SQTSLLYVFSLAGRMTQNTVIVNGV AMASRPTQPTHVNVHIHQESALTQL LKAG\GSLKKFLFHPGDTV PSTARIG YEQLAL\GV TQIFAGALRGVILGVC *SWGPGTVLRASGCAFWAGSVVIA AGAGAI VHEKHPGKLAGYISSLLTL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | A\GFATAMAAVVLCVNSFIWQTEPF LYIDTVCDRSDPVFPTTGYRWDAA KSRRNQWQKEECRAYM\QMLRKLF \TAIRALFLAVCVLKVIVSLVSLGVG LRNLCGQSSQPLNE/EKGSEKRLLG ENS\VPPSPSREQTSTAIVL |
| 1068 | 6565 | A | 1121 | 504 | 1026 | KIKRKKKRPHIPVLRIPGLLNIPCL WLEWVTLSPSKRFAFAVGGN GGESGWLGGTRP/PSPRGMHLP GSSSSESEPHRNCPCPGSAQPCGHQAGS EDPQNTGPVAS/EL*PPACWRLCGQ PGPL\GAPAAPLAGHPRPPWRQVGP GTSGSSQSWVSSCDHGGQHSGQH SWQ |
| 1069 | 6566 | A | 1122 | 461 | 548 | KNLEQKNAMIHSAGEHHQGAERRS TWEELEGPRVTSLTLLV*RAWSSGP APSPT*PPSCTPPRRSS*APAGPSDAS PSRRPRA/SPASRQAAPKDKLPETPR RRIEKEP\PGPFAPGIFE/GGFTVSGG REQETPFAGTSGCY/RPTPPHFCWL GSPPRSTSSKAGGPSSSPSPTEAES STARPAKSRTMPTSGWHIGSTRPPR RRPSPR*RTSCTAHRRTSCSFGTMP ARSRGLHSEIRRLQHQCTDLTYELT VKCSEQTGDGTSKSELKKRCEELE AQLKVKENENAELLKELGAEKRDD SQCWRTPSRSREKKYLGA |
| 1070 | 6567 | A | 1123 | 148 | 197 | DPLGFL*QKRNQQEDD |
| 1071 | 6568 | A | 1124 | 1333 | 2383 | RMKKEHVLHCQFSAWYPFRGVTI KSVILPLPQNVKDYLLDDGTLVVSG RDDPPTHSQPDSDEAEIQWSDDE NTATLTVAPEFP*SLPLKVQGSYQIP LGGQVSFPKV*FGS\APRD\AYWIA MNSSLKCKTSLDIFLLFKSSDFITRD FTQPFHCTDDSPD\ACIEYELVLEK WCEMIPGG\EFRCFVKENKLIGISQR DYTQYYDHISKQK\EEIRRCIQDFFK\ KHIPVQIL*MKDLVFDIYRDSRGK VWLIDF\NPFGEVTDSSLFTWEEL\AS ENNFKRRFLVKVDAQEODSPSFSVA QTSEVTVQPQPLICSYRL\PKDFVDL S\TGEDAHKLIDFLKLKRNQPEGR |
| 1072 | 6569 | A | 1125 | 162 | 413 | GADGQINQQTLD DRS GDECLDECP GPPRRGKGPPQREVQPASPPGT HQ*GSDGSSCTPSPV\SIGSPGLGPPI WRPHPKPG |
| 1073 | 6570 | A | 1126 | 2 | 228 | GGPRNKEPYPQGPKNRAQSPKNLV HSLTSM*SSP/LPFKPSKSTIDNCPLT HQ*NPLKP*PLFPPSPNIPPGFKKP |
| 1074 | 6571 | A | 1127 | 302 | 488 | SPICLTPKSSLTHSSDDYKYSVWQR AVAHTCNPSTLGAEAG/WVT*AEEF KTSLNIVRPCLY |
| 1075 | 6572 | A | 1128 | 66 | 703 | RRRLPSVAIMILPGPSSSHDEMFS DIYK\IRGDRGRGLCLEGGRGRWVS RTE\GTID\DSLIGG\NA\SAESPRGAK GTERHK*STGV\DIVMNHHLPGNKF SQKEASKKVHQRTMKSIKGGKP*K NRRPRKSKTFL*QGAAEQIKHILAN |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FKKLQF/YFIGENMNPRWAWVLLLDY*RDGVPP\YMIFFK\DG\LEMEKMLTNVAIILDLSPPCHP |
| 1076 | 6573 | A | 1129 | 1 | 1006 | LLLLGHASTSTGGGGKRASKMATT KRVLYVGGLAEEVDDKVLHAAFIP\WGDITD\QIPLDYETGEK\HRGFAFVEFELAEDAAAIDNMNESELFGR IRVNLAKPMR\IKEGSLARPACSDNDWLKKF\SGKTL*ED*RGRVRASQSRDPG/TGRAHLLKRRRSNPQVYWD IKIGNKPAGRIQMLLRSDVVPMTAE NFRCLCTHEKGFGFKGSSFHRIIPQFMCQG\GDFTNHNG/TLGGKSIYGEE VSMMENFILKAYGDQGLLS/MLACGDPNTNGSQF\FLTC*KTDWLGWASHVVFGEVHRKALGCLCGQIEAQG SKDGKPKQKVIIAGLWGSTC |
| 1077 | 6574 | A | 1130 | 1 | 574 | DTRFLERLRLSISFLVQTPIGHSTEEDQGLLSTSLWGK\VKCGKNAGRKKPLGKAPLVVLPPWDPKRFL*KSFGQTL SLCPLPHPWGKPPKSQRHHGKERCLTFPWGDAHKAPLDDPQRAPFAQA *VNLH\CDKPAMWDPENFQAPGEMLLVTVL\AIPFSGKEFHPWRLQGFLGRKMGDLELASALVPSRYH |
| 1078 | 6575 | A | 1131 | 200 | 740 | HGSMRRLLIPLALWLGAVGVGVVSQI*ENPSPGGLQVALEEFHKHPVPVQWAFQH/TAVLESAVDTPFPAGIFVRL EFKLQQTSCPEEGTWKKPRVQKSRPQWDGNRKLPWPCIQTWALEDKSS WARLVPPPIKTQVLAGGWRSTQEDPSCLRVRAC*RTPPSFYFPGQFAFSKIALPRS |
| 1079 | 6576 | A | 1132 | 79 | 933 | EWPSIDLVNELQVGISEKVSFLNRKIKPQVPLWYRLDGKVIILTAAAGQIGQAAALAFAREGAKVIATDINESK LQELEKYPGYSK/PRVLDVTKKKQI*SSLPMKLRDFDVLNVAGFCPS'RE LVLGL*GRKDWGLLR*ISMWRSTYLMDSRAFLPKML/RFRNLGNINMS CCGLPSVKGVVEQDVCTAQPASRGLASTKSVGCRFHSRQGHSGANLC VARGTVDTPISYKKEYNATRKS*TTARE*FP*RDKKPGKIPQLPEEISHAL RRISASDAESAYVTW |
| 1080 | 6577 | A | 1133 | 1601 | 1778 | MEQIRASGKLYKSLYQKREIYIYMCSTTYIYT*Y/HSTAYTYICLYVHIYIYMYRQYYVF |
| 1081 | 6578 | C | 1134 | 58 | 394 | MAEKPKLHYSNIRGRMESIRWLLAAAGVEFEKFIKSAEDLDKLRNDGY LMXQQVPMVEIDGMKLVQTRAILNYIASKYNLYGKXLKGESPFNLREQD AKXCLDPRGNPKIX* |
| 1082 | 6579 | A | 1135 | 133 | 985 | RNLRGIAILAGKPQVQFFHSRGRMESTRWLL\AAAGVEFEKFMK/SLA EDLDKFRNDGYFDVSSKCPMV*DL MGLKL\VQTRAILNLHLPANYNL/HYGGKDIKGREPLI*YCILGRY*PDFG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VEIV/LLLSCPYCSTLREQDCQALPW IKEKN*KNRPTFPCPLEKVLKRAHG TKTYLVGKKS*ARAGPFHLVELSS TTVEELDFQSLSPSFPLPERPLETPES RQPCPHSERKFPYSPGQPQGKPSPW. DEE/SL*EGRQGKDFSGFLINGSPWE GPRNLAINPMVS |
| 1083 | 6580 | B | 1140 | 866 | 942 | MDRHCPKLSGAPFGPPAPILGLTDP EFSHEPKLHHARILHRAPPTRDHP VGVISRLPRAGRGRAEGSPPGPDF* |
| 1084 | 6581 | A | 1141 | 405 | 536 | KSAPRPGVVAHTCNPSTLAGRG/G WIT*GQEFENSLANIVKCCFY |
| 1085 | 6582 | A | 1142 | 49 | 365 | TPDKPIRSHETLPIHEK*PRGKTGPPP DSDDPPPGSPSPQHVGN SQKINSKLP ISSGDHSPNPYHW*CPLPSVLGIP/PV RRDPLCGPESPQEEGGQQRNESFDIF |
| 1086 | 6583 | A | 1143 | 3 | 452 | |
| 1087 | 6584 | A | 1144 | 9 | 486 | NSARATDSERTHHGACLLPDKTNV KA\AWGKVGAHAGEYGAEALERM FLSFPTTK\TYFPHFDL\SHG\SAQG* RAHGK\KVA\DALTKRRGATWDDM /PQTALSALSDLHAHKL\RVGPGSTF KLL\SQLPCLGEPWAAHLPA\EFQPL AVARLPWNKVS WGFC |
| 1088 | 6585 | A | 1145 | 1890 | 2027 | KCLCPPR/RCPQPLTPYPC*GVKCPP SEIKYKP*MCPIGCPKPSIQC |
| 1089 | 6586 | A | 1146 | 1 | 903 | |
| 1090 | 6587 | A | 1147 | 1 | 1131 | |
| 1091 | 6588 | A | 1148 | 1 | 1376 | WALPAGFDGVM SHRKFSAPRHGSL GFLPRKRSSRHRGKVKSFPKDDPSK PVHLTAFLGYTPCL\AHIVREVDRPG SKV NKKEVVEAVTIVETPPMVVVGI VGYVETPRGLRTFKTVFAEHISDEC KRRFYKNWHKSKKKSFTKYCKKW QDEDGKKQLEKDFSSMKKYCQVIR VIAHTQMRLPLRQKKAHLM\EIQ VN\GGTCARES WDWPPREGLKQQ VPVNQVF\GQDENDRTSSGVTQGP KGLQRGSPSR\WHTQESCPRKDPPE GLRK\VACIGAMAIPARVALPLWQR AGQEKATH\HRT EINKKIL*DLAQQ YLIKGGKL/VSKNNASH*PMTLSDK S\NPLGGFVH\YGK*TND FVTFKSL VWLGP KKRVLTLRK\SLLVQTKAA GLWRRITLKF\IDTTSKFGHGRFQTM EEKKAFMGPLKKDRIAKEERSLMP GTDFASWWGLNKS YFPLK KKKK |
| 1092 | 6589 | A | 1149 | 3 | 497 | PTLLVPTDSERTHPWLLSPADKTN VKA\AWGKVGAHAGEYGAEALER MFLSFPTTKTYFPHFDL\SHG\SAQV *GPRARKVADAL\TNAVAQRGTDIA QRACPPLSDLHAHKL\RVGPGSTFK LLKATC/HCLGEPWAAHLPAEFQPL AVARLPWGQSFLGFLKQRC |
| 1093 | 6590 | A | 1150 | 26 | 508 | NSTDSE RTHPWLLSPADKDQRQGP AWG\KVGAHAVRSMCAEALERMF LSFPTTKTYFPHFDL\SHGFASQV*GP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RARKVADAL\TNAVAQRGTDIAQR AVPPLSDLHAHKL\RVGPGSTSKLL KPLACLVDPGPPTSPAEFHPLRLQG FPGDKFPGLSVGKFKI |
| 1094 | 6591 | A | 1151 | 3 | 520 | AKKHGHRGSSLTVFGGPHRLRENPP WCSSPADKTNVKAAWGKVGAAHA VRSMCAEALER\MFLSFPTTKTYFP HFDLSHGFCPG*RATAKKVADALT KRRGATWDDMPQTALSGPEATLH AHKAFGVEPGSTLKL\SHLPCW*P LARPPSPAEPDPWRVERLPWDKFP WVSC |
| 1095 | 6592 | A | 1152 | 232 | 783 | TCNPQTSSNGSQNSKLGRISRKWR MRRCFCFSITRWLECTSPRSRGRW KTDDVLLKLENMGVSELGQRI*LER FTKDTARFKDELDMKFICKDFWTT VFKKQIDNLRTNHQGIYVLAQGNKF RLLTQMSAGKQYLEHAS*V/Y*HLP CGLIRGGLSNLGIKSIVTAEVSSMP ACKFQVMIQKL |
| 1096 | 6593 | B | 1153 | 28 | 249 | MFLSFPTTKTYFPHFDLSHGSAARLR ATARRWRRADQRRGHVDDMPNAL SALSDDLHAHKL R VDPVNFKLLSHCL L* |
| 1097 | 6594 | A | 1154 | 3 | 511 | DKTNVKAAWGKVGAAHPGEVWCGP LERMFLSFPTTKTYFPHFDLSHGSA QVKGHGKNVADALTNAV/AHVDD MPNALSALSDDLHAHKL R VDPVNFK LLSHCLLVTLAAHLPAEFTP\AVARP SLGQVSWAFL*SNRCWTFQISLPAE FTP\AVHASLDKFLASVSTVLTSKYG |
| 1098 | 6595 | A | 1155 | 2 | 247 | PADKTNVKAAWGKVGAAH/AGEYG AE/ALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGKKVADALTQGELGG EVGGQGHQQA VA |
| 1099 | 6596 | B | 1156 | 74 | 195 | MFLSFPTTKTYFPHFDLSHGSAQVK GHGKKVADALTNAVXT* |
| 1100 | 6597 | A | 1157 | 3 | 224 | |
| 1101 | 6598 | A | 1158 | 3 | 136 | |
| 1102 | 6599 | A | 1159 | 1 | 371 | TQREPTMVLSPADKTNVKAA/WGM FLSFPTTKTYFPHFDLSHGSAQVKG HGKKVADALTNAVASVDDMPNAL SALSDDLHAHKL R VDPVNFKLLSHCL LVTLAAHLPAEFTLAVHAFLGQFP GFF |
| 1103 | 6600 | C | 1160 | 1 | 156 | MVRRPWRCSCSPPGXPPRRRVHP CGAXLPGQVSXFCEQRAELQIXLRL EL* |
| 1104 | 6601 | A | 1161 | 1 | 577 | AAWGKVGAAHAGEYGAEALERMF LSFPTTKTYFPHFDLSHGSAQVKGHG KKVADALTNAVAHVDDMPNALS LSDLHAHKL R VDPVNFKPPRPTSRT ST*ATALPRLRATARRWPTR*PTPW PRGRHAQRAVRPERPARAQASGGP GQLQLLSHCLLVTLAAHLPAEFTP AVHASLDKFLASVSTVLTSKYR |
| 1105 | 6602 | A | 1162 | 1 | 680 | ERTTMVLSPADKTNVKAAWGKVG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGH/GRMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLT SKYR |
| 1106 | 6603 | A | 1163 | 2 | 1758 | TMVLSP/ADKT/NVKA AWGKVGAAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDDLHAHKL/RSRTST*ATALPQVKGYGQEGGRRVDQRRGARGRHAQRAVRPERPALR NKLVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLT SKYR |
| 1107 | 6604 | A | 1164 | 121 | 521 | SFNKFFKKAKAVSQKKIPATKLRDKGLQTKYSCLYYYFYLRHGLALSPRLACSGTTTAHCILKHRGSSDPP/T*ASHVLKLQYFCTS**LGITGACHHASLLLKFFVETDLTVLPRLVSNFWPSSCPSLLKCWD |
| 1108 | 6605 | A | 1165 | 407 | 548 | VPFTKWHQKIEAGQAWWLMPVIPA VWEAEVAGGSLEIRSS*PAWATW |
| 1109 | 6606 | A | 1166 | 25 | 628 | EFHRLRENPPWCLSPADKTNVK/APAWGKVGAAHAGEYG\SEALER\MVLFPPPTPKPYFPHFDLSHG\SAQV*GPRARKVADAL\TNAVAQRGTDIAQRAVPPLSDLH\AHKL\RVGPGSTFKLLKATC/HCLGEPWAAHLPAEFQPLAVATSSLGTFKPGFLVEAPLLTFQITFKGWKLWLAIVFLPFGLPPSPSSPFLHPYPRGL |
| 1110 | 6607 | A | 1167 | 2 | 121 | TFVRLGTLSTPLWGSYDFFFPS*FSLFLFYSVHFMPLAF |
| 1111 | 6608 | A | 1168 | 3 | 582 | AKRELRFLLVYLHGDDHQDSDEFCRISQALRENTYPFLAMIMLKDRRMTVVGRLGLELIQPDDLINQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLRADQEKERKKREERERKRRKEEEVQQQKLAEEERRRQNLQEEKERKLECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVRTT |
| 1112 | 6609 | A | 1169 | 30 | 130 | QILLSPCLPPP*YLNKRWPEDNTCLL KTKLKRT |
| 1113 | 6610 | A | 1170 | 2 | 1412 | GIAGPTISCRGGGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNWNIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVS RPQPRGLLGWGYLIMLPFRFTYYTILDIFRFAPRFIRPEPARSR\VT*PRLGTTVSIYGTPEEKYGRAHPVFYQGTYSQALNDAKRELRFLLVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPEGYRVVSQALRENTYFLAMIMLKDRRE*PVVGRLEGLIQPDDLINQLTFIMDANQTYLGVSERLEREERNQTQVLRQQQDEAYLASLR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | ADQEKERKKREERERKRRKEEEVQ\QKLAEEERRRQ\NLQ\EEKERKLEC LPPAEPSPDDP*KVSKIIF\KLPNDSRV ERRIPLFHRSLTVIHD\FLSLKESPEK FQIEANFPRRVLPICIPSEE\WPNPPTL QEAGLSHTEVL\VFVQDLTDE |
| 1114 | 6611 | A | 1171 | 232 | 427 | STKISHTKKTARINKTKGGRGQAW WLSPIPTLWEIKVGGLFEPRRSRLQ *AVFMP\CTPSWATQ |
| 1115 | 6612 | A | 1172 | 232 | 427 | STKISHTKKTARINKTKGGRGQAW WLSPIPTLWEIKVGGLFEPRRSRLQ *AVFMP\CTPSWATQ |
| 1116 | 6613 | A | 1173 | 77 | 1775 | GRKVVM\DLIPNLAVETWLLAVSL\ VLLYLYGTRTHGLF\KKLGIAGGTPL PFLVNALYFRKGYWTFDMECYKK YRKVWGIYDC*QPMLAITDPDMIK TVLVKECYSVFTNR\RPFGP\VGFMK NAISIAEDEEWKRIRSLLSPTFT\SGK LQGDGPLSLPQYGDV\LRNLRREA \ETGKPVTLKDVF\GAYSMDVITSSSF G\VSIDSLNNPQDPFVGKHQGSF*GF NPLDPFVLLQLKVFPFLTPILEGIKY SLCFPRKSY*VFLNKIC*NRLKEGRL KETQKHRVDFLQLMIDSHKNSKDS ET\HKALSDLELMAQSIFIFAGYETT SSVLSFIIYELATHPDVQOKEQNEID TTLPNK\APPTYDTVLQLEYLDMVV NETLKLFPVAMRLERVCKKDVEIN GMFIPKGVGV\MI\PSYVLHHD\PKYW REPEKFLPERFSKKNKD\NIDPYIYTP FGSGPRNCIGMR\FALMNMKLALIR VLQNF\SF\KPKETQIPLEI/DAVGGL LLTEKPIVLKAESRDET\VS\GSLNFPK DILVCSLRKLVPQKHQRPSNYFTNR PLKRRRGFIPNVAAIK |
| 1117 | 6614 | A | 1174 | 3 | 403 | |
| 1118 | 6615 | A | 1175 | 2 | 465 | |
| 1119 | 6616 | A | 1176 | 1 | 1112 | AGEFPGQLHSRAS\FC\TARSGSAAAL RMRPVRLMKV\FVTRKIPRPCRVA LARAADCEVEQWDSDEPIPAKELER \GVAGAHGLL\CLLSDHVDKRILDA AGANLKIVISTMSV\GIDHLALDEIK\ KRGIRVGYTPRLSLTD\TTAELAVS\ LFLPT\CGRWPEAFREVKN\GGWTS WKPLWLCGYGLTQSTVGIIGLGPH* AQAIARRLKPF\GVQRF\LYTGRQPAR PEEAA\EFQAEFVSTPEAGWP\NLILI VVACSLTPAT\EGLCCKDFFQKMKE TAVFINISRGD\VVNQGRPC\TRALAS GKIAAAGTGM*TSPELPYKPPFSL TLERIVVILPHIG\SATPQEPGNTMFL VWAVNNLLDGLRGEP\MPSELKL |
| 1120 | 6617 | A | 1177 | 518 | 780 | EVLPSGPGLLALVLR\LGSEFKLPHH EVS\VGTHPCQTSGAPARHRSTRDP VFPLSRGHNNPVPSWKHRAALTRH QTFLYCERGLPACIH |
| 1121 | 6618 | A | 1178 | 117 | 1166 | ITMATGQKLMRAVRV\FKFGGPEVL KLRSDIAVPIPKDHQVLIK\HACG\V |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NPVETYIRSGTYSRKPLLPTPG\SD VA\GVI*A\VGDNASAFKKGDRVFT RQARSSGG/YMAEYGFFAGRTTLFY KLPGKTGTFKQGSLSDFPYFYCFIR GL\HS\ACV\KAGESVLVHGASGGV GLAACQIA\RAYGLEVLGTAGTEEG \QKICFCKNGAHEV\FNHREVNYIDK IKKYVGEKGDID\NEMLANVN\LSK DL\SLLSHG\GRVIVV\GSRGTIEINPR DTMGQRSPSIIGVTLFSSAKE\EFQQ YAAAL\QAGMGIGWGGPVIRSQYPL ERVAEAHEDIHGS\GATGKMDSSL MDD |
| 1122 | 6619 | A | 1179 | 264 | 647 | NLGTCPFPVPALQCLLLVETVSRGS LLPVSPLLFQLLYPSPPAPSYINS LPP*PCPASLPFYDSLVI*RPAPF*SH PSPSTPRTEGGV\PSQSHPPCCPQAP APPSLPASLSQRHLLPPLSHHSC |
| 1123 | 6620 | A | 1180 | 1 | 575 | NFALEAKNSARAISVVQTPIGHSTE EDQGLLSTSLWGK\VKCGKNAGRK KPLGKAPLVVL/HPWDPKGSFEQAL GNPVPPALCPSWGNPPKSAHGK\K VLT\SLGEMPIKHPG*SSKGTFAQPD VNCTCDK\LVHDPENFKLLGNVLV TVLGNPIFGKEFTPEGCRASWAERW VTWSWPVPCSSRIPLKPLGP |
| 1124 | 6621 | A | 1182 | 265 | 714 | HFTYKYTAGTTIKSKNICITPKSYSC TFLVINTLTTPLSNHYSGLLRLVLI VLEFFLFWRWSLALSPRLECSGMIS AHCNLCLLD*SDSPASASQVAGITG TRHQACLIFVFLVETGYPHVG*ARL ELLTSGDPSPPWPPKVLGLQT |
| 1125 | 6622 | A | 1183 | 84 | 1009 | HSMMMKIPWGSIPVLMLLLLGLID ISQAQLSCTGPPAIPGIPGTPGPAD GQPGDPRG*KERKGFQGLAGDHGE FGEKGRPRGFLGN\PGKKFGPKGV MGPKVGPAPGTPQAPKGDSDYK ATQKIAFSATRTINVP/LLRRSQTVRF GPR*FTNMNT\NYE\PRSGKFTLQGC PGLY*FNLSTPVSRG\NLCVNLMRG RERAQK\VTFC\DYCLTNTFPGPPP VGMGPQLKKAPKGGGGGEKKT\VF LQ\TDKN\SLTGAWEGA\NSIFSRV PGFFPDMGGPDLWAGFTSTPGSPCP ATLTIPPTTTI |
| 1126 | 6623 | A | 1184 | 115 | 361 | GWRGLPHCVPGRNCCSVLLMGS/C CL*GPHAL*KPSCSVRCCWPEAPLH SKTDPRLSAA*PPFC*VR*MRYGLR TVCAQILSV |
| 1127 | 6624 | A | 1185 | 3 | 734 | GGSRERARPSPESTRRLPSRRSAPHRP PPQPCEQDNSPRKIQFTVPLLEPHLD PEAAEQ\RRRRRPH\ATLVLTSD\QS SPETAEDRIPNPHLKSTL\AMSPRQR KKMTRITPTMKELQMMVEHSPGGN RQQGEEP*RGPLESTGLQES\RPPGI PDTEVECKCWAPFGTAKK\TAECIP KTHEGRGSKEPSTKEPSTH\IPPLDSK GANCGERGGGILGSRLQFGNAWT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PDLFLIPSLLGKISCF |
| 1128 | 6625 | A | 1186 | 1 | 1359 | GGPRDVNCRRCRRLRAAETPPAWHL CMRSGAPTPPAAAMESETEPEPVTL LVKSPNHRHRDLELSGDRGWSVG HLKAHLSRVYPERPHPEDQRLIYSG KLLLDHQCLRDLLPKQEKRHV\HL VCNVKSP/SQKLPEINAKVA*IPQRE PVGSNRGQY\PEDSSSDGFKGKGKF FR\NLSFPWGWENIFKGLEACPSRH FQGLGPGFLPVYTPYGV/WLQLSW FQQIYARQYYMQYLAATAASGAFV PPPSAQEIPVVSAPAPAP\HNQFPA\ ENQPANSGLAPSSGLFNPG\ANQN FAG*IAQGGPIVEEDDEIN\RDWLD WTYSAATFSVFLSILYFYSSLSRFLM VMGATVVMYLHHVG\WFPFRPRPV PNFPNDC\PPPDVVNSDPH\NN\LRE GTD\PELKDP\NHLPP\DRDVTRMGE AGPGPFLYGGTAWVCSFKDFSLASS FFPEGPPSPSAN |
| 1129 | 6626 | A | 1187 | 314 | 1614 | |
| 1130 | 6627 | A | 1188 | 128 | 1910 | RVVDRGRRWDSPSPLLGGGTWPGR SSLRFASASSDSDSDSGLYRASLHPS PGRAALGLCLYLTKTSCCAAIGTLY WGNIA YKQEAYSLSGENFFMSETE NSCSPFMSSLLQTEDTKKLQSKNL FILLIKPTNPKMSVNVNPQRCQTQ FYRLQDAPRLIAQG*GAKGNGNPR PVI/MSNMVDVGKGSIGPPNVSPPN IPIELGAQTQFDVKNDRIYVNG\SH GGELSCQDMLDGFH*KNFVLCPEEC GGFLETDLH\VNPK\KQTIGNS/CGK ACG\YRGMLDTHHKLCTFILKNPPE NSDSGTGKKEKEKKNRKGKDKEN GSVSSSETPPPPPPNEINPPPHTMEE EEDDDWGEDTTEEAQRRRMDEISD HAKVLTLSDDLERTIEERVNTLFFLF LNKIKEEGVIDSSDKEIVAEERLDV KAMGPLVLTEVLFNEKIREQ\KKY RRHFLRFCHNNKKAQRYLLHGLEC VVAMHQA\QLISKI\PHILKEMYDAD LLEEGFFISWSEKASKKYVSKELAK EIRVKAEPFIKWLKEAEEESSGEEEE DEDENIEVVYS\KAASVPNV\EFVKS DNKDDDD\IDIDAHKLGWMQPSLTV |
| 1131 | 6628 | A | 1189 | 132 | 362 | RRVDWKIQKISIGSSE*KLFNESHGI FLGLQRIDEELTGKSRKSQLVRVSK NYRSVIRACMEEMHQVAIAAKDPA NGRQFSSQVSILSAMELIWNLCEILF IEVAPAGPL |
| 1132 | 6629 | A | 1190 | 97 | 355 | AFSYNCPISKISCQRKSQHFHLGGGLY VILFLFQKGQGVCCQSHPERPEGNP RRHQGQKERSCVGKTLL*LPEQDFV PEKVSAFPWWSLCHHPVSVPKGA RRLSAESSRKTGGQSETSSRTEGEK LRRQNASPRTYGGTRDTFPGMSVG H |
| 1133 | 6630 | A | 1191 | 137 | 474 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1134 | 6631 | A | 1192 | 307 | 583 | |
| 1135 | 6632 | B | 1193 | 1 | 969 | MRPYSQTVFSTQYRWVEQHLGPQF VERIILTRDKTVVLGDLLIDDKDTV RGVHKSMCPGVTAASWGRAKDAM SICGCWLRELWDTSSRENSAAVKT GREADKPEVTKQTQFSTRKDEQAC SGYPYSDCWLAIELLHSAEPQAPRS RSDANASRSGPLRAGCETRLRLGV SCSACKPKPSVLRCLLSARPPLCGP LHASFLPGVDSKSGKTAPRTDCTQS TALTGSGGAGDTLRIDEELTGKSRK SHTQVFICTSPLLKYHHCVGEKYR WVEQHLGPQFVERIILTRDKTVVLG DLLIDDKDTVIRGWTRYPWQPSSLA CPD* |
| 1136 | 6633 | A | 1194 | 834 | 1834 | PSWCCRAGWMKPKDKMLSKEADAS PASAGICRDHGGPDEDNAHS*SWE HPDTRDAGAASGSTGTRNVERYLQ DSTFATSPHL\ESLLKIMLGDEAALL EQKELLSNWHFLVTRLLYSNPTV KPIDLHYAQASSLDFLG/E*EQPSN PWTTSCWQPLSLTSI/NVKECSIALS NWWFVAHLTDLLDHCKLLQSHNL YFGSNMREFLLLEYASGLFAHPSLW Q\VGVDYFDYCPELGRVSLGAAHLS GYL*TPRQKARKVLRICEAAADD* TSSQHL*DLSHESPSATIAWVLASF WSIRVKGCRLCPRSCQTGSSGITVSE AAFLIWISLATWGQP |
| 1137 | 6634 | A | 1195 | 32 | 393 | |
| 1138 | 6635 | A | 1196 | 102 | 888 | RNLQETAIMEKPKLHYFNARRRM ESTRWLL\AAAG\VEFEEKFIKIWQ KIWDKFKEMMGYFDVSQQVPN/VV *D*WGWKLVQTRAIQLTFASKLQP SYGGKDIKGRRALDLI/DVF*EGFSQ ILGLKLFPPFLPVM SHPEEKRCPSLA LGSKRKIKKIGYLPLPFEKSLKEPMG QDYPCWANKLEPGLDIHL\VGTFY YVE\ELGLLGLISSFPLLEGPWKTRI QLTCPTVEEVSLQPRAPREAPPRD EKPLEEAKEDFPGF |
| 1139 | 6636 | A | 1199 | 46 | 399 | PGSKYDKTAILVSHLNFLNLLIKQP NPTQISPQGMFKRGGAR/PLLKTGPF LPTWKGDSFCYKHSNSGWFEAKG FRRLPSFKNERKRNIIGSPPPRLVVIS SESPHAPFGTKSIPED |
| 1140 | 6637 | A | 1200 | 37 | 454 | PGSKYDKTVILVSHLNFLNLLIKQP NPTQISPQGRPPPPQCRVTEWTTAS TQTQAGLKLKDSDDFQVSRMKEKE T**GAHHQDL*LFPQKAPMPHL*QN PFLKTDSTRNQVRSRTFPTSITFQNV GRSLPNTIYSGKK |
| 1141 | 6638 | A | 1201 | 298 | 523 | LLKVQSRQKHWAVGLRTLVRGA VLIRVPPLREPLAPPILVGASSRENI SR*VTGCSPTHSSPTPLATSPRQRA |
| 1142 | 6639 | A | 1202 | 80 | 589 | IFLNLLIKQPNPTQISPQGRPPPHVQ GD*VYNYGPTPASQPERRALKRGI* RKGEGGPRERVWAGAPPGLPTPF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PENQGEKACG/GGRCLSPISLQGPR FPADWWEIPIL*SPDLHRDWGPAPP PPTSSNRPTPTVLRQERSGLG\PPSPP GHLGKLVFFQLAWDSFL |
| 1143 | 6640 | A | 1203 | 2 | 661 | FVEADRGLAVGSLRPLNLRGARAA AFRFAAGRESRGKGTGERRTRVA VAGKVTSVPFVVSQGREHSHAPTR LPTIPPAAMSAAG\ARGLRAA\YHRL LDKVELMLPEKLRP\LYNQSRQVPR TVFFWAPIMKWGV\VCAGLA\DMA QTLPEKP*AQLQSACFGWLTRGLIW \SRILHL*IIPNTNWSLFGW*FPFVG AAGASQLFRTWRYNPRTKKLKAH K |
| 1144 | 6641 | A | 1204 | 20 | 400 | |
| 1145 | 6642 | A | 1205 | 457 | 1011 | SRRPWGHFTEEDQGLLSQSLWGQ/V *NVEKMLGRKKPLGKAPLVVLPPW TPRGSFEKALGNLVLLPSCPSMGNP QKSRA PWARRVLTFPWGDAHKSTP G*SSKGTFCPA*SEPA/HCDKLH/VL DPENF\KLLG\NVLVTRFGQSIFGKE FHPLRCKAS\WQKMGELQVGHFPV LQIPLSSL\PMMQSFQG |
| 1146 | 6643 | A | 1206 | 3 | 452 | |
| 1147 | 6644 | A | 1207 | 9 | 485 | NSARATDSERTHHGARLLPDKTNV KA\AWGKVGAHAGEYGAEALERM FLSFPT\TKTYFPHFDL\SHGFCPRLK GPRQRRWPDALTK\AVA\HVDGHA QTALSGPEATLHGAQSFGVDPVQLS SS*SHLPCWLT\GRPPSPAEFNPCR V ARLPWNKFPWVSC |
| 1148 | 6645 | A | 1208 | 37 | 298 | RQGLPLSPRLECHDRIIAHCNLEVLG SSSPPTPASPIA*\TTGVGHHTQLPFK LPYFFHSGLFFFLKKILYQFCDTYRA RISSDFCR |
| 1149 | 6646 | A | 1209 | 49 | 564 | SQTPMGHFTEEDKATIT\SLWGK\N NVEK\SWKEKTPGKGSLLVLPWP TP RGSFDSFGQTCPSALCPSMGKPPKS RAPWPRRVLTSLGRCCQSTWDDPQ GAPFAQA*SELHCADKPAMWDPEN FKAPGEMLLVTRFGQFHFRANKFTP EGCRASWAERWVT\GVASALVPSR YH |
| 1150 | 6647 | A | 1210 | 134 | 673 | QRRTKATIT\SLWGKGEMWKDAGG ETPGKGSLVVYP\WTQ\RFFD\SFG\ NLSSAFCPSMGKPPKSRLHGK\KVL TSLGRCP*KHLDDLNGHLLPKPDV NLHCADKPAMWDPGGTFKLPGENV AGLTRFWAIPFSGKEF/TPLEVARLP WQKMAEDGDWQWASCPVPPRIPL EAHWPMISELFKG |
| 1151 | 6648 | C | 1211 | 50 | 373 | MGTVGSAAWAAAPVQTHMFCSSSSC ISSLSTLPDSAAPLSPLASSWPVPPRP LLHWPFQSSLLFSLSPSFXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX RALHTSLA* |
| 1152 | 6649 | C | 1212 | 45 | 424 | MNGDXGLCLAAAPDQTHMLGSSSS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | CISSLSTLPDSAAPLSPLASSWPVPP RPLLHWPFDQSSLLFSLSPSFXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXLTHTFLSLERGGVLSISIRMW VRLS* |
| 1153 | 6650 | A | 1213 | 97 | 1382 | SACAWRLPSPGPSAMWPLWRLVSL LALSQALPFEQRGFWDFTLDDGPF MMNDEEASGADTSGVLDPDSVTPT \YSAMCPF\GC\HCHLRVVQ\CAPT GLKSVPKEISPDITLLDLQNDISEL RKDDFKGLQHLYALVLVNNKISKI HEKAFSPLRKLQKLYISQNHLEIPP NLPSSLV\ELRIHDNRIRKVPKGVFS GLRNMNCIE\MGGNPLENSGF\EPG\ AFDGLKLN/YT*RHLQRSKLTGHSP KYLPELTNELHLDHNKIQGHRTGR DLLRYSKLYRLGLGHN\QIRMIENG\ SLSFLPTLREVHL\DNKKLAR\VPSG FP\DLKLLQVV/YILHSNNIHQSGVF NEFLFPWGFGEAGPYNGHSAFS TTPLPYW/ERLQPATFR\VVTDRLAI QFGQLQKVEAAAATLVSQWGS LG NRARHPDGEAEPGS |
| 1154 | 6651 | A | 1214 | 938 | 1501 | AGVGPDPGFLFQGIVANDSHPTALL KRMFASGGRRSWCQPFQGTPAMG GPWAKGCLGPASCAAKVGGPHPKT NPGPKPTGGQGFPATGLRGVGISPP K*PCQ*AVQPGSHCPATCAEPSPPW G/PGVPRFEAPPPQTPP*PRLWPETG EPPLGVQKPP/QPMPGPGAPLEN*S ASGGPRSPRGWESVWF |
| 1155 | 6652 | A | 1215 | 883 | 1216 | YISNSQLVQHFFFFFFFLFFFETESC PVAQAGTQWCDLGS LQPPPP\G*SN SPASASRVAGITGVHHHAGANFLYL *QRWGFTMLAQAGLELLTS*STR LG LPKCWGLQT |
| 1156 | 6653 | A | 1216 | 197 | 821 | RLFHSNQTV DHSQKNVDITLKGRP SNRVRA PKGTLR\RDFNPHQM*NSA LLGKEQQRGFRVD\KWWGYQKGN WPTRSGLFGSHVQD\MIKGWLPLGL PVTKMR\SVYAHFPHPTLLSRENGV SLLKSRNFLG\EKYIPQGFRMKTRVL LCQYLKAQKR*N*SLEGND\IGLV S\ NFSRL LIPASPTRLKTGIRK\FLDGI FCLLEKGLFRQA |
| 1157 | 6654 | A | 1217 | 241 | 514 | DGQRLGKPHFVLLVLQ*LQTGLWS WWGKLG VGE/MLGVGEILGSAFISP VLERVEGSGSGGNQAGPREEGWLG KPLRPEAPPSTFIQHHTLG |
| 1158 | 6655 | A | 1218 | 3 | 496 | SSGLFTQQSPEAWFCVSKCSYPAW QNVKVIVDSHKLQEIIQRS LIPFAQF PAMVTVCKAPGRFCHPCWHV*P/HP HSHDTEHGHHKCLVLCYPFTASA PPSCPAPLR CIYGCILSCLVDVPWRT DRLNKQRVC KEAQSRREGSPA WLI GQHSRLALPLLAALS |
| 1159 | 6656 | A | 1219 | 1326 | 2014 | QLMIYTFRTELAHWPGDQKH YFHT CVMILFFLRQSLALLPRLGVQW HDL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GSLQPA\PPPPGFRLFSCLSLPSS*DY RHVPPAPQLIFFFVLLVETGF/TPMLG RMVSIS*/PSDDPPTSASQSARITGVS HSWVNSCDLPLKNFFFFLEESHVS QAGVQWHDLGSLQPPLPGFKLFCL CLLNSWDYRHAPPCPANFCIFSRDG VSPCWPAPWSPSLHLVIRPPWPPEVL GLQA |
| 1160 | 6657 | A | 1222 | 1 | 459 | IEIHIKCGGIPAVLAAPAMGLELFLD LVSQPSRAVYIFAKKNGIPLELRTV DLVKGQHKSEFLQINSLGKLPTLK DGDFFILTE/SANRSVYLQGGCWHIT EMRFSKCKAEGPAKSRSAIYLSC KYQTPDHWYPSDLQARARVHEYL GWHAD |
| 1161 | 6658 | A | 1223 | 2 | 310 | |
| 1162 | 6659 | A | 1224 | 205 | 454 | |
| 1163 | 6660 | A | 1225 | 2 | 384 | |
| 1164 | 6661 | A | 1226 | 1 | 1276 | MPGLGFREKKGGSRTPVAPSRGCGL PAPILCTKWELPLSGSSRCLAAAL QGTWTAESSSLTPAFQSRGWGLIP YFPARRDPATAAAHTALSAFTAIPA VLAAPAMGLELFL\DLVSQPSRAVY IFAKKNGIPLELRTVDLVKGQHKSK EFLQINSLGKLPTLKDGDFFILTESLAI LIYLSC\KYQTA\DH\WYPSDLQGFG ARVHEVPWAWHADLHPVGTFWY YPWGVQGVWGHSLGVQVPEEKVG TQTRTAMDQALQWLEDKFLGDRPF LAGQQVTLADLMALEGS*CKPVAL GYELFEGRPRLAAWRR\RVFAFLG\ AELCQEAH\NILLSILEQAANKTLPT P\SPAEAYQAMLLRNRPGSPEGSGM GAKEISNKDSFCYLLAPFYLSLLPQS LLSKLQCEALHRQRHSSVLWQVLL LLRCKHT |
| 1165 | 6662 | A | 1227 | 151 | 278 | G*KYDSDIYHEAVVPHQNQMSARS DKEKKRFIFYSSYYIPFC |
| 1166 | 6663 | B | 1228 | 1 | 690 | MASWDEKDLTPQPDTRKGSVLRC GLSSRALRWAGRGHVAAGWRPLA PESAGGWGMAAAMVPGRSESWER GEPGRPALYFCGSIRGGREDRTLYE RIVSRLRRFGTVLTEHVAAAELGAR GEEAAGGDRLIHEQDLEWLQQADV VVAEVTQPSLGVGYELGRAVAFNK RILCLFRPQSGRVLSAMIRGAADGS RFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPTT* |
| 1167 | 6664 | B | 1229 | 1 | 975 | MSPPGREQGLLLNLLRPSGLDNAG KTILKKFNGEDIDTISPTLGFNIKTL EHRGFKLNIWDVGGQKSLRSYWRN YFESTDGLIWVVD SADRQRMQDCQ RELQSLLEEVEGSSYPLCTWRFFSY LRIEQMYNLVLYRDIQFPDFCFNSN TDWSKGLKTHARFGNTSLHVAHTD STNTTNFVDVWRGRKSLACLQL SSLTCIYTAGKMRLQDRIATFFFPKG MMLTTAALMLFFLHLGIFIRDVHNF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | CITYHYDHMSFHYTVVLMFSQVISI CWAAMGSLYAEMTENKYVCFSAL TILMLNGAMFFNRLSLEFLAIEYREE HH* |
| 1168 | 6665 | A | 1230 | 1 | 211 | |
| 1169 | 6666 | A | 1231 | 950 | 1326 | RPESQRANGVDSGPNLKTVPQPDTR KGSVLKWISKRGKPLAVEIEESHCLA CLPLRTECLGIKPIVHLFSCTRPVIV PSLELNYDVDSIAHMFVADLLLMIT LPSYDIPFYCLVFQNLVLEFQYL |
| 1170 | 6667 | A | 1232 | 271 | 927 | NQGLRHVRLCRMCLVNQMFASSIL GKSHHSLVPINQGHNAWKAAG\ PLPLKAGYC\QGFSPCHSLKYG\SW DEKDLTVPQRDTHKRSVLKVELVQ RGKNLPVEDGGKAHCLPELPPGELE CPG\ILKHGLYHWSSEMGEKPAPM VGG\RHV\CSNAALVIPLPLRCLGG EKHKSGL\HARPVI\VPSELELNHDTD SFAHMFADLLLITLPSYIYIFC |
| 1171 | 6668 | A | 1233 | 62 | 1158 | GHLCAFPETSLLQVRPGPLPSSFSG MDVGPSSLPHLGLKLLLLLLLLLPLR GQANTGCYGIPGMPGLPGAPG\KDG YDGLPGPKGEPG\PAISWIRGPKGQ KGEPG\LPGHSWGKMGPMPGPGDC QGLPGPLGDFPG\EPG*G\GRYKQKF QFSFSRLIRQTHQPPRTNSLIRFNAV L\TNPT*IYNTCTG*FTSKVPGLY\YF VYHASH\TANWCVVLYRSG\AKVV TFCGPHVPKPISSNSGGCACLRQV GRGRCGWLS\MTYYGHGWGIQGL* KSVFSGLPWLLPRTKGGARCGSRPT GPSPSPQLPAWTQPYWPVCILALDH SPHQMDFSPPGSPPLTHPHCTPLPM GSLPLNFFRSHCLCGSWDT |
| 1172 | 6669 | A | 1234 | 2 | 907 | AVAFGAKGTDPAEARSSRGIEEAGP RAHGRAGREPERRRSRQRRGGLQ ARRSTLLKTCARARATAPGAMKM VAPWTRFYNSCCLCCHVRTGTILL GVWYLIINAVVLVDFIECPG*SGSSI TFQVLELGGDFEFMDDAN\NGAFAI AISLLMILICAMATYGAYKQRAAWI IPFFCYQIFDFAL\TC*VAISGLIYANS IQENIRELPPKFPYRDDAMSVNP\TC LVFIILLFISISLTFKGYLISCVWNCY RYINGRNSA*CPWFMLPAMTLRCC YPPYDDATVNGAAKEPPPPYRVCLS L |
| 1173 | 6670 | A | 1235 | 966 | 1564 | NDFFKTNKSSIIRNSCLTAILVFLCC YDLTLTGTLF*ILTFRWL*LGLIIRLN \MASRSTIYVYGSQPSFLTFENTDF YQLWILFLVICLPFLFKLFTIFLWP KLLTLENQILHQIQCFSVVFLMSAPI TTVRGIHVLPVIVILQTDLAWINQLL HLLFSKLGVDSDSVQDWVSLMWN GTHGRKCRSQFYMPIKGHL |
| 1174 | 6671 | A | 1236 | 155 | 303 | AFQEGDPMFKPSRCPCPYLPKPCPS TCLP/SFAFRAVVTQVP*CCVCKCPG |
| 1175 | 6672 | A | 1237 | 739 | 1629 | GTSQMPTSAVPSLLSPSKFARKGFS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KVLQLCLYRRIGLCPAPPPPVPTQC PRPQELIGP/WRE*CPPGSFRNSPRNL FSFLQELPEESV |
| 1176 | 6673 | A | 1238 | 1 | 554 | NFALEAKNSARAISLVPDA\MGHF TEEDKAT\TSLWGKGEMWKDAGG ET\LGRL\LVYP\WT\QRFFD\SFGN LSSASHPWATPKVKAHGKKVLT\ SLGDA\TKHL\DDLKG\TFCPSLK*TC TC*QACNVGS*GTFKLPGEILLVTRF WQSHFRQKNFTPEGCRLSWAERW VTWSWPVPLFLPDYH |
| 1177 | 6674 | A | 1239 | 29 | 454 | |
| 1178 | 6675 | A | 1240 | 1 | 1368 | |
| 1179 | 6676 | A | 1241 | 1 | 1266 | LSRVAEFEHLGWSPKPPTTCTPACQ GLSGAAMKSLVLLLCLAQLWGCHS APHGPGLIYRQPNCDDEPETEEAALV AIDYINQNLPWGYKHTLNQID\EVK VWPQQPSGRAVLRFEIRTPWGTTLP CCWDPTLVGQDASLEGLSKEHAVE GDCDFQLLKLDGKFSVVYAKCD\S SQDSAEDV\RKVCQH\CPLLAPLND TRVVHAAKSCPGPPFNAQNNGFQF FSLEEISRAQLVPLPPSYV\EFVS G\TDLLFA*KKATEAAKCNLSGQKS NMGFCK\ATLSEKLGSGQRLQLTCT V\AQTPVT\SQPNPEGANEAVPTPV\ VDPADAPSPPLGAPGLLPSWLT PKT TMVLL\AAPPQHQLHRAHYDLCHT FMGVVSLGSPFRRKCSHPRKNT/RT VVEA*WLGAAAGATGFLPLFRGGI RHFKV |
| 1180 | 6677 | A | 1242 | 1134 | 1247 | |
| 1181 | 6678 | A | 1243 | 1330 | 1517 | KLNMVFKKISHGMQLRKSYNLFYQ KSGKIMT*IWEIFFPEFFIFPPTYLF LKREFLLNEPS |
| 1182 | 6679 | A | 1244 | 213 | 287 | |
| 1183 | 6680 | C | 1245 | 249 | 323 | MYKLRRKLEDNRNKIENENIVKSFR* |
| 1184 | 6681 | A | 1246 | 1021 | 1985 | IAWAFKINWLP\IFLIFS\VFYPIFGFI FFYLLYFSNTCLS/FVFPFSYLKLLTI FSFSILFLSSNFLSLYLPLAFCFLAC LFFFCFLFRFKFIFFLPKSMFLSSNF PIF/CIFFFFAFPYSCLPVFHCQTFYLL QIVVIL/IHSQLIFFSSAFSKCG*QGF *MTQFSLRHGFQGLLITFGLISF*KIA FKLF*SPTTFKLNFKLFK\YLHFNLK ALPSLLGLNSGLL*/FLSHQFSFKYIF YSMKKLHLNLRHVLETVLSFPSSCY SSKFVHFALSFLFPSLSFFFCFLFRF KFIFFL/RKSMFLSSNFPIFSILFYLP IF |
| 1185 | 6682 | A | 1248 | 147 | 460 | PFYKNCVSIVVVVFETGSCSVTQAG VQWHDFSSLRPRPPGSSDPPTSASR VAGTTGMCHHIQLIF*SFFIETGTHY VVQAGLKLLGSSHPPTFSLPKWLGL QA |
| 1186 | 6683 | A | 1249 | 168 | 407 | ISHTREHSLDFFSFLFFFETESH/STR RLEYNGGLSAHCNLHLLGSSDLPTS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AC*VAGTTSIWQHVQLTFVFFFLLI IIF |
| 1187 | 6684 | A | 1250 | 163 | 396 | TRFPILGSLA*IFFLFFFFFFETESH/STR RLEYNGGFSAHCNLHLLGSSDLPTS AC*VAGTTSIWQHVQLTFVFFFC |
| 1188 | 6685 | A | 1251 | 37 | 698 | RSSSPALEGGRKVDMECLGSTIGP GPGSGQPACPLIWLHC*NPVEQAGP KP/PARPARSGP/QPPPTAGPA/PVGP KPPPTAGPA/PVGP KPLPTAGPARS WRP*PSGARGIKETHTEI*VP/PQGGF ACLIPTAPTGPTD**WLHLDLPTTP\ QPHPEAVQHTGGSC LTPYDGPPPPQ PISSKHPLPSYPTPSPKLPLEHPSQIL GETDFSNHQILVSHSLVSV |
| 1189 | 6686 | C | 1252 | 150 | 308 | MALQORTHXLLLLLLTLLGLGLVQ XPMARMXCTSDSCGNTCTLRRQVA SDRY* |
| 1190 | 6687 | A | 1253 | 2 | 470 | |
| 1191 | 6688 | A | 1254 | 92 | 1047 | RAAWQGGAEASGPPSALRGGSALA AAARWGPAEEGARIPGSFFAWAAP AAPGAGAAAAPAPRADPGGRLLG EAGRGPNYAEAGTPTLHTLPRPHLR PCTHTHTRTPTPPRCKAGFKRTSLR FLPAPHHRTREEEAGEKQNFPLSC PFLRTCSEAEEPVEEMVMGLGVLL LVFVLGLGLTPPTLAQDNSRYTHF LTQHHIA\KTRGR\DPLSCKTFMRSR GLTSPCKD\NTFIHG\NKRTLKGQS CEN\KNGKPLTEKNLKE*SKSFLSQV T\TCK\LHGGSPA\WPPA\QYRATAGF RNVVVACENGLPVHLDQSIFRRP |
| 1192 | 6689 | A | 1255 | 199 | 792 | PGSTAAADQSRNWNPNRVRKKPD LEGGCGTVLSGRWRSRRNRRTSGQ SLVPVYIYSPEYVSMCDLAKIPKR ASMVHSLIEAYALHKQMRIVKPKV ASMEEMATFHTGCFICSISRSAKR AMMIIRTSLEYGVRFINFPATEGIFT LCSS*GGATITAAQCLIAGMCKVAI NWFGGWHHAKKKTCTVYVALYKAF |
| 1193 | 6690 | A | 1256 | 1368 | 2229 | WHPRQVLTGNDEVIGQVLSTLKSA DVPYTAALTA VRPSRVARD\VSVEA GGLGRQLLQKQPVSPVIHPPESYND TAPRILFWAQNFSA\YKDQWEDLT PLTFGVQELNLTGSFWNDSFARLS\ TYERIFATTATFSFIPAHQRYPPSAR HWFTMERLEVHNSGSVAYFNASQV TGPSIYSFHC\EYVSSLSQEG*SPRW ARTQPSSWQMML\QGFPDPGFSTL MGEQFSYA\SDCGQASSSPGIWMGL LTSLFMLFIFTYGLHMILSLKTMDRF \DEHKGPTISLTQIV |
| 1194 | 6691 | A | 1257 | 2 | 630 | PDSSGPHRLRENPPWCLSPA\DKTN VK/APAWGKVGAAHVRSMCAEAL ER\MVLFPPPTPKPYFPHFDLSHG\ S AQV*GPRARKVADALD/TNAV AHR GTD/DCPNGVVPPLSDLHAHKLARV GPGSTFKLLKATC/HCLGEPWAAHL PAEFQPLAVATSSSLGTFPGFLVEA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PLLTFTQITFKGWKPRVGHAFALW ASPQPLLPFPAPVPPWSFE |
| 1195 | 6692 | A | 1258 | 207 | 591 | |
| 1196 | 6693 | A | 1259 | 1 | 541 | WNLSASPARQHPLLPHPVSCILLKPS SKKCLPNLTGYRFSQKNMEDYL QALSSPH\DISLAVRKIALLLKPDKEI EH\QGNHMTVRTLSTFRNYTVQF*/ HVGVEFEEDLRSVDGRKCCQGC PW HCNFSQSHELLSSRAMFSTAYKIQL ALHHGFCIHSFSKLQMEKYL GKIKI KNNNTK |
| 1197 | 6694 | A | 1260 | 214 | 491 | ESHGAQIYIPHFCVPWSRWGNVRR CEALAVIYVTNNKIYVLS DPEISCLQ PTSIN*QSNLLACK*GKN/RKTGQAR CHACNPSTLEGRSRJN |
| 1198 | 6695 | C | 1261 | 48 | 173 | MVRKRMEMKMRKLSQLRASGQLK MMRMXMSIPRSRRPRGIX* |
| 1199 | 6696 | A | 1262 | 59 | 306 | FGTDRTAVQTSSSQRLCLPWVAQK TYWLLVPSSLLKDLKEKKEVVEEA* NGRDAPANGNAVSVCFAPWPQLP PHKIFPVLL |
| 1200 | 6697 | A | 1263 | 279 | 889 | TLAVFLIPCIGSPACPTMSDAA\VDT SSEITTKDLKEKKEVVEEA\ENGRD APANGNAVEEEDGDEDEEAESATG KAGQPED\EDDDVDYQ GKQKTDE D*IRQQKRKKLNLKKRPAHRGQC HPADDTRSPPPNP NHENLQQGREKR NQNFQGP AFFLKSTLKRKFVCIFYL HFIFLYILLRVSHFLMISDDQTSLPER SLSYF |
| 1201 | 6698 | A | 1264 | 358 | 508 | DDVDVTKKQKTDEDD*TAKKRKV KLKKKKAAVTYSPSTSRLRYLYVFT FE |
| 1202 | 6699 | B | 1265 | 46 | 386 | XIRHESGSRSHSHCSTLSSIGDVAKK LGEMWNNTAADDKQPYEKKA AKL KEYEKDIAAYRAKGKPDAAKKG VVKAEKSKKKKEEEDEE DEE DEE EEEDXEDDDEEEDDDDE* |
| 1203 | 6700 | A | 1266 | 263 | 484 | |
| 1204 | 6701 | A | 1267 | 157 | 886 | TWKGKDLKKPRANMSSYAFFVQTC RGG\HKKKHPDASVNF/ESFSKKCS ERWKTMSA*R/EKGKFEDMAKAD KARYER\EMKTYIPPQRGRQKRKF DSQLHPRGPPSGLLSSSCSEYRPKIK\ GEHP\GL\SIGDVAKKLGRDVGINTA AD\DKQPY\ERRAAKLKEYEKDIA AYRAKGKPDAAKKG\VVKAEKSKK KKEEEEGEEDEE DEE DEE IEE\DEED EEDEEEDDGLMNKLGSGAVVFFSCL |
| 1205 | 6702 | A | 1270 | 2 | 343 | |
| 1206 | 6703 | A | 1271 | 3 | 647 | |
| 1207 | 6704 | A | 1272 | 59 | 1297 | NHASVQVKLWILSRSYLQLTMEAN GL*PQGLPDLKNDTFL*AAWGEETD YTPVWCMRQAGRYLPEFRETRAAQ DFFSTCRSPEACCELTLQPLRRFPLD AAIIFSDILVVPQMFSPPPGTGQWKV TMVPGKGPSFPEPLREEQDLERL\RD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PEVVASELGYGFQAITLTRQRLA GTCAG*LAFAGAPMEP*MTYM\VE G\GGSST\MAQA\KRWLYQRPQASH \QLLRILTD/ALWLPYL\GQVVAGA \QALQLFESHAGHF\WPHSSFNKFCT ALTSRDVAQAK*RPRLPGSQALATR CPCIFA\RDGHFAPGRSLAQAG\YE\ VVGLDWTVAPK\KARECVGKT\VT\ LQGNL\DPCA\LYA\SEEEIGQ\LVKQ MLDDFGPHRY\ITPHLGHGLYPDMD PEHVGA FVDAVHKHSRLLRQN |
| 1208 | 6705 | A | 1273 | 7 | 1047 | |
| 1209 | 6706 | A | 1274 | 7 | 960 | |
| 1210 | 6707 | A | 1275 | 3 | 53 | |
| 1211 | 6708 | A | 1276 | 237 | 441 | AHFLHIVLVLLSCWYSVRSRCTSQ QGVQSD\LAQLLPLRQRLEGEALV ALGAGVERRHVRPGPRNST |
| 1212 | 6709 | A | 1277 | 94 | 1003 | VRVSLSLRLECNGAILPHCNLHLP SSDSPASASQVAGITGVCHHAPPIFV LLVETGFHHVGQAGLELLTSSDLPA WASQSAGITGGSH/LCLANVKYFKS HFKIFVIDETWFQHT*LLSLSSCD*V *TSI*/PQVLD*NVLCPDV/SQ*LLPW LIKIFLKYTLDCW*KRQAWLYWY* FGTELFGCP*GRQTLCTFFLRSL/DS VAQAGVQ*CDLGSLLQPLPPRFK*FS CLSFPNSWDYRCAPPLPANFCIFSRD /MGFAMLVRLVSELLTSGDPPASAS QSAGITGMSYRAWPKPYAFEVECR PCDN |
| 1213 | 6710 | A | 1278 | 4077 | 5102 | KEASPAKRASGEGSRRLRVEAGGR CGKVCSGRGGGSPELRLRRQKMLR ASSQRNAAGHRGWASGSRGSPTA AAERPKKGGGGSRAAQTASSSGTR RRRRRLRESRRPRSRSGCRPPAFQ AAPDPPLPLPAGSHFRQATAELA/G RAPRRKWPKPAFAS/VGRGRGRAL ATFPTASED/SPRPPAAPR*HPGQGR GAGRRGLWEARGGAPAAFGAPQL ASCKGRR/HTPSTINLFLNDPPPLP KH\PH*ASPPTLGIEFQHEIWRGQTS KLSQHPSFSLRTLTYSSSTQAAFEFL FCRCLPTGHVPSSLLHSAADTAVSG DYATEGWECHCCWGCWEAKVGV LLH |
| 1214 | 6711 | A | 1279 | 316 | 1180 | KEASPAKRASGEGSRRLRVEAGGR CGKVCSGRGGGSPELRLRRQKMLR ASSQRNAAGHRGWASGSRGSPTA AAERPKKGGGGSRAAQTASSSGTR RRRRRLRESRRPRSRSGCRPPAFQ AAPDPPLPLPAGSHFRQATAELA/G RAPRRKWPKPAFAS/VGRGRGRAL ATFPTASED/SPRPPAAPR*HPGQGR GAGRRGLWEARGGAPAAFGAPQL ASTQAAFEFLFCRCLPTGHVPSS/TP PFSSRYSSFRRLCLIFRGCWTEVLNE GGANSDSWSLTKLESSESSECS |
| 1215 | 6712 | A | 1280 | 2 | 315 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1216 | 6713 | A | 1281 | 195 | 739 | KFSSRITVCHWKDVLLSGFQEPDRG SAMDYVRKYAAIFL\VTLSVFL\HV LHSAPDVQDCP\EFTLARENPFLLSPAR VPPIQLQCMGLPASPRAYPTPTKGPR KDGCWVPKEPSPSESPCLW*PKIHI NRGPQ*MGGFPKVGEPTACPLGS YLFYIPQIFKMFLPQVLSWMDWLDL LGIGKI |
| 1217 | 6714 | B | 1282 | 29 | 200 | MSRTRLVCPSLIPFCIYVVDVGFSPG PQCTSHEPKDIAKCELAFLHHQR FYKNEGX* |
| 1218 | 6715 | A | 1283 | 138 | 1908 | ASRTAVARWECVLQNVREPSR AWPSQLRPIASTATKCREICGPGYST PLEAMKGPREENVYLPCILPETQGT EGPRLSWATVDVDPKSPQYCQVIH RLPMPNLKDELHHSWNTCIGSCF G*LAPSRGTK\LVLPFHLLFGIYVG GTWGSEPRAPKLAQGSLSPRDIHAK C\NWAFLHTSHCLASGEVMISSLGD VKGNGKGGFVLLDGETFEVKGTWE RPGGAAPLGDFWYQPRHNVMI EWAAPNVLRDGFNPADVEAGLYGS HLYVWDWQRIE\VQTLCLKDGLIPL EIRFLHNPDRCPKAFVG\CALQAPNI QRFLQRTTRGGTLFSGRR*FQVAPPRK LKGWLLPKMPGL\ITILASPWNDG FLYFSNWLAWGP*GKYDISDPQRP ALTGQLFLGGSIVKEGPVQVLEDEE L/TSPSPEPLVVKGKRVGEGPQMIQ LSLDGKRLNNHHGRCTSALGQSSF YP*SQSGERLLVNAGRVEW*DNSK KGA*KLNPQLSWVDFGEGAPLPK PLPH*ARYPAGGDCSSDIWILNSPPS HPHSLFWALHFPGGPGLSFCISLGTR TLGKHVPTTAKLRLWQCVES |
| 1219 | 6716 | A | 1284 | 155 | 336 | HFKIINRGWAPWFMPVIPALWEAE GGHLKL**AMIVPLHSSLGDTVRL KYLCLISLIF |
| 1220 | 6717 | B | 1285 | 251 | 570 | XELLVQLASLQTSFVTLDEAIKITNR RVNAIEHVIIIPRIERTLAYIITELDER EREEFYRLKKIQEKKKILKEKSEKD LEQRRAGEVLEPANLLAEKDED LLFE* |
| 1221 | 6718 | A | 1286 | 83 | 977 | HNQLTPVEEDTVESQFWSYCSLGCP AGDPSRKVIVRMSGKDRIEIPSRM AQTIMKARLKGAQTGRNL/L*RKKS DALTSFDFRQILKKVIGDLKCLMGVE VMREAAFFTSWKPSFTAGDFQALT VIPKCSIKGGKLVSE/DEGKVIVRP VFTFASNFEHYH*RN*PVMELTGLA RGGE\QLAKLKRNYAKAVELLVEL ASLQTSFVTLDEAIKITQQAC*MPIE HVIIIPRIERTLAYYSSQSWRRERE EFYRLKKIQEKKKILKEKSEKDLEQ RRAAGRCWS\LLIFLAEEKDRGSFL F |
| 1222 | 6719 | A | 1287 | 1 | 3249 | |
| 1223 | 6720 | A | 1288 | 504 | 932 | RYRCGVGSVLQAGGLILHLRKEGIL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HNKGKIEGMGLLEYVQGSLLQGW VMFVSVTAFFFSLLFLGMFLSGMV AQIDANWNFLDFAYHFTVFVFYFG AFFMEAAATSLHDLH*NTTITGQPL LRDNQYNINVAASIFAFYDDS |
| 1224 | 6721 | A | 1289 | 66 | 1363 | RTAVMPREDRATWKSNYFLKIIQLL DDYPKCFIVGADNVGSKQMQQIRM SLRGKAVVLMGKNTMHAQAPFEG TL*NNPSLWRKLLPHIRGEFGLLFH PGRTLTE\RD MFAGPIRLPTAARCW CQLPPCEVTVP\AQNTGLGPEKTSF FPGL*VSPTK\ISQGAPIENPEVNVPA ESRTGDKSGKPSEATLLNMLNISP FSLWGWSSSQVFD\NASIYKP*KCLI SPEETLHSR\FLGGCPQMLPSVCLQI GYPTVASVPHSINGYKRVLA\SV TDYTFPLAEKVKAFLADPSAFVAA APC/AVVAPPAAPAAAAAPAKVEA KEESESEDEDMGFAAAVLPGGTKP GALPPLAPGLALPRGPRCDPEAFRK RFRSQPRQDGGGHAELQKFTLPSLY FFSPKPSGCEPRANAKSSLNFVFSKY SLSTYYEQGL |
| 1225 | 6722 | A | 1290 | 3 | 231 | CSSSTSPSSEYCPSWGTEFRSGEMGS K*SSL*GASSLSPTDGRGTGSSSSSS GGGGPGGVLGPLGCGGLGLPLN |
| 1226 | 6723 | A | 1291 | 221 | 984 | ETGLMCSSPLDGQNSV*RLTPWTLA PGTTAEVNQEDQKKSQIL*KKWQA AANSSRLVKNS*MP\T*KIQNGRMD KNSPTKYLLSSRDSS\THKESHLKD IALILPSSSEGSISELEQLSNSLPNKEL MTSICDCLLATLANSESSYNCLLTC VRTMMFLAEHDYGLFHLKSSLRKN SSALHSLLRVVSTFSKDTGELASSF LEFMRQILNSDTIAPVCVAALSVSM CSHRSAPTWFPPKGLKGARTTSRNS SEA |
| 1227 | 6724 | A | 1292 | 817 | 1826 | SCYPFCTS*KSFHSFCHTNDTVQSFK SI*LKR\SDT*SANRSSNNPLITPACSS PVTP*APHSASEDTNLVPALSCRTFK AIGWRSATCKFKACMVQSTNWP SCFVFFNCK*LNPFIKLGISKA VTH FAPLSSLYKSKSSVNFTEASIAPEFSL SGP*SFILLISISKVVLYGQLKYKSGT SSLSYGSYVIGGTEAKSSAVYSTSKF GYLNVSRSKSAIPSSSLEICS*PSSPSP SSSSSPSSSSSSSSSGILSTVRRSSSS SSSSSTSTSSSSSPSSCCSSSTSPSS EYCPSWGTEFRSGEMGSK*SSL*GA SSSLSPDTGRGTGSSSSSSGGGGPGR SSWSPWLWSWRASIKLIFFLPISMF WDSFSNLGCGLGEGGWREGGGG GRVSVMTLSLYPLDPYIASVRQLYQ PLSTRPSVFTFELGLKMMEVFSSYS RLPNLSKTGALGLPYTVEE |
| 1228 | 6725 | A | 1293 | 25 | 771 | LDGPQGTSRPWGLPSLPPPRAGAGL SQFGSSLRPARTPPSSGSKMSTEA QRVDDSPSTRA\QSSDGDQRESVQQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | EPEREQVQPKKKEGKISSKTAAKLS TSAKRIQKELAEITLDPNNL*VAGP KGDNIYEWSTILGPPGVSVEGGVF FLDITFSPDYFPKPPK\VTFRTRIYHC NINIQGVICLDILKDNWSPALTISKV LLSICSLTDCNPADPLVGSATQYM TNRAEHRM\ARQWTKRYAT |
| 1229 | 6726 | A | 1294 | 449 | 826 | QKSRRLLIDDLFFFFFFCETGSCSVTQA GVQWHNHGSLQPPPPG\NDPPTSA SQVAGVSVACHHSRVCARVCVCV CVCVCVCVESGLKLLGSSNSPSLAS QNARIIGMS*IVPKKLYFKSKVKGRI |
| 1230 | 6727 | A | 1295 | 1 | 727 | NTEDQRNEEKAQREANKKIEKQLQ KDKQVYRATHRLLLLGAGESGKSTI VKQMRILHVNGFNGDEKATKVQDI KNLKEAIETTVAAMSNLVPPVELA NPENQFRVDHILSVMNVPDFDFPPE FYEHA\KALWEDEGVRACYERSNEY QLIDCAQYFLDKIDVIKQADYVPSD QDLLR\CRVLTSGIFETKFQV\DK\V NFHIV*RGVGQ\RDERRKWIQCFND VTAIFVVASSSYNMVIREDN |
| 1231 | 6728 | A | 1296 | 2 | 1271 | PVRSSAPRRGHSVASAPRSGLRQVA GRRGAALPCSLAPGCGAAAGASPC PGAGRRRAAGGRCLACECTSLTCA GESGKSTIVKQMRILHVNGFNGEGG EEDPQAARSNSDGEKATKVQDIKN NLKEAIETTVAAMSNLVPPVELANP ENQFRVDYILSVMNVPDFDFPPEFY EHAKALWEDEGVRACYERSNEYQL IDCAQYFLDKIDVIKQADYVPSDQD LLRCRVLTSGIFETKFQV\DKVNFHM FDVGGQ\RDERRKWIQCFNDVTAIF VVASSSYNMVIREDNQTNRLQEAL NLFKSIWNNRWLR\TISVILFLNKQ\ DLLAEKVLGKSKIE\DYFPE\FAR\Y TTPE\DATPEP\GEDP\R*TRAK\YFIR\ DEFLRISTASGDGGHYCYPHFTCAV DTENIRRVFNDCRDIIQRMHLRQYE LL |
| 1232 | 6729 | A | 1297 | 235 | 1571 | GRPRPPPPQGRAPPPPPRMGCLG NSKTEDQRNEEKAQREANKKIEKQ LQKDKQVYRATHRLLLLGAGESGK STIVKQMRILHVNGFNGEGGEEDPQ AARSNSDGSEKATKVQDIKNLKE AIETTVAAMSNLVPPVELANPENQF RVDYILSVMNVPDFDFPPEFYEHAK VLWEDEGVRACY\ERSNEYQLIDC AQYFLDK\IDVIKQAD\YVPSDQDL LR\CARVLTSGIFETKFQV\DKVNF\HMF FDVGGQ\RDERRKWIQCFNDV TAIFVVGSSSYNMVIREDTGHNGL AGRL*TS\PKGIWDNRWAAAPSLVIL FLTKQ/EILLA*ESPLAGNSKUKDYF PE\FAR\YTTPEGCYSRPGE\GPHGV YRGQVTPFEDEF\LRSSNCPVEDGRH YCYPHFTCAVDTEN\IRRVFNGLAV DIHFSGMHLSFSYGAGFKEGEPPKF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NLKA |
| 1233 | 6730 | A | 1298 | 176 | 505 | ILKFPWIDIFLYSFNLVFLIFETRPHFI LSPRLECSGMTSAHCNLCPCSSDP PTSAS*VAGTTGTQHHA WLI*LFGE RELHHVTQAGLKLLS*VILSPQPPK VLGLQA |
| 1234 | 6731 | A | 1299 | 310 | 326 | SQHFGKLRRVHSLNSGVQDQPGQH EETSSLLKIQQLARHGCVC LWAQL LRRLGWEDHLNLGGRGCNEPRWC HCTPA*VTE*DSISKNNNNN*QAGV QWHHLGSLQPLPPRFK |
| 1235 | 6732 | B | 1300 | 99 | 430 | XVITQRELVSQRQVSNDLTEQAATFG LILDDVSLTYLTFGKEFTEAVEAKQ VAQQEAERARFVKEKAEQKKAE QKKKVEQKKKAAVISAEGDSKATE LIANSLAHRGGPP* |
| 1236 | 6733 | A | 1301 | 64 | 967 | NFRVEAGVRGVQQKETCAFKVLESI GKLG\LA LSVAGGAENSALYNVDA GHRAVIFDPIPGQK*QDIVVGEGTHF \LIPWVQKPQLSNDCSRPRNCCQS ITGSK\DLQNV\NITLRHPSSGPVRQP SFPRIFTSIGED\YDERVLA VPSQLEN LKSVVAPFDAG\ELITQR\ELVSRQV\ SDDL\TERA\ATFGLILDDVSLTHLTF GKL\LTEAVEAKQVAQQGKQRRAR FV/VLEKAEQKKKAAIISAEGDSKA AELIANSLATAGDGLIELRKLEAAE DIAYQLSRSRNITYLPAGQSVLLQLP Q |
| 1237 | 6734 | A | 1302 | 424 | 598 | |
| 1238 | 6735 | A | 1303 | 3 | 371 | |
| 1239 | 6736 | A | 1304 | 1 | 1596 | |
| 1240 | 6737 | A | 1305 | 2 | 556 | WDMMYVTRFASFRLRNVLPSFISDW LYVQKMNTWFKHENYGLMPLNGY LKMEIFFIQKRGALI**IYLSIKPSVK EFTETSAVFEDGTMFEAIDSVIFATG YDYSYPFLDETIMKSRNNEVTLFKG IFPPLMEKPTLAVIGLVQSLGAAIPT ADLQAWWA AKVFASRWALLSFIHFI NEHLLNTCY |
| 1241 | 6738 | A | 1306 | 955 | 1187 | IFFFFFFFKMESCPFAQAGVQWCDLG SLQALPPGFTPFSCLSLLSSWDYRRP PPHLANFLYF**TWVFTVLARMVSI S |
| 1242 | 6739 | A | 1307 | 6345 | 9041 | |
| 1243 | 6740 | A | 1308 | 236 | 437 | LLTLRWSHSSHVLLKTRGQPRRSG WCL*SH/HFGRPRRADHLRSGVQDQ PGQHSEIVSTKNTKIGWAWWQVPV IPAT*E |
| 1244 | 6741 | C | 1309 | 182 | 433 | MHLDLFLNKTLPQIRGVESEQSSRL HPLPDPRGDRHRMADNLPMEIHGS SATSSGKPSDFNQAAVDGAGERGG KEVLGGTLDVL* |
| 1245 | 6742 | C | 1310 | 72 | 254 | MVSTQLRQASDPRTTIGRERFELL RRVDKLMSPRLPTGTLNPHHFWTL SIPQVGRCNAP* |
| 1246 | 6743 | A | 1311 | 225 | 735 | GELRVNSLHVSTHFQIPEETDIGWL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VSPGQGPAPPFEDIQLWPPGSLMAA EPTDQSLEESH*DRWITTFTFARIQ EGRK\D*PQRSNEFKE\VTQQLPHL\ LKDVGSLDRKN*GAWDVNQDFGG SRFN\EY\WRLIGGA WPKEIRKEEKT LKIQUERSKAAWLEDGVGQGR |
| 1247 | 6744 | A | 1312 | 165 | 629 | TGEMLIRKHCLYIVCKLSLLFIFRDM SCSVAQVAGMQWHATNAVDGD*LT ASLKLLGSSNPPPCNPKRAGIIGMH QHIQLIFCWSFF*KQAFRLITKALRN FKKI*FQNTLVTKY*HCSLTFFFCH FNENRILHLLAQMAKQDSGLLRV AWEA |
| 1248 | 6745 | A | 1313 | 76 | 523 | ELGRNLWNASQGRGLEWVSNRKF WAVYAYITFLSHPERVVNKHNCPL FE*KGECWEW*EARAQ\DRVQKQ MWLLRIQTSFSSRKETQSLRVTFWR YPVSPSPISMR*MSPGNSYRTLYKR NVPLKAHFPTAVLAVVPPAVTNQG KEQG |
| 1249 | 6746 | A | 1314 | 55 | 391 | |
| 1250 | 6747 | A | 1315 | 996 | 1334 | WASVGLSGPRSPSSRPQ*ARPRPG APASLRQADLGRGWRDLGAPRPR PPRTGGWRSCCRGRGPGSRPRGAR AGLPGAPGGWRRSRRSWTRARA ATRPRAAARGSRTPRG |
| 1251 | 6748 | A | 1316 | 1 | 993 | |
| 1252 | 6749 | A | 1317 | 72 | 496 | PPWARGSARRPPAWRTVRMPSCHP RMFGAPQKTFLRVSVWSRCRPWGI VMRMM*PMRGQVRRHNSCMAKPT EE*NPTVSATFCCCSFVSCSWPPVTR YSSILFTAAM |
| 1253 | 6750 | C | 1318 | 202 | 378 | MTPYLTFLSPLPPKGEIWGLLLFLT PLGFLPSLPLLPCPAPAGVRRQW DGPTEGA* |
| 1254 | 6751 | A | 1319 | 1 | 1541 | |
| 1255 | 6752 | A | 1320 | 9 | 345 | YLSEVGVSVGIVIRPRQWIRPEGDP FHGGRLKMDPLRAQQLAAELEVEM MADMYNRMTSACHRKCVPPPFKE AELSKGESVCLDRCVSKYLADIHGA *WGKKFDRVLLQG |
| 1256 | 6753 | A | 1321 | 199 | 985 | VRGSGADPGGRLCSASVRRGGPLE GAFNSRTRQATMTENSTSAPAAKIP KRAK\ASK\KSTDHPQVFQT*IVACN SSPRRTGAGS\SRQSIQ\KYIKSHYKV G*ERLTSQ\KLSIKRL\VTGVP SRQ TK\GVGASGSFRL\AKSDEPKKSVAF KKTKEIKKVATPKKASKPKKAAS KAPNPRNPKSSPVKKA\KKKLAAPG PKKA\NPKTKVKAKPGKAFKAHWR PYLV*PKCKCPVAKEGRARRKLTMI VFFLRDTPSWSPIFCK |
| 1257 | 6754 | A | 1322 | 3 | 129 | |
| 1258 | 6755 | A | 1323 | 376 | 545 | NILHRLFTFREKTSYAPFVVRRFHSH GRHTPPALKWEVWVRKKGPGE DSDMALSYSPPPPPPPMVMG*/SP PSH*PLLLCRRVKKEGF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1259 | 6756 | A | 1324 | 14 | 262 | FQTQTKYQAPLHPAPGHRPTPLPPP PPASHCHLFLWSVCKRSNKPQAPFI SPAPPSNPLPEPGPCSSLCQPWGRTG EGLAPPD |
| 1260 | 6757 | A | 1325 | 234 | 275 | |
| 1261 | 6758 | A | 1326 | 52 | 454 | SQTQREPTMVLSPADKTNVKAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR |
| 1262 | 6759 | A | 1327 | 3 | 616 | PTLLVPTDSERTHPWLLSPADKDQR QGPAWG*G*GSHPPSNVAKTLERIM VLFPPPTPKPYFPAHFDL\SHG\SAQV\ KGHGK\KVADALTNAVAHV\DDMP NALSA\LSDLHAHKL\R\DPFNFKL L\SHCLLG*PWAHLPRPSFTPCGCK ASL\DKFPGLFVEAPLLEPSKLPLKL GSLRLAMLLCPFGPFPQPLLFPAPV PPWSLK |
| 1263 | 6760 | A | 1333 | 732 | 1634 | RRFWQVENHEILTEQAFVGQKPIFR/ MKSLKEKLKTLATKRKPKNIGDILT KRKNNRTGSEAGEPQRWKPRRCPI RRAQEKNSQRPRKRREGKVPIWRK KPLKTGRDRSW*P*KLLALCPSTVG IRSAG |
| 1264 | 6761 | A | 1334 | 1 | 531 | FFFLHVVAHLIFTATQMGSNILITVL QMRSPRRRVEYLAQDHTPFATPHS KSHRQLRLSTSMVITYHLPLQTISS LVPYSQWGHLLQSPGPKLGNRKPFLL TPPSPSPTPSKWN\SPGTMYFFRVLI QSPLSSPRPRC*PIVRCPAAAPGSSLP STLFAGPSPPFPASYTLRLRCAF |
| 1265 | 6762 | A | 1335 | 130 | 361 | GACCPLSPGGESGT*C/SPRGPRKPS GPSPKAKCS*QSTGCGQCASSPPSPS PGRAPCDSPILACDLGQGGFLQLHT H |
| 1266 | 6763 | A | 1336 | 144 | 224 | |
| 1267 | 6764 | A | 1337 | 1111 | 1200 | PGVVTLLGGGACSEPRCATALQPGR ESETLP*TLHSHNQSKPLPPICYPI VNGNFILLVAQVKKPKAGCGGPR L*SQHFGRPRQADHLRPEVQDQTG QHGKTASL/LKNTKISQVS/WTLGG GACSEPRCATALQPGRESETLP |
| 1268 | 6765 | A | 1338 | 344 | 512 | ETLYTME*YTAIEKNEIMSFAGTWL ELEA\VIL\SNLV*EQKTKMLPCSPL MGWELK |
| 1269 | 6766 | A | 1339 | 274 | 393 | |
| 1270 | 6767 | A | 1340 | 1 | 561 | VRSAVGGTGMSSGASRKSWDPGKP WPPDWPIGRK\MK\VLWAALLVHI SCQNPMPKW*QAV*NKSRPELR\Q QTEWQ\SGQ\RWEL\ALGRF\WDYL RWVQTLSEQVQEELLASSQVTQ\ELR ALMDETMKELKAYKSELEEQLTP VAEETRARLVK\EPQAAQARLGAD MEDVRDRLVHYMFVDV*AI |
| 1271 | 6768 | A | 1341 | 1 | 746 | MAAAGAFRLRRAASALLRSPRLP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ARSCRPRPDSITRSPPDVRLPLEKQL KNAINQRGTKGPYIRYYPEVVDHY ENPRNVGSLDKTSKNVGTGLVGAP ACGDVMKLQIQVG*KRGRFVGC*G FKTFSAVGSAIASSSLSHLNGVKGK TVEEALTIKNTDIA\KELCLSFPWK LALAPMLGLKVAFKAALADYKIET RTQKKGEAEKKWSPPLGEASSRPTP AVPQPAVPVTLDVSGSRLPSPTEGA L |
| 1272 | 6769 | A | 1342 | 160 | 381 | SWGLDSALGVSDTTHHPKVVGRAK HRGFLKWLPPPPGPPLGKRNCQPYP NPQLPESGPPQQYFYLKCCPFYEL |
| 1273 | 6770 | A | 1343 | 653 | 814 | WDSTPLPSSFTDWMLWPEKRQVGA CSHPTPNFL/C*GKLNISPNSPCQPKV LDLT |
| 1274 | 6771 | A | 1344 | 954 | 1245 | DLSLTTSRQRKHEFKEVILPNYTHD KLYLINSNHPTKMCP*NQVLKKLIHK ITQQWITGAMIHAYNPSTLGGRWG WIT*SQELETTLPHIRGTLIHKI |
| 1275 | 6772 | C | 1345 | 155 | 431 | MRERGLGPLGVFRSDAGLKSLEPEG RRESGALEECVIHTQRVCDWKVPE HPLAPLLLVSVAVLRILAKPLPTQR DLFLLSRSSLFNQHFPLC* |
| 1276 | 6773 | A | 1346 | 2 | 70 | |
| 1277 | 6774 | A | 1347 | 1 | 271 | LFF*TESCSVTRLQCSGMISAHCNLH LPGSSNSPASASRVAGTTGARHHAQ LIF/VVFLVETGFHHVGGDGLDLL/N LVICPPRPPKVL*LQA |
| 1278 | 6775 | A | 1348 | 117 | 229 | KKTMFRQKLFYKRRKQLQKGPRP*G SAKKKLCFGKSYFIRGSSFRKGQGH EERGLKYKKKTGEGV |
| 1279 | 6776 | A | 1349 | 255 | 381 | IHFSINSOLFSPSSPPNKKG*FPKVT* KR/P*NGPRYIPQRF |
| 1280 | 6777 | A | 1350 | 72 | 577 | TTGVRGALQREGGSLPTQPQGERA LGGRRRNQAGDPGFA\G*RGAWP TGCKQGRGGSPSPQPLGSGGR\QNL ARLKPPRPPP/PQEGDKGRPRQQG PSWRSKSSPPILPTSYPGGDKGVVP KHKLEAVNSVRARSSVSRNKCWSN RMDIALRCPVTVAHELTYS DAL |
| 1281 | 6778 | A | 1351 | 160 | 336 | |
| 1282 | 6779 | A | 1352 | 1625 | 1920 | LSFPAKKGNDCLPHVPGLSFKGRVP ESRQEFCEQTQESSLENPRLCIPV/CHP WAPWRWEPGETAEPVLRKEAF* PGPPCPPPNRVSETREAVLLQPRI |
| 1283 | 6780 | A | 1353 | 9 | 249 | KVHTKPRTSSICRSHIGFCLFF*ETES CSVTPPGVQWCNLGSLQTPPPGSS DSPASAS*VAGTTGMHHRAQLII*F YVFTGFFWQ*QLSDGILTH |
| 1284 | 6781 | A | 1354 | 426 | 744 | DNLLKSFHLIISINCLFFCFFFL*TESC SVSRKCSGAJLAHCNLCLLGSSDS HISASLVAYRCLPPCQANCFFSFLAE TGFHHVVGQAGLELKIQLAECSG MRQ |
| 1285 | 6782 | A | 1355 | 184 | 422 | GYIQGSPALVSTHGGHAV*PPTQSK PTEHAHP LQPRRWARTRVGE GIPC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AHPSPSCSPRPLATQKRFQANRRGR LEGLC |
| 1286 | 6783 | A | 1356 | 3 | 1221 | HFIYLFIFIFLRQSLALPLRPECSGAIS AHY/RHLCCLPGSSDPPN\SASRVPGT TGMPRCTWLIFVFLVEMGFHHVGQ AGLKLLTSGDPPALASQNGGITSVS HRVQPKNFFE*SRYYYLNFKN*DS KRLKK*KIRQLEN/RRNMIQILLFF* L*NSCSRMKDNS*AREKYLOHILRG LRFLTCKDSTKLDLKTNRNTTLE* MENMMKQFTEEKIQMPNKLKRC* TSLGVREMQIEVIRYYFSRSS*QKFK RVV/IIPGQLQRKCQF/PCTW*KSKPL KRFSEEI*YNINQIHLFEAGSCCVVQ DRVQ*YHHSSL*PQPPRIKQSFHLSL PTSWDYWHMPP/HPS*FCVCLFCFF SRDEVSPGCSSWS*TPELKLSSHLNL PKCRDARPEPPCVAQYDINQNCKK HVLS |
| 1287 | 6784 | A | 1357 | 703 | 918 | TREVEVAVSRDHATALQPGQQRQD SVSKKKKKGRVQWLAPVIPSTLGD QGGWIT*GQEFETSLTNKVKPHLY |
| 1288 | 6785 | A | 1358 | 273 | 561 | DRQAEKKRNIL**NEIVLDLPR*PHT AS*ISSTT**FENTALRPGVVAHACN PSTLGGGA/GQIT*GQEFETSLANV VKPISTKNIKINWEWWCRL |
| 1289 | 6786 | A | 1359 | 375 | 663 | LITKQLGLGVVAHVCIPQHFGRPRW ADHLSPAGVQDQPGQ\QGETQSPQK NTKISQVWWHVPEVLAP*KAEAKG LLEPGRQRLPPTLHSRLGGSETL |
| 1290 | 6787 | C | 1363 | 79 | 153 | MPDMIRQHSSCLIKRVYLTRWFGR* |
| 1291 | 6788 | A | 1364 | 4776 | 9134 | WLHDSVNILKNIEHFFFFFFWRQSL APSSRLECSGAISAHCNLHLPSSDS PASASQVAGITGAHHHAQLIFVFLV ETSSHVVGQASLKLLTSSDPLALAS QNAGITGMSHHTWPNH*IEHF*WV NCMVWEHYLNKAILKFYKEIKSRR DPTPKAYLIWGR*C*/TVL*NKEQVT DTKFLT*LFKGVGRM*KFTVPAPEV VRVS*LYLA*DKCLVIIVAMLMDRN VIFLKGPLMGFVG*LCSGFQGEWF LFESYPSLPTSPTTLSPALPKYFL*VN VTKANFLQ*SIPFYIMVLTFPST*S QYTNFFFSF/HFFFFFF/CFFETESHS VTQAGVQW*DLGSL*PLPPRFQ*FS CLSLSSWDYRHAPLRPANFCIF**R /SGVSPCWPGWS*TPDLK |
| 1292 | 6789 | A | 1365 | 3 | 287 | |
| 1293 | 6790 | A | 1366 | 75 | 301 | AHKKLRAAPLAPMTGTH*K\VFVK AGDKVKAGN\PSWVMFPMKMEHTI KSPKDGTVKKVIFYREGAQANRHHS FSRV |
| 1294 | 6791 | C | 1367 | 155 | 377 | MKASSFKKLQKFYIDPYKLLPLQRF LPRPPGEKGPPRGGRGGRGGRG GGGRGGGRGGGFXXXXXXXXXXGF RG* |
| 1295 | 6792 | A | 1368 | 363 | 423 | SIKGTENGFLIVL*PKSQV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1296 | 6793 | A | 1369 | 157 | 723 | KTLWRYGNRG/GFQRGGST/RAGGC /GAQQQGPEGHVAPY*GEFLHPCE DDIVCKCTTDENKVP/YFNAPVY*E TKEQMGKVDAIFGQLRDFYFSVKW SENMRLSSFKKLQKFYIDPYKLLPL QRFLPARSPGEKGPPKASGGRGGRGG GRGGGGRRGGRRGGGFRGGRGRÆG GGFRGGRGGGFRGRRTLSETC |
| 1297 | 6794 | A | 1370 | 1 | 810 | ASPPLVCTHARSFSVLAPLFLHFPLL PDRRSRSFRAVHFWGPRSSPPHAAV RLREARRGRDRREKAESPTGEKSTS PSSRRQRGPPTKVRPPAPFTMQP ASAKWY\DRRDYVLKWEFVFLNTL RDVNVNFÆKSKTYNFSCLGG\SDN F*GILNEIDLFHACID\PNDSKHKRTD RSILACCLRKRIWASSWPKGLTKÆ RGKGLIWV\SVDFNNWKDWEDDS DEDMSNFDRFSEMMNMGGD\EV VDYPEVDG\ADDDSDSDDEKMPD LE |
| 1298 | 6795 | A | 1371 | 1 | 588 | |
| 1299 | 6796 | A | 1372 | 179 | 989 | KWRNQSWRWPKPGTNWMLSCSVC WRRVTWTGSVWMRKLKHPQTPT /IKDCSIAATGKRPSARFPHQRRKKR REMDDGLAEGGPQRSNTYVIKLF RSVDLAQFSENTPLYPICRAWMRNS PSVRDAECSPSS\PLPLPEDEEG\SE VTNSKSR*CVQACPPHTHPGGQPKN ACR\SRIP\SPLAALRMQGT*RWSPF EPEPSPSTLIYRNMQRWKRIQRW RPPACLPLVGPFAESPLCLSRWK EASHRNQLRYSESMKILREMYERQ |
| 1300 | 6797 | A | 1373 | 245 | 336 | HIPSQGQDGK*VKNRARKIVSYSRG GWHSG |
| 1301 | 6798 | A | 1374 | 127 | 872 | EATGQTVGTVPSSLSRPRPPLHSSSG GVRIQTLFATSRPLDKTASIFLVLSN ACIF*KILIA*KEIQDS*SHH*K*LLLI RLDFLSSFFPP*LIN*FFFFPGNSLVH RLFFFNLGMVAHTYNPSTLGGQSG RIA*A*EFKASLGNLVGPHFFFLGGG VGYKSPFIKPILNKKKTKSLQKKKR YRKRIPLLHMVPKREKNKGDNQRQH AQQIKASFSYFFNVQNTSKGYTYLK QELSDAGHAGPGKPFQ |
| 1302 | 6799 | A | 1375 | 37 | 80 | |
| 1303 | 6800 | A | 1376 | 1452 | 1700 | |
| 1304 | 6801 | A | 1377 | 316 | 373 | |
| 1305 | 6802 | A | 1378 | 144 | 356 | FQFRLTSLRNSTDVHRCPLPPPPAS PPPYPGPWGMGCCGRFPKGGQGP PRLSGLG*FLSFFALGFSDG |
| 1306 | 6803 | A | 1379 | 860 | 924 | |
| 1307 | 6804 | A | 1380 | 263 | 616 | TTCFSFESRASCHFHVASAVSPPTPL CSPATLMAQDKAGKPSPRK/PSLAP EKPLSPLSPQ*RHSPKPKAPHVESP SGPSPTRAKKRV*FSSPPSLWGQEP GHÆCPLPYLGEGAPA |
| 1308 | 6805 | A | 1381 | 152 | 272 | YSVLKFNYEILKNCFSFFV*VSEPPF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KTILVYFTLTEKL |
| 1309 | 6806 | C | 1382 | 71 | 316 | MCHHSQLTFLYFVKTKSHCVAQAG LELLASSDPLDSTSQSVGITGMSHH TQPLILFFNFSVSVKYTKIMVLKNGF RNSYKK* |
| 1310 | 6807 | B | 1383 | 165 | 520 | XNLKLLDNWDSVTSTFSKLREQLG PVTQEFWDNLEKETEGLRQEMSKD LEEVKAKVQPYLDDFQKKWQEEM ELYRQKVEPLRAELQEGARQKLLP VLESFKVSFLSALEEYTKKLNTQ* |
| 1311 | 6808 | A | 1384 | 3 | 558 | |
| 1312 | 6809 | A | 1385 | 3 | 118 | |
| 1313 | 6810 | B | 1386 | 28 | 384 | MKAAVLTAVLFLTGSQARHFWQ QDEPPQSPWDRVKDLATVYVDVLK DSGKDSVTSTFSKLREQLGPTQEF WDNLEKETEGLRQEMSKDLEEVKA KVQPYLDDFQKKWQEEMELYRQK * |
| 1314 | 6811 | A | 1387 | 2 | 1093 | GGASCCLPRSLWLPSSRFRPCPRPG LWVPEVFSRSVPFSSPGCNEWGSTG LLHAEGTPLSQALLLQVPHGPFRM KAAVLTAVLFS DG*ARRRHFWQG G*SPPRAAWDRVKDLATRVPTV LKEQRTETYVSQFEG\SALGK\QLNL KAPLTTGDSVDLPPFS\KLREQF\GP C*PRDFLGINLGKRETEGP*GKGR*G KDLWKEVKAKVAALTDDFQERS WQEEIGAFTROKVEPLARKNFQEG\ ARPESLHELARRSLSPLEEMRDRA RAHVDAALRT\HLAPYSDELRLQRLG ARL\GALRENGGARMGQYHA\QAT EHLSTLSEKAKPALEDLRQGLLPVL ESFKVSFLSALEEYTKKLNTQ |
| 1315 | 6812 | A | 1388 | 1 | 2076 | |
| 1316 | 6813 | B | 1389 | 560 | 752 | XSVAAVTALNSES NFARA YAQGISR TKYWELIYEDSMDLIAKLPCVAAKI YRNLYREGSVTRGH* |
| 1317 | 6814 | A | 1391 | 1031 | 1407 | CVGGRAQVEKEGAALRLRPATVPR ALMSLSSLVKPETA/ALCGTEMQDF FTPLLCDFKS\PGISFCKGT*MCLRSC *HNVRRWR/DQPTPVSTVTPVPTLT CVPSPHFPVPER\GAGCLHLCLKFM VH |
| 1318 | 6815 | B | 1392 | 97 | 880 | MAPRTVLLLLSAALALTETWAGSH SMRYFYTSVSRPGRGEPRFISVGYV DDTQFVRFDSDAASPREEPRAPWIE QEGPEYWDRNTQICKTNTQTDRES LRTAARLLQPERGRTMYGCDVGPD GRLLRGHNQFAYDGKDYLALNEDL SSWTAADTAAQITQRKWEAARVAE QLRTYLEGTCVEWLRRYLENGKET LQRADPPKTHVTHHPISDHEATLRC WALGFYPAGDHTDLAAGMPRTKL RNTEL VETRPAGR* |
| 1319 | 6816 | A | 1401 | 1380 | 2180 | EIQSEWNLQDLAELQLEERLAGAWE E/LSFRAVRMPSP\FRSSALMGVMCG SRSADNLSWPFFH*NVMPEPVTELM |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QEQSYLKSELGLGLGEMGFEIPPGE SS\ESV\FSRAQQDSFCECSGPSNATR KMGVPS\TASVGKSKTPLVARKKV RASVALTPTAPSR\TGSVQTP\PDLE SSE\EVDAAE\EGSPRKL*GPKSESEV/ EKEGHGKLP\MPAAEEMHKN\VEA RLSLQQVIR\EIKESIVGEIR\REIGKL DFWAAVSS\SKASNSR\QDYH |
| 1320 | 6817 | A | 1402 | 119 | 301 | INDKRKKKRPARGAGGLHLQLCL SQPPQPRGHPAPIPTGQAGPRDSGP GASP*/GRDPPSD*WTPADLGSDPW AGPLPTPQEP*GSRWPSSATVSLAS TATGTPCTYSHGTGWTQRLWTRGL PLSRDPPSD |
| 1321 | 6818 | A | 1403 | 1451 | 2495 | RGLAGNFEDRKSAHYVFQTFRGGE RRSLELEAHLEGWSLGLRFLGGLK GPPA\QGHFHPSLPISWRGAGVPHS R/SPFPTLGIPG*IFPPKPGRRPRGPPR KEDLGPGMVG/RPSGPLQLPSAVL SADPAGPRPHVPFCEP/SPSHGVRAS PGSKWVEEEIGGEEGRQ/PKCRQAF QEAWLMQG/GARGQGLPGS/GCWR INKPSKPSKRGKGLTCQTFSTNIC* SPPLMPRSLPGPSFILHLISSQQP*SG LLFIDPIPEKGRGGLSERWGRAFG DSVACSFQKPTPGPWEVFEQDAWP NPWP/QGPPPENFPKGNPSHSRNIHK GDEQSPVRTKTEPTPWGGKHSQFA SR |
| 1322 | 6819 | A | 1404 | 3222 | 5798 | PLLTPLVSKVTAAGVPLFFFFFFF* DIVSLCHPGWSAVV*P*LTAASNS*\ VKQSSHLSPSSWDNRYAPPRPANY FYYFYFL*RLDLALFPKLLNCWAQ VILPSQPPKVLGL*AQSSEGGIHSGL SLPSPCFLCNPI |
| 1323 | 6820 | A | 1405 | 38 | 402 | |
| 1324 | 6821 | A | 1406 | 2 | 380 | |
| 1325 | 6822 | A | 1407 | 1 | 477 | |
| 1326 | 6823 | A | 1408 | 1 | 1104 | |
| 1327 | 6824 | A | 1409 | 524 | 1584 | IVKMEKYSIMKSMNMHLTERKKDH FRNDTNTQSFYREKWIYVHKESTKE RHGYCTLGEAFNRDLDFSSAIQDIRTF WYVVKLLQLIAKSQLTSLSGVA\QK NYFNILDKIVQKVLDLHISLLFKDL PQVLSSNLCTLIRGVGKSVLVGNIN IWICRLETILAW\QQQLQGLQMD*G K*TMGLTL\SDLPLAHGWNNILLPV FQDGWGHSTFRPR*PPRLYMAVG EDRQLWKKL\CQYHFAEKQFCR\H LILSEKGHS/VEWEVGCNFATFRKH YPAKEQYGRQHCIFCRHCSILFWKD SGHP\CTAADPDSCFTPVSSQQFIAL FQVLRACPLPIPYWRFVNPCCPVQG LIVSVL |
| 1328 | 6825 | A | 1411 | 588 | 855 | VLLSSYLTYSLVFICWLFICLFICIFI FMYVTM*IWFVAVFVWNLVFPYKV VK/TPWRSRIHVHCLYF**NYSPYAF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LYSA*CYSLCVH |
| 1329 | 6826 | A | 1415 | 277 | 509 | YMLSCHHTFVQTHRMYNTKHEP*C KLWTLK*DNLSM*VHQL*KFPTLVG DVDS/ERRLCMYGDRGYMGNLYIL LSILL |
| 1330 | 6827 | A | 1417 | 15717 | 16041 | |
| 1331 | 6828 | A | 1418 | 41 | 544 | TKLVMMQKLLKCSRLVLALALILV LESSVQGYPTTRKPRHQWVRCNPDS SSAHCLEEKGHMFELLPGESNKIPR LRTDLFPKTRIQ\DLN\RIPLSEDYS GSGFGSGSGS\SGS\GSWFLTGNNGN RNYQL\VDE\SDAFQ*QPLGSLDRNL PASDSQDLGQHGLEEDSMV |
| 1332 | 6829 | A | 1419 | 168 | 467 | |
| 1333 | 6830 | A | 1420 | 2 | 196 | ASTRSRRSGSRGLTRRAAFGV RAGE GWVCGGPAGSRRRRKLPLTGPGSG SFQCRSRGGRGSVNMKGDPNKP GKMSSYAFFVQTCREEHKKKHPD FSVNFAEF\SKKCSER\WKTMSCKG RSSKF*RIWAKS*QSFAIDRIEMENL RFLPKGDKKGKKKDPNAPKRPPS AFFLFCSEHRPKIK\IEHPGLSIGDTA KKLGEMWSEQSAKDKQPYEQKAA KL\EKYEKDIAAYRAKGKSEAGK KGP\SRPTG\SKKKNPPRSWRGWEG *EA**DPASGIWGAGRRGLGLWRA GGQSEEAETAPDRARFWFMSMT RWTRICQHG |
| 1334 | 6831 | A | 1421 | 3 | 107 | |
| 1335 | 6832 | A | 1422 | 450 | 851 | KTEFTQNYFWKSCTGVDGFFFSILF CLFV*DGVL LCHPGWECSGCDLHS LATSASQVQAILVPHQPSK*AWDYR RAPPQLG*YLYC\CRDRVFTMFVPG LSNFW\PHV\HLPQ\PPKVLRIIGREP TCAPASMAF |
| 1336 | 6833 | A | 1423 | 6 | 461 | AEMTPLHSSVGSRVRLHLKKKNYI KKPRKALFISIFGIFFHLIYVSTYIYL STFSFTSLILMEFILCVV*VLHLQLK NAILMAYWY/TFILITWLPSSSEEDLK VL*LFMPKNELIFSKCFHFLFIVPKFT LLDHLAFLRLKLAFWRLGWST |
| 1337 | 6834 | A | 1424 | 222 | 350 | GAHTWTGISQAALQPTAPGRLSRTL LFLC*KCGEICNLLSGC |
| 1338 | 6835 | A | 1425 | 198 | 385 | |
| 1339 | 6836 | C | 1426 | 207 | 385 | MFFYKLAQMXQISVSTLKFKLVLFV PTGXQVNGGEPSTLYGRWGRXGSA PSWRYQPFCP* |
| 1340 | 6837 | A | 1427 | 327 | 516 | |
| 1341 | 6838 | A | 1428 | 58 | 255 | FSPDFYRGYIYFYHYFGFEKFFFTPS NFFISQSR*FFCVKMFSFFNLRFKIPL PNHVDFA LCFFVV |
| 1342 | 6839 | B | 1429 | 242 | 509 | MRPRKAFLLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DXGENDLEVKEENGVLVLNDANFD NFVADKMDTARDLPPX* |
| 1343 | 6840 | A | 1430 | 338 | 511 | NSFSKSKTPCVAHGRGVHAEAGNK RQYLGFLFFF*FFILWCFTSCSEY |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1344 | 6841 | A | 1431 | 2 | 454 | |
| 1345 | 6842 | A | 1432 | 671 | 955 | FFFF*IFTLGCFTSCSEY*ITMNDVK* FSPEFLPEGYLLFLSLFGV*KIFFYTL LISLFLKAD/RFFCVKMFSFFNLRFKI PLPNHADFALCFFVV |
| 1346 | 6843 | B | 1433 | 46 | 3152 | MRPRKAFLLLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEEEDD DEEEDDLEVKEENGVLVLNDANFD NFVADKDTVLLIFYAPWCGHCKQF APEYEKIANILKDKDPPIPVAKIDAT SASVLASRFDVSGYPTIKILKKGQA VDYEGSRTQEEIVAKVREVSQPDW TPPPEVTLVLTKEVFDEVVNDADIL VEFYAPWCGHCKKLAPEYEKAAKE LSKRSPPIPLAKVDATAETDLAKRF DVSGYPTLKIFRKGRPYDYNGPREK YGIVDYMIEQSGPPSKEILTLKQVQE FLKDGDVVIIGVFKGESDPA YQQY QDAANNLREDYKFHHTFSTEIAKFL KVSQGGQLVVMQPEKFQSKYEPRSH MMDVQGSTQDSAIDFVLKYALPL VGHKVSNDKRYTRRPLVVVYYS VDFSFDYRAATQFWRKVLVAKD FPEYTFIADEEDYAGEVKDLGLSE SGEDVNAAILDESGKKFAMEPEEFD SDTLREFVTAFKKGKLKPKVKSQPV PKNNKGPVKVVVGKTFDSIVMDPK KDVLIIFYAPWCGHCKQLEPVYNS LAKKYKGQKGLVIAKMDATANDV PSDRYKVEGFPTIYFAPSGDKKNPV KFEGGDRDLEHLSKFIEEHATKLSR TKEELMDVQGSTQDSAIDFVLKY ALPLVGHKVSNDKRYTRRPLVV VYYSVDFSFDYRAATQFWRKVLV VAKDFPEYTFIADEEDYAGEVKD LGLSEGEDVNAAILDESGKKFAME PEEFDSDTLREFVTAFKKGKLKPKV KSQVPKNNKGPVKVVVGKTFDSI VMDPKKDVLIIFYAPWCGHCKQLE PVYNSLAKKYKGQKGLVIAKMDAT ANDVPSDRYKVEGFPTIYFAPSGDK KNPVKFEGGDRDLEHLSKFIEEHAT KLSRTKEEL* |
| 1347 | 6844 | A | 1434 | 785 | 1271 | LCTDQLHNFNNYFQDKDKCFYFPM FWSFLGLETEAACFKPDSKGKALQ NRKYFN\VYLPSATSRDLWISPGWS QPFFFFFFFFFFFF*RA |
| 1348 | 6845 | A | 1446 | 549 | 791 | GLLSN*NFFFSILIFFQTESRSVA\RL ECNGAISAHCKLRLPGSRHSPASAS RVAGTTGAHHHAWLIFFVFLVETG FHHVSQDGLDLL/NLVIHLPRPPKVL G*QAGVQWCDLRSLQAPPPGFTFPS CLSLPSSWDYRCPPCLANFFCIFS DRVSPC |
| 1349 | 6846 | A | 1447 | 59 | 485 | NSPCSGSSIATASPERRKGINPAPPST PAAPCRS*ACTAAAAAAVR\DDRLN VTEELTSNDKTRILNVQSRLTDAKR INWRTVLSGGSLYIEIPGGALPEGSK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DSFAVLLEFAEEQLRADHVFICFHK NREDRAALLRTFSFL |
| 1350 | 6847 | A | 1448 | 125 | 927 | NPPCSGSSIGPCSPKRRKGIKPGPPIH RKPAPSGS* \ACTAAAAA \AVRVPGS PSTAV \VTRVRG \LGGAPDAPHPLK DPRVGEGNSQRNPNI \SANLFYS \DD RLNEQKEL \TSHDKDEHSRPSRLT DGKTPLNWRNNC*SGGSLFNIKPA GRRWPEGSKGQLLQFLLEFA*GATC GADPKVFICFQTRTREKAEPPLLR \T FSFFGLCRLVRPGGIPLVPKETPDAC FMALQRSRESLPGEEEEVGARLRG WAIPPPWGHPLVCTGG |
| 1351 | 6848 | A | 1449 | 1 | 866 | ESVDLAAEAVRIRRSPLIFSKAVHIM AAAFRKAAKSRQREHRERSQPGFR KHLGLLEKKKDYKLRADDYRKKT RITSKALRK \KALEKNPDEFYKMT RVKLQGWSYILLRETKGRK*PQEQL KADEELQDVKYIEMKRVAEAKKIE RLKSELHL \VWDFQGKQKNKHVFF FDT \KKEVEQFDV \ATHLQTAPELV DRVFNRPRIETLQKEKVKGVTNQT GLKRIAKERQKQYNCPAHQRIE \RE KKLIPLLPQKIQTRKDLMDKTQKVK \VKKETVNSP \AIYKFQKSVENR |
| 1352 | 6849 | A | 1450 | 3 | 896 | LRAVRVGLLLGGGGVYGS \RFR \FTF PGCRA \LSPWRVRVQR \RRCMSTM FA \DTLLIVFISVCTALLAEG \T \WVL \VYRTDK \YTRL*AEVEKQSKKLGK GRKET \T \EFSWFGQKKKIERQEE T*RNNNRDLS \MVR \MKS \MFAIGFC FTAL \MGMFNSIFDGRV \VAKASF*P LFSYIQ \GLSH \RNLLG \DDTHRLVPF IFL \YLCTMSIR \QNIQK \LGLAP \SR AATKQGRVDFLGPPPPSGEVLLEL KELFIFYSF \LGH \THIRMGQLFCSQE PIGSLYYLGLFLVLNYFLSLLGYD |
| 1353 | 6850 | A | 1451 | 2 | 125 | |
| 1354 | 6851 | A | 1452 | 18 | 1374 | LAEQIVPRGVGIRPPDKADQAPCRS PIRTPAPESWHCDSRQRFRQDSSRM KMRVLGLVVCLVLWTLHSESGG KLTA \VDPETNMNVSEIISYWGFSE EYL \VETEDGYILCLNRIPHGRKNHS \\ DKGPKPVVFLQHGLLADSSNWVT \\ NLGNSRLGFILADAAIDVWMGNTR GNTWSPKHKTLSVSQDEFWAFSYD EMAKYDLPASINFL \LNKTG \QE QV YYVGHSGGTTIGFIAFSQMLELAK GLKMFFAWGPVASVAFCTSPMAKL GRLPDHLIKDLFGDEEFLPQSAFWK VAGVPHLATHVIL \KELCGNLCFLL CGFNERNLNMSRVDVYTTHSPAGT FVQNM*HWSQAVKFQKFQAFDWG SSAKNYFHYNQSYPTYNVKDMLV PTAV* \TGGHDWLEDVYGVNI*LTQ ITNLVFHESIPEWEHLDFIWGLDAP WRLYNKIINLMRKYQ |
| 1355 | 6852 | A | 1453 | 165 | 1353 | LPKPRLGPGQPEKDRTESSVRMAIT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LEEAPWLGWLLVKALMRFAFMVV NNLVAIPSYICYVILQPLRVLDSKR FWYIEGIMYKWLLGMVASWGWYA GYTEMEWGEDIRAVSKDEAVTLV NHQATGDVCTLMMCLQDKGLVVA HMMWLMDHIFKYTNFGIVSLVHGD FFIRQGRSYRDQQLLLKKHLENNY RSRDRKWIVLFPEGGFLRKRRETSQ AFAKKNKLPFLTNTVTLPRSGPTKIL NALVAQQ\KNGSPAGEDAKELASK SKGLQWIIDTR*PYPKAEPI/DNIQT WVFGYRKPTVTHV\HYGIFPAIKDV PALETEDLTTWLNQRFVEKEDLLSH FYETGAFFPSKKGHKEAVSREMTLS NLWIFLIQSLAFLSGYMWYNIQYF YHCLF |
| 1356 | 6853 | A | 1454 | 313 | 650 | FVICV*TYTGMNTHSPHTKTL SFLS DSG*FFYCRSL/CNIG*QKTYPQPNR LHTHTHTHTHTHRGYFSHTSSTVEK ALLTRIEGSEEDNGFYGWALRTI LVAFKSQCMH |
| 1357 | 6854 | A | 1455 | 2 | 401 | VSVGGLVGEVACACRDCIPETMAE GDNRSTNLLAETASLEEQLQGWG EVMLMADKVLRWERA WFPPI/MG IIYYLDPSVLSGVSCFVMFLCLADY LVPILAPRIFGSNKWTTEQQQRFHEI CSNLVKTRRA |
| 1358 | 6855 | A | 1456 | 18 | 741 | AACGAFSRVVVGVRVSVGGLVGEV ACACRDCIPETMAEGDNRSTNLLA AETASLEEQLQGWGEEMLMADKV LPWERA WPPAIMGVVSLVFLIIYY LDPSVLSGVSCFVMFLCLADYLVP LAPRIFGSNKWTTEQQQRFHEICS NLVKTRRRRAVGW\WKRLFTLKEEK PKMYFMTMIVSLAA/VLLAWGQQV HNLLTYLIVTSLLLLPWT*TQHGHI FERTLGMANMEINKLLKHK**TN |
| 1359 | 6856 | A | 1457 | 2 | 529 | GRVDPKAKKEAPAPPKAEAKAKA LKA/RRKAVLKGVHS\HKKKKIPHV HPPFRRPGRHLR\LRROPK\YPPEEP RPRRNKLDHYA\IKFPLTTESAMK KIEDNNTLVFIVGCLKPTKHQV*Q GC*RKLFWTLDVGAKVNTPGFGPD GRRRKA YVPTWLPDLPIAFGMFAN KIWGF |
| 1360 | 6857 | A | 1459 | 323 | 624 | IVVHLVPTTQRSGKGKIMELVERSV VARVEVGHRGFLERGLPIAINDM KKSPEIISGRMTFVQPRNWLLFACH ATNEVAQLIQGGRLIKHEMTKTASA |
| 1361 | 6858 | A | 1460 | 438 | 549 | |
| 1362 | 6859 | A | 1461 | 210 | 556 | QFWGPVATWGLPIDAINDMKKSPEI IQWGG*HFALCICYSLTFMEILPYK VQPSGTWASCFACHGTNEVRPSFI QGEGRIPNTRMDLKRASGINQWG KGKNKVFEGDSLCPGCC |
| 1363 | 6860 | C | 1462 | 110 | 509 | MLLICSFAPATLXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXVSA* |
| 1364 | 6861 | A | 1463 | 93 | 180 | |
| 1365 | 6862 | C | 1464 | 128 | 382 | MYLGISRRLSSMLTFLAYLHPRERP PHRAPXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXQQAQG TGISIPRTCTSTGL* |
| 1366 | 6863 | A | 1465 | 3 | 140 | |
| 1367 | 6864 | A | 1466 | 1 | 609 | |
| 1368 | 6865 | B | 1467 | 1 | 690 | MASWDEKDLTVPQPDTRKGSVLR GLSSRALRWAGRGHVAAGWRPLA PESAGGWGMAAAMVPGRSESWER GEPGRPALYFCGSIRGGREDRTLYE RIVSRLRRFGTVLTEHVAAELGAR GEEAAGGDRLIHEQDLEWLQQADV VVAEVTQPSLGVGYELGRAVAFNK RILCLFRPQSGRVLSAMIRGAADGS RFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPTT* |
| 1369 | 6866 | B | 1468 | 1 | 975 | MSPPGREQGLLLNLLRPSGLDNAG KTTILKKFNGEDIDTISPTLGFNITL EHRGFKLNIWDVGGQKSLRSYWRN YFESTDGLIWVVDSDRQRMQDCQ RELQSLLEEVGSSYPLCTWRFFSY LRIEQMYNLVLYRDIQFPDFCFNSN TDWSKGLKTHARFGNTSLHVAHTD STNTTNFVDVWRGRTKSLACLLQL SSLTCIYTAGKMRLQDRIATFFFPKG MMLTTAALMLFFLHLGIFIRDVHNF CITYHYDHMSFHYTVVLMFSQVISI CWAAMGSLYAEMTENKYVCFSAL TILMLNGAMFFNRLSLEFLAIEYREE HH* |
| 1370 | 6867 | A | 1469 | 25 | 353 | EVCYYSSEAFFSELIKVILRHLCV AGKGLCSIPQLNTREGSVLRRISK GSPLAVEIEEGHCLCLPLGTECLGI KPIVHLLNSEIGEKPPFSPLSPCSSA AFLLLR |
| 1371 | 6868 | A | 1470 | 79 | 467 | RPESQRANGVDSGPNLKTVPQPDTR KGSVLKWISKRGKPLAVEIEESHCLA CLPLRTECLGIKPIVHLFSTRPVIV PSLELHYDIDSIAHMFVADLLLIITLL SYYIPFYLGFQNAIGITGINHRAWFY |
| 1372 | 6869 | A | 1471 | 368 | 611 | LCPSHFAPTTLTQSGSSLKTCVVLNS RFKACRAVPGPCLVNQMFASSILG KSHHSLVPINQGHNALWKAAGPL PLKAGY |
| 1373 | 6870 | A | 1472 | 441 | 1178 | FVALPQPLCPSHFDPTTLIQSGAHKN MCCIKSRFKRDLGLCRTCLVNKMF TSSILGKSHCHSLVSINQGHNA PWK AAGPLPFRAGYCQGFSPCDSLKYG SWDEKDLTVPQPDTRKGSVLRWIS QRGKPLAVEMEEGHCLCLPLGTEC LGIK/PPIVHLFNSEIGENRPMVGG RHVLQ*CCLG*FL*LPLRCLGGEKH KSGL/HVHIPVIVLSLELNYDIDSFA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HMFF/SVDLLLIITLLSYIPFC |
| 1374 | 6871 | A | 1473 | 1540 | 1812 | GKFQLIKTLQNPVVCSLPVIPALWG GQRWVDHLRLGVDR*PGQHGETPS LLKNNNNNTKISWAWWHEPVIPA\ MGEAEAGESLEPGRRRLQ |
| 1375 | 6872 | A | 1477 | 1 | 354 | |
| 1376 | 6873 | A | 1478 | 1 | 411 | |
| 1377 | 6874 | A | 1479 | 2 | 265 | RMYGKIIFVLLLSGIRNVHPK*IVSIS ASSTTGAMHTSTSSSVTKSYISSQT NGITLINWWAM\ARVIFEVMLVVV GMILISYCIR |
| 1378 | 6875 | A | 1480 | 111 | 520 | |
| 1379 | 6876 | A | 1481 | 106 | 395 | EEALPPPLHCTWVPFSPFECLQEMS KEIVSISALSTTEVAMHTSTSSSVTK SYISSQTNGRKRDNLSDRFHCTSSC SDNTSLFLCVMGWYYWERS |
| 1380 | 6877 | A | 1483 | 3 | 1078 | TRAAGLRAGVRVPRSPGPSRRMPA RSGAQFCRRMGQKKQPARAGQP HSSSDAAQ\APAEQPHSSSNPAQAP CPRERCL\GPPTTPGPYR\SIYFSSPK GHLTRLGV\EFFDQPAVPLARAFLG QVLVRRLPNGTELRGPHRWETEA/ YTLGPED\EAAPLQGGWPGKTPR\ RGMFH*KPGD/LWVVYIYGYMYFC MNISSQGDGA\CVFL\RALEAPGKS WRPMRQLRS\TLR\KGTRQARVLKG PPKLCSP\SKL\CQALPINKSF*PEG TLAQDEAVWLERGPLEPSEPAVVG S/APRVGVGHAGEWARK\PLRFYV\ RGSPWASVVDRAEQDTQACAKG LPRQDFLHCLKTRINVLFLEKKKKK |
| 1381 | 6878 | A | 1484 | 3 | 452 | |
| 1382 | 6879 | A | 1485 | 26 | 493 | NSTDSETHPWLLSPARQRPTSRPA WGKVGAAHVRSMCAEALERMFLS FPT\TKTYFPHFDL\SHGFCPG*RATG KKVDDSDAQTPWPTWDDMPKRRRC PP*SDLHAHKLS/RLDPV\NFKAPKA TCLAG*PLAAHLP\AEFQPLAVARLP WGQISWGFC |
| 1383 | 6880 | C | 1486 | 30 | 200 | MCISYTKGHFVVVWWVFPGFSLIF RYISCPAPCRSSRMQSQCAHSSQSE VPGHRA* |
| 1384 | 6881 | A | 1487 | 31 | 664 | APALPGCEHMAIRELKVCLLGDT GVGKSSIVWRFVQDHFHDNISPTIG\ ASFMTKTVPCGNELHKFLIWDTAG QERFHS LAPMYRGSAAAVIVYDF TEAGFHFHPLKKWV\KRLKELGPE\ NIVMAIAGNKCDSLDR\REVPEGM KEY\AESIGAIVVETSAKNAY*YRKS SFKEISRDPHPWTPHENGNGTIKS *EANPCKPVRRC |
| 1385 | 6882 | A | 1488 | 124 | 1180 | DLGKPLFKVQEEGGRPPTLNQSEVV ALCPQGPANHDARSLIMDSPRAG THQGPLDAKTEVGADRCTSTAYQE QRPQVEQDGKQAPLSPGLPAMGGP GPGPKDPAGCGGAGA\GGSEPLVT VTVQCAFTVALRARRGADLSSLRA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LLGQAFPHQVAQLGQLSYLAPGEDG HWVPIPEEESLQRAWQDAAACPRG LQLQCRGAGGRPVLVYQVVAPPPK RGTPKPKRALDPFPPSPPPPKGPE DLGFRQGD TVDVLCE\VGWAWPFP GSTVVPGVWGA*SSACAVSRRGTQ KATPG*RPAPDVPLAVDQAWLEG HCDGRIGIFPKCFVVPAGPRMSGAP GRLPRSQQGDQP |
| 1386 | 6883 | A | 1489 | 1 | 229 | |
| 1387 | 6884 | A | 1490 | 3 | 461 | AASTRFRASGQFVMAGAGSAAVSG AGTPVAGPTGRDLFAEGLLEFLRP AVQQLDSHGHA VRESQVELRDQID NLATELCRIN*GQKVALDLDPYVK KA/ILNARRRV\VLVNNILQ\NAQER LRRVNHRI\VAREQPARRAMLDSGIY PPGSPGK |
| 1388 | 6885 | A | 1491 | 1274 | 1416 | FGIFSQFSVLH*SGK*A*NYYYYYY YYCYFYKMEYGSFFNLQVTF |
| 1389 | 6886 | A | 1492 | 243 | 1125 | FQQRLYRAARRFTMVKIAFNTPTA VQKEEARQDVEALLSRTVRTQILT G\KELRVCHPGKKEGSSGEMLWFTL FRAFQFILG\GLYLFGGACIYK/YTF MPKRHHFTVGEMCFFDSED PANFPF GGGEP*LSCLVT*/EEADIREDDNIAI IDVPVPSFS\SDSPAANYFMTFEKG MTA\YLDLLLG\NC\YLMPLQYFYL LWPPKKIWVELFGQTGRVGRY\LP QTYVVR\EDLVAVSRKIRDVSNLGIF IYQLCNRKSFRLRRRDLLLGFNK RAIDKCWKIRHFPN\EFIVETKICQE |
| 1390 | 6887 | B | 1493 | 28 | 282 | MYHDWRLVPKHEEEAFTAFTPAPE DSLASVPYPPLLRAMIAERQKNGD TSTEEMMLNVQRIRMEPWDYPAKQ EDKGRAKGTPV* |
| 1391 | 6888 | A | 1494 | 2 | 187 | QNDRKMETQA/PEEPMLNVQRIRM EPWDYPAKQEDKGRAKGTPHPTPR AHAGESGKRSLPFPH |
| 1392 | 6889 | A | 1495 | 302 | 771 | RKRGVCTHLLCRRRSASNCRAPALP SLTFEGQDAPGLPVVQVLRRVVG HPREAPVARLVVLPQPGGLARDQAA QAEEREAAEQ/LQ/AGGSRGARRPRP GPAAGVQRTAASRSRSPRRAGSRA ACSVAPAGRARGGPAPRSAADAPS SAPWRVRVLSG |
| 1393 | 6890 | A | 1496 | 497 | 1212 | SWPGGEAGTARRPGCLPAPA*TR*R PPRAWAPAASHGT*RVRSPAPRSQ SSLMKKKRR\FEGQDAPGLPVVQV VQSHKQAGSARKALGPRGQEVGAS /DHANLQGGGEAGRPAGCRVGVRT GCTHLLRVVGPHPREAPVARLVV LPQPGGLARDQAAQAEEREASEQLQ SGSRGARRPRPGPAAGVQRTAASRS RSPRRSGSRAACSVAPAGRARGGP APRSAADAPSSAPWRVRVLS |
| 1394 | 6891 | A | 1497 | 852 | 1562 | FGKAGWELNRRRERGSWRVEEKDL QRWGVCGGGLCLPKPVRRSGVCLS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LKHISGGLRTLSQAPNWRNNSNGR VRGKHSNLNAQPFHPSLSYELKPCC VSQGLQRGILPPPQVSGPTFCSPKAL TPPSVRVLPPPPP*CAVCMSVNSP PALPTPLAKVSPADLAPRD*AHISG* RG*PLGHPHLSPLMLFTSPEPSE/PPP YPPSAP\SSSFSPARPAPPTVWPPPM QHRLWLPFPSS |
| 1395 | 6892 | C | 1498 | 127 | 355 | MKNRILQRNGXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXX* |
| 1396 | 6893 | A | 1499 | 529 | 2082 | FLDLLHFTTSLIIPHYKRIRDITYTIR HFPFVHLSPKCLDRLPSLFLIHLGV/ VIL*ALEPIH*SSSFLH*LKIFSSPLW NI*VSPTFDSHF/CFLILNLFLLSFPL SALI/NFQLQF*IKNETFHTLLIG*SEH *I/HT*MISTLFWLFL/LLLTGSLV*A RIFSCVHTQYHHACAIEKEMYSSL FLFFMNSKSCILFCIIGPEFFDILL IC/LFFFLD*IIFSSIPALQ*YYLWALN AHSSQKARDSMLS/F*/ILVCWIAVT LG*DTLLAVTLE*DILSKVHCFMDPI SSSFLVFNPHFGWENFPQRYFPQVR VQRRLS*KFA*QEKCPPLWMFLPEQ SALTMKFLGYQKISLKALKDVPID FWAFSVG**QIC*QSISHPFLC*ANR DDLICFLPGHFNIFLLSLIFQNFTILC LDVRLYWALSIWRLSL/RLFFN/IFFF LFLHLTSLASLPGTPNITY*MTMSL FFLY\FYYLSLFALYLGEIPSTLFFQT VYQILLAVLFYFQDLPYSQSSLSFP |
| 1397 | 6894 | A | 1500 | 3 | 930 | SSRGRAGGVWRFERDEDGTGAGCG QWTRFCREPKMAVNVYSTSVTSDN LSRHDMLA\WINESLQLNLTKIEQL CSGAAYCQFMDMLFPGSIALKKVK FQAKLEH\EYIQNFKILQAGFK\RMG VDKIIPVDKLLKGK\FQDNFEFVQW VKKFFDANYDGKDYDPVA\AR\QG QETAVAPSLVAPALNPKK\KPLTSSS AAPQR\PISTQRTA\AAPKAG/PLGV VRKNPGVG\NGDDEAAELMQQGQR I*NLLFEDLGGKERDFYFGKLRNIEL ICQENEGENDPVLQRIVDILYATDE GFVILDEGGPQEEQEY |
| 1398 | 6895 | A | 1501 | 3 | 87 | |
| 1399 | 6896 | A | 1502 | 1 | 667 | RRSSARRGGRSEPGRAAGGGAED TRRRAGDMDRGEQGLLRDPVPEE GEDVAATISATETLSEEEQEELRREL AKVE\EEIQTLSASVKQQRKHLA EIQAGNLGINSLQELKQNIAGGW*D VTVT\SA YKKT\SETLS\QAGQKA\SA AFSSVGSVITKKLEDVKNFPNFLNH FEEKVENLKS\VRGH/TKPAGGDF\ GEVLNSAANASATTTEPLPEKTQES L |
| 1400 | 6897 | A | 1503 | 1 | 395 | AKAKMADVLDLHEAGGEDFAMDE DGDESIHKLKEKAKKRKGRGFG/SR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | *VWGKWGRVA**GRSYGFWSPPH HRNNGRKEEFSVISCMSLIEEGSRA RMREDYDSVEHDGDEPGPQRSVEG WILFVTGVHEEA |
| 1401 | 6898 | A | 1504 | 146 | 833 | CLSGTDEISIEGEMADVLDLHEAGG EDFAMDEDGDESIHKLKEKAKKRK GRGFGSEEGSRARMREDYDSVEQD GDEPGPQRSVEGWILFVTGSP*RKP PEEDIHDKFARIMGEIKNISSSTFDR RTG/YILKGYTSLNIETYKEAQA MEGLNG\QDLMGQLGGVDWCFVR GPPK\GKRRGGRRRSR\SPDRRPSLT GPLLSRCSLQDSIWTMAALGQIGLG WELCCVYI |
| 1402 | 6899 | A | 1505 | 717 | 1563 | APLPAVLTQTIHLVTGTAFHSGKVD IVTIGYPFIDLNDMVCMSQYDSTHG *FHSTVKTEGKLVINGNCITHHPR RDPTKIK*DDAGTEYVVESTGVFMT MEKAEAHSAAPSADG\LNDEKYENSL KIIGNASCATKGFAP/LPAKVIHDF GIVEGLMAMVHAITATQKTVDGPS KK\WHDSHGALQNIIPASTGATK/A GMAFLVSTTNVLVMDLTLEGILGY TEHQVVASDFNSITHSSTFKAGVGI ALNNHFVKLISWYENEFGYSNRVV DLMVHMASKGSS |
| 1403 | 6900 | A | 1506 | 625 | 2919 | |
| 1404 | 6901 | A | 1507 | 2 | 76 | HHYAKLGTRAVRRARRCAGWQSY VDNLMCDGCCQEAAIAGYCDAY VWAATAGGVFQSITPIEIDMIVGKD \RKGFF\TSGTLGAKKCSVIRDSLY VDGDCTMDIRDKQS/QGGEPT\YNV A\VGRSG\RALV\VMGKGKVFHRR HTLTRKAYETPLYT*RQAWHEGSA KGSKMCRLAELRG |
| 1405 | 6902 | A | 1509 | 63 | 290 | GGILLSISRPYKTKPTHGIGKYKHLI KAEEPKKKKKGKVAVRANLGTDY NYGVLNIHLTA YDMTLAESYAQY VHN |
| 1406 | 6903 | A | 1510 | 315 | 1092 | RPRSSKRMSGTSEKVLCLRNNTIFK QAFSLRFRTSGEKPIYSVGGILLSIS RPYKSK\PTHGIGKYKHLIKAEEP KKKGKVE\VRANLGTDYEYGVN\H HLTA YDMTLAESYAPLFSTTFCNSL SH*KSEESYAMPTQNHKKWLPVCR DQGQPKCLLGLKCLPHERVIVQIS GLSATFARKFSWKIIPKPVLP*RESG LFS*REHTERKTSRGRFQRFDP ELGRTFWAKFEVATVDPFHCQQWSYLSA KEKSLLGS |
| 1407 | 6904 | A | 1511 | 284 | 758 | KQNPSSPLQRLIAGSNLDSEPRIQTD ILKQATKDRVSDFHKLKQSRFFDEN ESPVD PQHGSKLADYNGDDGNVGE YEADKQAEAYNEEEDGDGGEEDV PPDEEREL/PNGKKQAMESNISMMS FKS*RNA SENLKCKMKSFYFVLS D FCKDELYQL |
| 1408 | 6905 | A | 1512 | 148 | 476 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1409 | 6906 | A | 1513 | 204 | 620 | GDAMAAVTPRPPLPEGCRAPSSAPT VSLPELRSLLASGRARLFDVRSREE AAAGTIPGALNIPVSELESALQMDQ LAFQGFIFLLEKPKLGR*ASSFSFLFR WGKRGLQATQLARS LGYTGGFATY AGAY*EWLEKES |
| 1410 | 6907 | A | 1514 | 1386 | 1711 | FPKSIMGLVTIQDMNLCKFIGLSHL PALVLLYC/DVRACVMMSGC/LRKT EKNLKSRPSFFACSILSRNVQCNTW KIGMFKDI*GFFCFPYFYLFVSVCIFA YL CRFSGF |
| 1411 | 6908 | A | 1515 | 481 | 1380 | TSKQNAAPLVKYFQEKGLIMTFDA DRDEDEVFYDISMAVDNKLFPNKE AAAGSSDLDPMSILDGTGEIDTGSDY EDQGDDQLNVFGEDTMGGFMEDL RKCKIIFIIGGPGSGKGQTQCEKLVEK YGFTHLSTGELLREELAS*SERSKLI KDIMERGDLVPSGIVLELLKEAMVG \SLGDTRGFLID\GYPRE\VKQGEEF\ GRRIWRPHSWVICME\CSADTMTN RL\LQRSRSSLPVDDTTK\TMAKRLE AYYR\ASIPVIAYYETKTQLHKINAE GTPEDVFLQLCTS*LTLFSEGKNA CLG |
| 1412 | 6909 | A | 1516 | 47 | 416 | NSYIYMCIYSYINTIYIHLYLESNISLP LNIYISTPT/HIY*RHTV*VHTKAYV HML*HVYIHFCLCVHKSFKGTIYRD ASFLESCSKVNTECHKLRKV KRYS RIHHTGIHQSSLITSPFTF |
| 1413 | 6910 | A | 1520 | 1386 | 1666 | SLMAPQKMGR TSCSPSERLGN*GPE TGSDSHKTPQQGCKGGRTRGSIVSL GDRRPLAP/GACFAGDKDFLGLRSP GVGTALLGCT SINQRLLWA |
| 1414 | 6911 | A | 1521 | 304 | 1253 | VTNEMSQGVGKYDFYIGLGLAMSS SIFIGGSFILKKKGLRLARKGSMRA GQGGHAYLKEWLWWAGLLSMGA GEVANFA\AYAFAPANSSGLHLGAL \SVLVKCPFFLSYFLNERLN LHGKIG CLLSILGSIVMVIIHAPKEEEEIETLNE MSHKLGD P GFVV FATLVVIVALILIF VVGPRHGQTNILVYITICSVIGA FSV SCVKGLGIAIKELFEGSLCCGIPWA WILL LSLIVCVSTQINYLN RALDIFN TSIVTPIYYVF FTTSVLTC SAILFKGV GKDMPVGR CPLVL*SGFFT IIVGGY SCCMPLKTSALA |
| 1415 | 6912 | A | 1522 | 20 | 131 | KEILPKQAFAVAPTYITEPVEIKFFFF SRIRL*VPPG |
| 1416 | 6913 | C | 1523 | 7 | 348 | MSKLYIMQFXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXHY TV* |
| 1417 | 6914 | A | 1524 | 1103 | 1388 | VLLIFNFLPMALYFVCF SF/CFFETE A HSVT*ARVQWHDLGSLQPLPP*FK* FSCFSLPCS*YYRHLPYPANFCIFSR DGVSPCCPGWS*TPNLR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1418 | 6915 | A | 1525 | 149 | 421 | |
| 1419 | 6916 | A | 1526 | 1 | 1107 | |
| 1420 | 6917 | A | 1527 | 25 | 1486 | GPQQPHSRSTHASGRPQSLSPVLSLS PDSMSFTTRSTFSTNYRSLGSVQAPS YGARPVSSAASVYAGAGGSGSRISA SRSTSFRGGMGSGGLATGVVAGGL AGMGGIQNEKETMQSLNDRSLASYL DRVRSLETENRRLESKIREHLEKK GPQVRDWSHYFKNEDL\RAQIFA NTCGTMPRIRSARIDNA\RLA\ADDF RVKYEDRSWPMCPVLWRTDIHGLP KVH/IDDTNYHTDLQLETEEALK\E ELLFQ*RRNHEEGS*KALRRQ\SSS GMNAWRLD\APKSQDLAK\IMADIR AQ\YDELGSKKNPRGSLDKYWSQ Q\NEESTTGGSPQKSAEVG\AVETHA HRSCLKRTVPVLGRSTLDSMRNLKG QLWRTSLREG*RPAYALTRLEPAPT GSLHLESELAQTRARGTAARPRE YEALLNIK\VKLEAEIATYRRL\LED GEDFNLGDA LDSSNSMQTIQKTTTR RIVDGKVVSETNDTKVLRH |
| 1421 | 6918 | A | 1530 | 277 | 693 | PWHCPDSHYSQQPGSTASSSVPART GGPCWSSSCSPN*CCTSCCSTTPTPT LDPR/GSRHCQLPWLKQLPKGM/CT STCLHGSCGCICGSCGPGCIDGPTL GRNHNEPHHHSHGDLPYRFPEHAH HGHATLMGLMDTPLV |
| 1422 | 6919 | A | 1531 | 1 | 364 | PFVSLGLMCFGALIGLCACICRSLYP TIATGILHLLADTML*SPGHMEVSC VDAPAEIPS*APN*QPTSFPAMCGSH PGCPALTSLQRTSATAILLHPCETLI KNQLAEPNQPMELIEIK |
| 1423 | 6920 | A | 1532 | 1 | 898 | RGESRVLWSELEGEAGGAGGWASS LNARMDNRFATAFVIACVLSLISTIY MEG\SIGTDFWYEYRSPGQENSSDL NKSIWDEFISDEADDATYN\DALFR YNGTVGFLRRVYSPYPKTLHWVLA HHERTESFDVVTK\CVSFTL\TEQFM EK\VDPGK/HTNSRGLDLLRTYL\W RCQFLLPFVSLGFDVLWGALIGLC A\CICRSLYPTIATGILHLLAGLCTLG SVSCYVAGIELLHQKLELPD NVSGE FG\WSFCLACVSAP*QF/LWASALFI WAAHTNRKE\YTLMK\AYRVGMSK KPACF |
| 1424 | 6921 | A | 1533 | 939 | 1591 | LQSLCRVLLQMESGSRDTIPGVCKR ERENREDTEVLQPRFPYQGGQLVG KAATPQPGF*STVGWTLQPQ*P*YP AGQGCPPRCPPAPSS*GSKRPPEPQ QGRLGPKPGSPA*GNASPPKCPA PVPTPCPPTLCTGEKTGGARAGPW VGAGSPW*DPR*DGPIPCVGDPLSP HPCCVIVALLPFNVSVPGGRGGAPP QPP*T*PKAMAVAPPFV |
| 1425 | 6922 | A | 1534 | 34 | 912 | GRIRMQRQSTTGGRGIMEGPRGWL VLSVLAISLASMVTEDLCRAPDGKK GEAGRPGRGRPGGLKGEQGEPPGAP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GIRTGIQGLKGDQGEPSGNPGK VGYPGPSGLGARGIPGIKGTKGSP GNIKDQPRPAFSAIR\RNPPMGG\NV V\FDTV\TNQEEPVDPSG\RLVCP EPGYYYFT\FQGAGPQWEICLSIVSL LQGARVRRSPGAF*HPPTRGFLFQV VSGGMGL\QLQQGDQ\WVVEKKPP QKGSIFYQGE\ADS\VFTGFL\IFPIC LSQGRTPSPPTSLASMLRL |
| 1426 | 6923 | A | 1535 | 919 | 1260 | YSVSEFRGQTLTAKFCFFERESHV PRLECRGTILAHCNLCPLGSSDSPAS ASRVAG\TTGACHNARLIFVFLVET GFHHVVQAGLNS*PQVIHPPCPPKV LGLQACTWHLAH |
| 1427 | 6924 | C | 1536 | 130 | 441 | MVQNKGLPANSQRGTEAXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXX* |
| 1428 | 6925 | C | 1537 | 5 | 316 | MVQNKGLPANSQRGTEAXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXX* |
| 1429 | 6926 | C | 1538 | 74 | 91 | MTLAM* |
| 1430 | 6927 | A | 1539 | 368 | 430 | |
| 1431 | 6928 | C | 1540 | 191 | 592 | MGQQPGQARAPSYCRCPLSPGSGR ALRWERPGGGQGPKEIVLSGCVPE KGPQTPAQPHSLRHLQNPEATARTG EEATSAAGGPWASPSFGGTQLCSDT MPALLGARSTCWIATHHVCTLPLS ECGPINILLE* |
| 1432 | 6929 | A | 1541 | 58 | 1531 | VIAVTSALPGRTQAAWTRVVKMDL LAAKMAVGGGSLMTDLTSSISKPL VPVGNKPLIWYPLNLLERVGFEEVI VVTTRDVQKALCAEFKMKMKPDIV CISDDADMGTADSLRYIYPKLKTD VLVLSCDLITDVALHEVVDLFRAYD ASLAMLMRKGQDSIEVPVGQKGKK KAVEQRDFIGVDSTGKRLLFMANE ADLDEELVIKGSILQKHPRIRFHTGL VDAHLYCLKKYIVDFLMENG\SITSI RSEL\IPYLVRGKQFSSASSQOGTRK EKEGGSKGKRGLKSFRISYSFY*KE ANYTGTGAPY\DAC*NACRGDRWE DLSRSQVRCYVHIMKEGLCSRSTL GLYMEANRQ\VPKFLSALCPGRTHQ SISSSPDCQHYTWVGVD\SLIGPRDH RLGEKVIPLSASVIGSSL\CLIKDRVT IT\NCLLMNSVTFWRKEANIQGSVI L\NNAVIEKGADIK\DCCLIGKWARRI EAKAKRSVCR*S*GNDQLMEI |
| 1433 | 6930 | A | 1542 | 315 | 644 | EEETPKDQCLGAHFSSDTFPRQSRL LGVHGRGAGSLCTGLLSEHCPSTPP SGSPRVTYLPHAPPLPPSP\SWAPTP PAHR*KPSTEPFPGPSTQVV*PLPMF TTKGPAPP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1434 | 6931 | A | 1545 | 1 | 364 | FFFF*DGVSLLWPRLERNGVISAHC NLCLPASNDSPASASLVAGITSAC/R PLPPKQK*LFFFLRWSLALSPGWSA VARSWLNATSPGYF**KQGFHHAG QDGLGLLIHPPWPPEVLGLQA |
| 1435 | 6932 | A | 1546 | 1 | 391 | |
| 1436 | 6933 | A | 1547 | 2 | 2371 | GPPGRARARGLRRAPAAFLRRSLSL PAAFSSAAGPSSPQRSQEGRREPRT RSSRGRGSRPRRLRLRRGRSAIH GEGRTAKGSAAWSARTFRSPPGVG RDPMRAHEGREIPSLGGARRREVL QAGRSQRAAGRRLRRRQELGLVGS GRPGGPPPGPGRRGTCAAALPPEWP RRRTGLPRRGPRPPLAMAKWLNKY FSLGNSKTKSPQP\PRPDYREQRRR GERPSQPPQAV\QASSA\ASASCGP ATASCFSASSGSLPDDSGSTSDLIRA YRAQKERHFQDPYNGPGSSLRKL AMCRLDYCGSGEPGGVQRAFSAS SASGAAGCCASSGAGAAASSSSSS GSPHLYRSSERRPATPAEVRYISPK HRLIKVESAAAGGGAGDPLGGACAG GRTWSPTACGG*KLLNKCSSSSAEE SGAGMKDKVTIADDYLDPFDAKND LKSISGKGESAGYMEPYEEQRIMTE Y*RQECVRSQH*GIQLYETP*EPGQ NFESESESTVNPRMRENKLPQDYEQ /RPAD*YDQPLELNPV/TQFPALAA QFNGNEKPQSSPSR\DRRRLRA PGGGFKPIKHGSPEFCGILGERVDP AVPL\EKQIWIYHGAISRGDAEN/LCL RLCKECSYLVNSQTSKHDYPLSLR SNQGFMHMKLAKTKEKYVLGQKS PP\FDSVPEVIHYTT\RKLP\IKGAE HLSLLYPVAVRTLLSGPDSALLCDR AWRLARCQRPTNQPPATVAGCVV CVVCMVLAHHCMSLECCCHLRGLE KAWIKTEGRQHTTPSPNPNEALEFL |
| 1437 | 6934 | A | 1548 | 304 | 678 | PQVILPPLVSQGCWELPDVSPLRPSL VW*FL/RK*KLDLPCDPAIPLLGVP RKIKACFHTKTCIQFIATLFGIAKKK GKQPKQPSAGEWINTWW/HIHTMK HCSAVKKEQTITISLFRSRIWRI |
| 1438 | 6935 | A | 1549 | 80 | 623 | LGGVTRGFNMRIEKC YFCSGPIYPG HGMMFVRNDCKVFRFCKSKCHK FKKKRNPRKVRWTKAFRKAAGKE LTVDNSFEFEKRRK*TYSNYQRDLL GIKTNDAMKRVEEIKQKPPS*YNEQ IE/GKIKSYRKFDIKRSPSQNIPSL RAPPCQAKGKQLGEEMGTARLQGG CGHGKMPP |
| 1439 | 6936 | A | 1550 | 1021 | 1544 | EPTKKCCVYYAQFLSLPSLFFPTGSE EQDSIYFILFFEMEFRS\VTQAGVQW CDLGS LQPPPPGFKRFSLSLPSSWD NRLLPQGPANFCIFSR/GWGFHRVG QAGLFSRDGVSPS*SGWSRTPDLVI RPPWPPRVLECSGQYIIFPWLFSRFS LSIFSKFDCNLSQFGFIWICLFYSS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1440 | 6937 | A | 1551 | 2 | 210 | |
| 1441 | 6938 | A | 1552 | 2 | 310 | IGVKMEEYAREPCPWRIVDDCGGA FTMGT\GGGIFQAIKGFRNSPVG HRLRGS\LTAIKTRAPQLGGSFAVW GGLFSMIDCSMVQVRGKEDPWNSI TSGCLNGEPYWQARNGTQWPMVG VSPQWVGIFPSF*FEGSWYLCLTRF ASGTVFPMGP\QFA\EDPSPVCLSTQ LPSL\PFGGGIFQAIKGFRNSPVG HRLRGS\LTAIKTRAPQLGGSFAVW GGLFSMIDCSMVQVRGKEDPWELH HKWVP |
| 1442 | 6939 | A | 1553 | 1 | 4629 | |
| 1443 | 6940 | A | 1554 | 96 | 721 | PGQLSSLTPPRPASLLPWRAAYLFL LFLPAGLLAQGGYDLDP\PPFDHG QYTHYMDQIDNP\DYDYQEGTPR PSEGQFQ\QSQQEVQGVIPSPNPR AQGNAEL\EPTEPGPLDCREEQYPC TRL\YSIHRPCK\QCLNEVCFYSLRR VYVINKEICV\RTVC\AHE\ELLRA\D LCSGTSFSKCGR*WASSGLACQSV ASCA\RSCGSF |
| 1444 | 6941 | A | 1555 | 262 | 732 | FQNKGNFFSTKRTEVSPSTQFNFA RKNTTLIRISHSSLGQVRIRLVWFG LVWFWFLETGV/CTLVIRGWEFQW CDQNSLQP*TPGLQRI\PTSASQSTG ITGVSHSLVRYV\FVTEIQLKFWILI TKITVLLVYN*L*NKGY*YIFITFFL NLQN |
| 1445 | 6942 | A | 1556 | 162 | 496 | HSYIHIVHVCNFFMYSFAVFVFKKH LLLCLYNRTVIIYYNLGKL*INS*FK QPVYMHI*VLYC/INLCFTYMKAA RILLICNYTHKIYICMIHEIYLEMFII LMDILWCE |
| 1446 | 6943 | A | 1557 | 2 | 247 | GEIVVFKVEGRDIPVHRVIKVHEKD NGDIKFLTKGDNNEVDDRGLYKEG QNWLEKKDVVGRAR/GYALLAVM GAYVLLKRES |
| 1447 | 6944 | A | 1558 | 1 | 503 | VRAGAVGAHLPASGLDIFGDLKKM NKRQLYYQVLTAMIVSSALMIWK GLIVLTGSESPIVVLSGSMEPAFHR GDLLFLT\NFREDPIRA/GDNGDIKFL TKGDNNEVDDRGLSKEGQNWLEK KD\VVGRARGFLPYVGMVTIIMND YPKFKYALLAVMGAYVLLKRES |
| 1448 | 6945 | A | 1559 | 180 | 257 | |
| 1449 | 6946 | A | 1560 | 2 | 676 | FVRCSAAVCATQSRRAARSPENPA MVRAGPPWGLNLPASRLGISSADL KKMNKRQLYYQSFKPSPWIVSSAL MIWKGLIVLTGSESPIVVLSGSME PAFHRGDL\FLT\NFREDPIRAGEIV VFKV*RPRTFPISSQR*SKVHEKD\N GDIKFLDLKGDNN*SLMD*EALYK KARNWLEKKDVVGRARGFLPYVG MVTIKMNDYPKFKYALLAVMGA\YVFLKR |
| 1450 | 6947 | C | 1561 | 449 | 820 | MVIXGQISPMTATSGQKAFLAGPLG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SLGTLPRSQAVKRRLLLKLTKDRI RDVLLLMFLKGHRETHGQCLQRQQ TKESTSIVVLALCGLYGKQVVTLN VGIPFSINVYFTTPKSPLIMKLI* |
| 1451 | 6948 | A | 1562 | 251 | 473 | |
| 1452 | 6949 | A | 1563 | 22 | 212 | |
| 1453 | 6950 | A | 1564 | 160 | 397 | |
| 1454 | 6951 | A | 1565 | 17 | 262 | LFWAKALNRHFSKKHIQMANQH MKRCSTSSAIREIQVKIAMVYN*YTI *HSQ\YSLQLPFPLWKTWVKFLT VVKLLNCSVK |
| 1455 | 6952 | A | 1566 | 2 | 294 | GNKMAAPKGSWVVRTQLGLPPLL LTMALAGGSG\TASAEAFDSVLGDT ASCHRAQLTYPLHTYPKVGPRVRS GLRPFPCSPFLGSPHVCRLWQPGC |
| 1456 | 6953 | A | 1567 | 366 | 1412 | QRGTRWRRERGSWVVRTQLGLPPL LLTMALAGGSGTASAEAFDSVLG DTASCHRAQLTYPLHTYPKEEEL YACQRCRLFSICQFVDD\GIDLTRT KLECESACTEAYSQSDEQYALPFL GCQNSACHFAELRQEQLYVPRWP KMAPTFFL*LLGEGSFWELT*WDSA QSFITSSWTFYLQA\DDGKIVIFPV* SQKSQYAPHFGAREPTNFEENHLLS KMSSDLQMGKFHQAHQGIFLKNEE RDGLFKKPSILNSGWILTT\TLVLS\V MVLLWICCATVATAVEQYVPSGE AGVTMGDLEFMNEQKLNRYPASF SCGLVRSKTEDHEEAGPSYLPKVN LAPFLEI |
| 1457 | 6954 | B | 1568 | 76 | 384 | MSGWGVLSGRLNPAAREKDVERFF KGYGRIRDIDLKRGFGFVEFEDPRD ADDAVYELDGKELCSEVVTIEHAR ARSRGGRGRGRYSDRFSSRRPRND RRNAPP* |
| 1458 | 6955 | A | 1569 | 3 | 229 | |
| 1459 | 6956 | A | 1570 | 152 | 536 | PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDP K\DADDAVYELDGKEL\CSEVVTIEH ARARSRGGRGRGRYSDRFSSRRPR NDRRNAPPVVTENRLIVENLSSRVS WQVC |
| 1460 | 6957 | A | 1571 | 771 | 1383 | ILIEYKCGKCHVCTLSNIFSFSVLVFF ISCDCLCVFPPLLCTQLSCVKDLK DFMRPAGE\VTFA\DAHRPK\LNEGV VEFASYGDLKNAIEKL\SEKEINGRK IKLIEGSKRHSRHSRHSRHSRTRSSRS RSRHSRHSRHSRHSRHSRHSRHSR DVPVLLSRSPRA*EEPRNRGSSSRSK SPASVDRQRSRHSRHSRHSRSDSGN |
| 1461 | 6958 | A | 1572 | 236 | 1377 | PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDPR DADDAVYELDGKELCSEVVTIEHA RARSRGGRGRGRY\SDRFSSRRPRN DR/RVCEGWMAALNNYW*G*PFKI QESLAVMILGPAV*SVLLFPR*PIVL DESI*VIEHKSIDGSH*NGL*YLMA* |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TCPQLNTSAVIAFLPL*IRIFFLRNAP PVRTENRLIVENLSSRVSWQDLKDF MRQAGEVTFADAHKPLNEGVEF ASYGDLKNAIEKLSGKEINGRKIKLI EGSKRHRSRSRSRSTRSSSRSRSR RSRSRKSYSRSRSRSRSRSRSKSRV SRSSPCPEKS\QKRGSS\SR\SKSPSHL WNRPEVPGPRSRSQIQLDQWPIKPV K |
| 1462 | 6959 | A | 1573 | 568 | 770 | PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDPR DADDAVYELDGKELCS\ERVITIEHA RARFTRLGRGRGRYSDFNNSAEL RNDRRNAPPVRPAENRLIVENLSSRV SWQDLKDFMRQAGE\VTLPDTTRL NLNEGVEFASMGDLRNAIEKLSG RELNGRKIKLIERPAKRPQ*VQQSRS SDPGTQKSPLGPRSRSPSPVANLN SRSKK/RRGSREPGSPEPSRSC*VGS SPVP*ERFFKGYGRIRDIDLKRGFGF VEFEDPRDADDAVYELDGKELCS |
| 1463 | 6960 | A | 1574 | 22 | 202 | TKSSS*CDSVATCGIIFSCPHNLSKI HDSISPRVC\SICKPHGSIHKLCIKIKF HIFAR |
| 1464 | 6961 | A | 1575 | 1 | 1878 | MQYSHHCEHLLERLNKQREAGFLC DCTIVIGEFQKAHRNVLASFSEYFG AIYRSTSENNVFLDQSQVKADGFQK LLEFIYTGTNLDSWNVKEIHQAAD YLKVEEVVTKCKIKMEDFAFIANPS STEISSITGNIELNQQTCLLTRDYN NREKSEVSTDLIQANPKQGALAKKS SQTKKKKKAFNSPKTGQNKTVQYP SDILENASVELFLDANKLPTPVVEQ VAQINDNSELELTAVVENTFPAQDI VHTVTVKRKRKGSQPNCALKEHSM SNIASVKSPYEAENSGEELDQRYSK AKPMCNTCGKVFSEASSLRHMRI HKGVPKYVCHLCGKAFTQCNQLE NACKELHTGEKPYKCGICVIKGFQAQ KC\QLVFHSRMHHGEEKPYKCDVC NLQFATSSNLKIHARKHSGEKPYVC DRCG\QRFAQASTLTY\HVRR\HYW EEKPYV\CDTCG\KAFAVLLVLFHS FLRK\HTGEKPYICGICGKSFSSGEL NKHFRSHTGERPFICELCGNSYADI KNLKKHKT\K\H\GADKTPRTPSA\ EDPNLGVKQDP\IQKSPFNPETYGCE SPS*YELYPLALPLGTED\HHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIF LQQLY |
| 1465 | 6962 | A | 1576 | 42 | 134 | |
| 1466 | 6963 | A | 1577 | 154 | 768 | HVACGLLWYVSPSAHLNLDGTITT K/ENLGTVNEILLGSNPTEAELQDMI NEVMSDGNGTIDFPAEFLTMMARK MK\DTDSE/EKEIRRKHSRVFGLRVG NGLYL\ACRNFRHV\MTNLGRRKF NQIEEV*WN*SRGSQILDG*WSKLT YEEFVQMMTAKVRPLSRNVLNFLV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QNCFICLFLWFVTLSCKKVFSPTCQ KKNMHVIGN |
| 1467 | 6964 | A | 1578 | 3 | 202 | RRMVSAFSCRCMPSEPCIAVTAPCM MAGQAPAERTAQ*PLYF/CTLFQGS LSPT*REVGWPLGPAGM |
| 1468 | 6965 | A | 1579 | 133 | 378 | |
| 1469 | 6966 | A | 1580 | 891 | 1744 | DMFPITPSRSVLPSFLLTYLPRQSL/N SVAQAGVHWCDLSSLQPPPPGFKQ FSCLSLPSTW*LGLQACTTVPS*FFV VVVCIFFFFLVETGF/TLGWARLVLN L*LQ/CDPPTWASQSAG/ITDVSHHA QPILRFKCLS*CIRSFNEGRIKGTRQ NKVELSL/CFLRQESHVSTQAGVQW CNLSSLQPLPPGFKQFSHLTGLPKC WDYRSKRPRPANQTSILGC*RKDPY *LHWAKKATEDIKLESCRLTPGKAR PTANFLRQGQFFWGPILGGLLGPQE GFPFLFFKGF |
| 1470 | 6967 | A | 1581 | 2119 | 2436 | TTRYLKKTSTTGQRKKRGRGNGSF PTENLVPSGTVTGSQQLGPPFR*N/H TEECWGPPTADGRAGKGPRQQPGR AQRIYRWDPDGTWTHHRPCGSR GTDQPETK |
| 1471 | 6968 | A | 1582 | 208 | 296 | |
| 1472 | 6969 | A | 1583 | 185 | 947 | SHCSSGMEIPVDQLPSLPRAALVAQ NYINYQQGTPHRVFEVQKVQSQQA WKD\PGKEGHKYS/HLKFAV*KKL YKKQVKG*TCTA\EVLLPFQRGQET LHQEVNFHILKEKLGKNPD\EEDNT FYQRLKSMKEPLQAQNI\PD\NFGN VSQEMTLVLNLAWVACGLI**WQK FLLKTTWYK\MVKI\QTCQARCQRI DDFIELDYPPFYFINIASQEII\WQM QVLWHPQYGTKVKHNSRLPKEVHL GYTPKPLTLEV |
| 1473 | 6970 | A | 1584 | 5060 | 5662 | ESQAAPPPRPSTLHRPARATAITAC WSSQASGPQAVRRRLTPLSSPAAR DLVSKEGFRRARHVVGIEIRRTAQA AAALRRGDYRAFGRLMVESHSLR *GPLGAPLLPGTGRPRPTPSISLQD DYEVSCELDQLVEAALAVPGVYG SRMTGGGFGGCTVTLLASAAPHA MRHIQEHYGGTATFYLSQAADGAK VLCL |
| 1474 | 6971 | A | 1585 | 2 | 987 | LREGCPQR*RQPTQLDWPYF/CPFSP VC*KTKTKKPYPCAPKLGHVRCPT ASTLQAHTGPCPPSPQTGPQTRAGL LHICVGVGARFLFLLSLSPFGDIPL |
| 1475 | 6972 | A | 1586 | 318 | 382 | |
| 1476 | 6973 | B | 1587 | 106 | 293 | MAGRVCCLCQGSAGSGAIGPVEAAI RTKLEEALSPEVLELSFRGTEPPTT PAGPRSAGRAGS* |
| 1477 | 6974 | A | 1588 | 442 | 905 | PMLSGRLVLGLVSMAGRVCCLCQGS AGSGAIGPVEAAIRTKLEEALSPEV LELRNESGGHAVPAWAVRLHFRVG CW*ALVFEGLSPLTTDTGLFHAALA EELGRFRSHALAI\PGTDPPPQWREN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | \SQLEQLAPPCLG\GKQENFLGTPLE PPKRG |
| 1478 | 6975 | A | 1589 | 1206 | 1335 | KTQERYFNLKQN*TGQAWWLMH/I WEAEAKGSLEPRSLRPAWAT |
| 1479 | 6976 | A | 1590 | 136 | 837 | PSEKTSPDRDKKKRAVRSILFLELQ NIIQDHDQGOEKENESQIMKEENT GAGAEAKREEDMNPVKSSKKHKS EEHNDKEHSSDKGRERLNSSENGE/ AQAQTPRKEGH/RKGRGHSRERSRE RRHRIRGRERKKSRERSRERKKSR SRSRERKKSRERSRERKRRIRSRSR IQRHRA*D*KAGVGPRSRSDRKKR IEKPRRFSRKFKPDSQVHLPLEGRTQ PWDAQEAFS |
| 1480 | 6977 | A | 1591 | 209 | 1545 | PYYFLQANSPPGPLLTPALLPHRILS DVTQGLPHAHSACLEKLKRSYEFY RYFETQHQSVPQCLSKTQOKSREL NNVHTAVR/SLWQLHLKALLNEVII LEDELEKLGCTKETQELVSEAYPILE QKLK\LIQPHVQASNNCWEEAISQV DKLLRR\NTDKKG\KPEIAC*KPTCY SSTF*RQPTLHIADQDPIPEEQE\EA YVDDIDIDSAFQNRHDFYLSQEDK ERQKREHEESKRVLQELKSVLGFK ASEAEQKW\KQLLFSG\HAVLK\SL FPVGPQWEPISNSEPSMNSDMGKVS KNDTEESNKSATTDNEISRTEYLC ENSLEGKNKDNSSNEVFPGAEER MCYQCESEDEPQSKIGSLTTAPPT PRDSLQPSIKQRL\ARLQL\SPDFTT AGPCWQEVGCLDLLPFTTMAGNR LFGDEEEEQIIEENKNEIEEK |
| 1481 | 6978 | A | 1592 | 1 | 296 | DFPLPTLLKTGP GPGF/YNGPP*GER FYVASPG*IWAPQGFF*KGPPSSSSS SSSQRSKPLFPCFANKTG*VGCFLVI SQRDQIPYPRPTPPTLPWLQP |
| 1482 | 6979 | C | 1593 | 15 | 350 | MLISLNINQTL LYCNKTENCXXXXX XXXXXXXXGGPFKRTPGGPKFNRG WQGKIFPLKGGLLKPHWGIFXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXEKGEKQPEKPGG* |
| 1483 | 6980 | A | 1594 | 11 | 129 | APWLSVLY*SESPEAQPPYMMGPLE SP*AQRCPGLERGR |
| 1484 | 6981 | A | 1595 | 2 | 660 | NFPTARLFRLFYPLFPLKIFIPKAFN FCREVGPFCPPPK*GFFPKIPK*VFN RPP/SK GKSF TLPAPVKFGPPRGPFK RAPSSSSSSSPVV*APWPTVLY*SE SPEAQPPYMMGPLESP*APHEGVTA WVES*GPCPA*PWGRQAAPQPPPP QERAG*EPESKFGPGSK/PPERPVYA GNSPVLRSGLTSPSPSPAPPGGFKY MEERSKADLGPGMEKG |
| 1485 | 6982 | A | 1597 | 1 | 680 | ESRIRRRSSRRPREPPGPSRRRRRRR PDPRTMPSEKTFKQRRTFEQRVEDV RL\REQHPTQIPR**LERSKGNNQPP \VLDK\TKFLVDPDHVNMSEL\IR\IR RRLQLNANQA\FLLV\NGHS\MVS VSPHP\SEVYESEKDE\DGFLYMV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LCPPPE/YGLR*TLNV*N*KKKNAAS S*NCLNPLPKEKIKECYPTIDQFIPI TDHETSSVPTLGVLGSCVCVSSRKT |
| 1486 | 6983 | A | 1598 | 2 | 508 | PDSSGPHRLRENPPMVAVSCPTKTN VKGPPGGKVGAGAG\EYG\SEALER MFLSFPT\TKTYFPHFDL\SHGLCPR LKGHG\KKVADALTNAVAHVDD MP\NGVVRP*SDLHAHKL\RVDPVN FKLLSH\CLLVTLA\AHLPAEF\TPA VPRPPWDKFPWLSVKHRCLTFKYR |
| 1487 | 6984 | A | 1599 | 295 | 758 | VLSRKCQRSLTAFSSKCPNSWFSITQ TECKTMTGMPQHVTQQ*RPINTS HQYSVKLGHP\DTLNQGEFKELVR\ KDLQNFLKKENKNEKVIEWHMRGP GTQNAQAELSRFIMLMGEA*PG AFPRRKIARGLTEGPGHPNK*PGPG GGAPP |
| 1488 | 6985 | A | 1600 | 411 | 1259 | SQGTTSRGSWEFPHSPEIETSCLAE LFEKAAAHQLGLIQVAKQGATLCT LYAKYKQVKVGNCTPKPSFFDFE GKQKWEAWKALGDSSPHQAMQE YIAVVIKLDPGW/ISSDIQRRNGKEA NTGFGGPGVISSLYHEETIREEDKNIF DYCRGKQH*PYNQKPSNPKNVDVN VKDEEGRAPLHWGL*SEDIKELVH SVAANIELTLNCQDNERPKQALHY ASACGVSGIL*ELAAPSLGADPDSPR PGWLPARGGDRLONSFFGAAAAHN WQGLIKRLENC SL |
| 1489 | 6986 | A | 1601 | 177 | 409 | FLQASGILKGFEPNLL\NLVLTVTI*Y MRDPDDQYKLTGGHPGKLGVLVFR G\TSLVL\ICPQDGMEAIPNPFIQQQ DA |
| 1490 | 6987 | A | 1602 | 1 | 165 | PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPVEKSAVTAL WGKVNVD\VGKALGRLLVVL WDPKRSFQSPLGESVPTP*MVHLTP VERVCRYCPVGQGERG |
| 1491 | 6988 | A | 1603 | 240 | 461 | |
| 1492 | 6989 | A | 1604 | 2 | 206 | |
| 1493 | 6990 | A | 1605 | 2940 | 3296 | |
| 1494 | 6991 | A | 1606 | 189 | 736 | ENKISSVFKADFLPPAPCSLPGLEVS VSPKGNKTSGRESFGWAIWMEGL VFSRLSPEYYELA\RPHLRDEEKS\CP CLAQE\GPQG\DLLTKTPELGP*ITR TCLTIVQKT*RK MVDKP\TQRSVS NAATRVCRTGRSRWRDVCRNFMR RYQSRVTQGLVAG\ELAQQNLVST SRLCIPSTGPL |
| 1495 | 6992 | A | 1607 | 3 | 452 | |
| 1496 | 6993 | A | 1608 | 3 | 485 | PTLLVPTDSERTHPWLLSPADKTN VKGPPGGKVGAGAVRSMCAEAL RMFLSFPTTKTYFPHFDLSHG\SAQ V*GPRARKVADALTNAVA\HVGR LPNALVPPLSDLHAHKL\RVGPGSTF KLLKATCLAGLTL\AHLPARVQPL AVASLPWDKVS WASC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1497 | 6994 | A | 1612 | 77 | 636 | QPQTDITMVHLTPVE\KSAVTALWG\KVNLD\VGKALGRLL\VV\YPWD POKVL*NPLGESVPTP*MLVKWGKP PKGEKAQWQKKKCSGAL*VNGPGL T/HGQPSKGTFGPH*SELHC\DKLH\ VDP\ENFRLPGQQCLVCVAGPITLG KEFTP\QLQACLFRKLVA\GVANAL GPTSNHLSLAFLAGPISN |
| 1498 | 6995 | C | 1613 | 167 | 391 | MNVFMCRLGTTFFHLVLLLPSVLP SL RKT VFLNPF SIKQRFQRWKHWVFQ VASELTDAILSSCGHLFLPGSHNLS* |
| 1499 | 6996 | A | 1614 | 1402 | 1871 | GLQGSQSLHIPSLTGLRHACITLGKT AHSSRLHPSPAPPPYL*STDTRDNN APEPTPPRSWTWRA*/PMGRGSSQE GQASQQPWPGEKGSGCEMPPLVY KVKPEP*P/SPDPWGL*QSMPLDYL HLSVILRWRRGGGQWQGATKISRR DRRGGALLHL |
| 1500 | 6997 | A | 1615 | 8 | 551 | SAQMAVTTADPRVRPRVRTQLCSL ASLIQTLLVHLTPVE\KSAVTALWG KVNVD\VGGEDLS\RLLPVYPWTQ TFFD\SFADQSTPDAAMGNPKVKAH SKKVLG\AFSGGPGCTWDNLKGTFAHTEVSLHC*QACTWDP\ENFRLLG\ NVLVCCCWAHSLLGKEFQPHQLQA CLIKKIGWLGVG |
| 1501 | 6998 | A | 1616 | 3 | 389 | |
| 1502 | 6999 | A | 1617 | 1 | 672 | |
| 1503 | 7000 | A | 1618 | 18 | 621 | RSLRCSRHSCLATSSPLPCARRAWH PARGKADQPFCSRAGPSVPAAPR GENREKEETTRIGPGVMESKEKRAV NSLSMENANQENEEKEQVANKGEP LALPLDAGEYCVPRGNRR\RFVRQ PILQYRWDMHRLGEPTGQGMKR RE*WKRIGEEVRQLMEKSWRGKSQ L\SHSLRGESGTDPPSPMTHHD*VF ALMPLNP |
| 1504 | 7001 | A | 1621 | 3 | 700 | HASDRRHGSHACSRVSSGHQAGL LGGGWEEDRECGQRAEGMMFWA ALALAATSPSRLLLSPGKGPVPSRL PLSDAASPTWLKLT*RR*RSQIYQT G\QEGPLLPSQIGVILRDSHGVA\QV RF\VTGNKIL\RILKS*GTCS*IFLIDL YHLN*ESQFAVRKGILRREQERDKG G*NFPSDF*IGEAGFHPFWLRYKQ QAESSLPNWEIWNHLTASALGRINL VWCTPSN |
| 1505 | 7002 | A | 1622 | 1 | 340 | GEHSMAPPAHFRALLYHPGTATLV PHPASISQHSPPWGNA/RG*PV*RQ RHLTAPRSPPHPRFRHKPGKDPREN PSRWPEVPSLPQTHVVPQGAAWDT VNTTVCKNRSTKPQD |
| 1506 | 7003 | A | 1623 | 3 | 1076 | HPVPSSSYSVHTLSPAAMTEQMTLR GTLKGHNG\WVTQIATTPQFPENNL PASR\EKAILRKPARGWSQPMNFQ RRSRIHSHLLRMVVIS*DGQFC/AF QGFWDWKPCALGDLTNG/TPTRGR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FCGPIPKDVLSVAFSSDNRQRLSLGS RE*THQSLWN\TLGVCKFNLSRNES H/SESWVLCV\RFLAPTTSKPLSIGLP VAWDK\LVQ\WKPG\LNCKADAPN PHLATTGFL\NTGDLSSSRWDPLCA SGG\KDGQA\MLWDL\NEGQPPLQR *NGGD\NNA\LCFSP\RYWLCAAT GPS\KIWDLEGKI\NDELKQEVISTS SKAEPPOCTSLAWSADGQTLFAGY TDNLVRVWQVTIGTR |
| 1507 | 7004 | A | 1624 | 1 | 1189 | LQGGGRRGCGASFSKPSSAILVAAA THALAAAMTEQMTLRGTLKGHNG\ WVTQ\IATTPQFPENNLPA SR\EKAI LRKPARGWSQPMNFQRRSRRIHSHF VSDVVIS*DGQFC/AFQGFWDWKP CALGDLTNGHPHEGDFVGPYPRNV LSVALSSDNRQRLSLGSRE*THQSL WNTPGWCANTTVPG*EPTQEWVS CVPLPRPNNQQTPIIVLLWPGNNLV QVMETWANCKLKDPT/NHWPTPGY SETPVTVLSRMDPFCA\SGGQGMAQ AHVYGD\NEG\KHLHARMVGTSI NA\LCFSP*PATWLCAATGPS\KIW GFRGERSIVDELKQEVISTSSKAEP QCTSLAWSADGQTLFAGYTDNLVR VWQVTIGTRLEVYGRALPIKKKTGF SEKKKK |
| 1508 | 7005 | A | 1625 | 3 | 445 | GEFADSF/SSMGSPVNAQDFCTDLA VSSANFIPTVTAISTSPDLQWL VQPA LVSSVAPSQTRAPHFPGVPAPSSGA YSRAGVVKTMTGGRAQSIGRRGKV EQETDQLEDEKSALQTEIANLLKEK EKLEFILAHRPACKNPDDLGFPE |
| 1509 | 7006 | A | 1626 | 7 | 514 | |
| 1510 | 7007 | A | 1627 | 3 | 462 | RRSERAVTVLLPSSASQRPPVSAPRP LARLCLTATMMFSGFNADYEASSS RCSSA\SPAGNSLSYYHSPRRPPFSA WGSPVNAQDFCTGPGPFSSANF\IP TGHLPSWTSPDLQWL VQ\PALVSS VAPSQTRAPSTFSESPPPTAGA\YSR AGVVKTMTGGRAKSIG\RRGKVEQ LSPEEEERRRIRRE RN\KMAAAKCR NR\RELTDTLQA\ETEQL*DERTAF WT\RM SHPVEEEGKLEFILAHR\PA \CKIPDDLGLPRKRMSVASLDLTGG LPRGLPPRRSEEAFTL\PLLNDP*/DP KPSVEPVK\SISSMELKTEPFDDFLFP ASSRPSGSETARSPDMDLSGSFYA ADWEPLHSGSLGMGAHGHRGWEP LCTPVVTCTPSCNCLHVFLRLHLPR G*LLPQLCSCPPQGOQQQ*AF\LA QLTHAAGPVRGQGRGGS RHPQVPL PELVHYREEKHIFP*RVPRPGIASLT TTHPADLLFQHGARLSTRDFCTGP GPFSSANFHSGLAILDQSGPCSG WCKPALVSSVGPIADQSPFNLFQVP TPYRWGLAPGLAL |
| 1511 | 7008 | B | 1628 | 43 | 674 | MDWTWSILFLVAATTGVHSQVHLV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QSGAEVKKPGASVKVSCKASFNSF DTYGFNWVRQAPGQGLEWMGWV SAFNGDTNYIRKLQGRVTMTTDSST STAYLELRSLKSDDSAIYYCAATNS DKYFWGQGTLVTVSAASPTSPKVF PLSLCSTQPDGNVVIACL VQGFFPQ EPLSVTWSESGQGVTARNFPPSQDA FGDLYTTSSQLTLPATH* |
| 1512 | 7009 | A | 1629 | 3 | 1639 | SPGIFRGFQSVIRTEQRELTMESGLN WLLLVAVLKGVQCEVQILESGGGQ VQPGGSRTLSCAASGFIFSNYVMTW VRQAPGKGLEWVSSTAASGANTFY AESVKGRFTVSRESENMMYLQMS SLRDEDTGIYYCAKDGDVPNLGVA WIVAGPGNVRPRKWFDWVGQGT VTVSSASPTSPKVFPLSLCSTQPDGN VVIA\SCLVQGFFPQEPLSVTWSESG QGV TARNFPPSQ\MASGDLYTTSSQ LTLPATQCLA\PKSVTCHVKHYTNP HPDVDG\PCVPSTPPTP/CSLNSTYP ISLMLPPPTVTAPTGPSKDLFLGSEA NLCTLTGLE\NASGCHFQSEGLQV GKSAVQGP\PEA*PSVAAYSVVQLS CRGWREAMEPLVRPFTCTAAHPV VQGPALTAHPLQNPNTFPGRVHP FAPAVGRVCPFNDLLTLHCLAR\AF SPQGPCWVRWLQGS PKLPPRKST*L G/PFPAGA QARAPTTFAVTSILGR/V QPEDWEE/EGTPFSCMAGHEALAL AFTQKTIDRLARKPTHVNV\SAVMP EVDGTCY |
| 1513 | 7010 | A | 1630 | 3 | 497 | SSGPTRLRENHPWLLSPADKTTVKG PL/WGKVGAAHAAEYG\SEALGEGFS LSFPQPPKTYFPATSDLE/HNGFAPG LKGHGQRKFGRTR*PKSRGGNVD\D MPQTALSAPERPCTAHKL\RVDPV\ NFQASLSHC/LCLVTLAAHLPAEFT PAVRLLWSKFLAS\VSTVL |
| 1514 | 7011 | A | 1631 | 9 | 489 | NSARATDSERTHHGARLLPDKTKA QRPPRLKLGANA\GEYG\SEAL\ERM FLSFPNPPKTYFRQFRP*ANGFAQG* RGHGQRRWPDALTQ\A\VA\HVDEH APNGAVRP*SDLH\AHKL\RVDPVN FQASLSHCLAW*PWPAHLPRPSSTP GGATPSLEQSSWASC |
| 1515 | 7012 | A | 1632 | 2291 | 2960 | INCPAQAKVADILQFNFKKFVCLF/D FLRQSLALSPRLQVQWYDLSSLQSP SPRFKQFSLRLPSS*NYRCASPRPT NFLIF/M*RWGFTMLARLVFVLLTSS DPPTSA/SHSAGITSVSHCTRPLQSIFI *PLEQVS*VKDKNNNKKTHFFVLFC FLRQSHSVTQAGMQWHDQSSLLL QPPRLKQFSHFRLSSWYYRCLANF *IFCKDGVLLCCPW*SQTPGLK |
| 1516 | 7013 | A | 1633 | 1 | 1233 | |
| 1517 | 7014 | A | 1634 | 233 | 884 | ESPGVGCSARRGPRPRSPGPPPAAP GTPRPHGIPLYTRAGHQ**GEIRRRP CTFISKFLRPQGGASERQLPDLQAR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AWQELLGRPFNKHWHWFR*SPCKG IGVTRCIRINP*KWIPLIGPGQHS LSSQELFRLLPSEL\TLWG*PPIEVS YRIGEDGSHLCACMKPSA\GGSTQ QNTNVQMVD\SRISCKEELLGRTE PFPKTTNMMTVSG |
| 1518 | 7015 | A | 1635 | 2 | 402 | SQTQREPTMVLSPADKTNVKA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASL DKFLASVSTVLTISKYR |
| 1519 | 7016 | A | 1636 | 2 | 522 | GLEFGTSHRLRENPPWCLSPADKTN VKA\AWGKVGAGHAGEYGAEALER MFLSFPTTKTYFPHFDLSHGSAQ G*RAHGK\KVA\DALTK\AVA\H VDDMP/HNGAVPPLSDLHGAQAF GWDPVQLQSS*SHLPCW*PLARPP SPAEFQPLAVATSSLGQSFLGFL LKHRCNLNLPNYR |
| 1520 | 7017 | A | 1637 | 344 | 742 | GFLIGVNEKTCFFTSPMLHDSYFF FLVNVIRCHFICGTLYWAKHIFS FVPFFLSFLFTSFISLFLPFPFF LFFFFFW*LLLPTPFYVSFAMK G*SFNF*FFIFCRLLTLLQNIK* TREMTTFDYFLSVFL |
| 1521 | 7018 | A | 1638 | 1 | 519 | PLKRSDGCNDGRPTRPPTRADTTAY TSNLKQTLVLVHLTTEEKSAVTALW GKVN\VEKVGGKALGRLLVVYPWT QRF\FESFGDLSTPD\AVMGNPKV KAHSQESSPRGL*WWAWLTWDNL KGTFAHTEVSLHCDKLHRGSLKN FRLLGQRAWSVVAGPIHFWQKNF NPTSCRLA |
| 1522 | 7019 | A | 1639 | 3 | 452 | |
| 1523 | 7020 | A | 1640 | 3 | 484 | PTLLVPTDSERTHPWLLSPADKDQR QGPAWGKVGAGHAVRSMCAEALER MFLSFPTTKTYFPHFDLSHG\SAQV *GPRARKVADALD/TNAVAVNGRTL PNALVRPL\SDLHAHKL\RVDPVQF SSFL\SHCLLG*PWAVHLPRPSFN PWRLQGFLGDKVSWAFC |
| 1524 | 7021 | A | 1641 | 180 | 613 | SFAGISNGLAGRSVKDSGKAQAKA VSR\ISQRAGLQSQWGR\NRH*K SRDASH\ERGGATA\AVYSA\ALE YLPQKVLELAGKASKDFKGKAYYPL RHLQ\LAIRG\DEELDSL\IKATVAG GGVPTTSHQISDRGGKKKDNQKTV |
| 1525 | 7022 | A | 1642 | 107 | 368 | IYIILRD*VLSTFVCFILCKAIYKNIW TAFWKCS*ILCSI/LCNYVCTCTSVY ALCYIYIIDLR*QQTYLCESKCTCIC MYVCIFLC |
| 1526 | 7023 | A | 1643 | 790 | 1252 | CAKPETQNNGNLRLVRLRPLHFGHT LN*VRT*LKRRIFFFLRQSLALSPRV ECSGMISAHCKFCFLGSGHSPASAS* VAGTTARRQHA\WFLCVFSRDEFH RISKDGLNLL/NLVICPPRPPKVLGL QHEPPCPAKRRNFLSKIMGGHCFEL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SSCN |
| 1527 | 7024 | C | 1645 | 171 | 329 | MGARASGRSPLCQVGRQEQGLRGR NGPLPASRLPQQPVVPATPQSPRD DLA* |
| 1528 | 7025 | B | 1646 | 196 | 514 | MGRDTGPELCLHDSSLPAADDGPSL PTKQNEEFRPFIRRLPEFKFWHAAT KGILVAMVCTFFDAFNVPVFWPILV MYFIMLFCITMKRQIKHMIKYRYIPF THGKRX* |
| 1529 | 7026 | A | 1647 | 43 | 321 | |
| 1530 | 7027 | A | 1648 | 35 | 821 | GRPRLGRSGAASYRMSEGDSVGES VHGKPSVVYRFFTRLGQIYQSWLD KSTPYTAVRWVVTGLGSFVYMIRV YLLQGWYIVTYALGIYHLNLFIAFL SPKVDPSLMEDSDDGPSLPTKQNEE FRPFIRRLPEFKFWDASVCGDGRCS CKAGGGRQCPVLAADAALTFSPHL KHAATKGILVAMVCTFFDAFNVPV FWPILVMYFIMLFCITMKRQIKHMI KYRYIPFTHGKRRYRGKEDAGKAF GQLEAGLRLPHVLQEQL |
| 1531 | 7028 | A | 1649 | 156 | 818 | HSYRMSEGDSVGESVHGKPSVVYR FFTRLGQIYQSWLDKSTPYTAVRW VVTGLGSFVYIDSEFTCLQGWIYIC* PMPLGIYHLNLFHKLSFSPKWDPSL M\EGLODDGSFGYPTKQERREF/RA PFIRKGS PGVLNFWHAGYPRASLVA LWSC TFDAFQTSPVFWPILVMYF HHASSCITDGRRANSRHMDLSYRY MPVSHMGK/RGRYRGKEDAGKAF AS |
| 1532 | 7029 | A | 1650 | 154 | 685 | PPLHLRDCFSPPGRALSPVGFYPYR\ RSVPATWLKLT\SDDVKE\QIYKLGQ EGPLLLSQIG\VILRDS\HG\VAQVRL G\TGHDTFKILKSKGLAPDLPEDLY HLIK\KA\VAVRKH\LERNRKD*GC* NSRLILIESRISPFWLRYK\TKR\VL PPNWEIWNHLTASAPGRINLVWCT QAIK |
| 1533 | 7030 | C | 1651 | 127 | 435 | MAASXNPEVLDITEETLHSRFLEGV RNVASVCLQIGYPTXASVPHSIINGY KRVLALSVETDYTFPLAEKVKAFLA DPSAFVAAAXLGCCHHSCSXCCCCSP S* |
| 1534 | 7031 | A | 1652 | 1 | 689 | KCFI/VGADNVASKQMQQIRMSFRG KAVC*WGKNTMMRKPIRGHLENNP ALEKLLPHIRGNVGFVFTKEDLTEIR DMLLANKVPAAARAGAIAPCEVTV PAQNTGLGPEKTSFFQALGITTISR GTIELGVRNVASVCLQIGYPTVASV PHSIINGYKRVLALSVETDYTFPLAE KVKAFLADPSAF/VAAAP/VAAATT AAPRAAAAPAKVEAKEESESEDED MGFGLFD |
| 1535 | 7032 | A | 1653 | 68 | 1110 | RTAVMPREDRATWKSNYFLKIIQLL DDYPKCFIVGADNVGSKQMQQIRI VPWGEACVLMGQKTMMGQAHPK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GTL*NNPSLWRKLLPAHIRG\NLGFC FTQGGPSLEIKGHVCLANKGLPSWL PVVGANC PHGEVTGGQPQNTG/LSG PEKTSFFPGL*ATTKVISQGAPIENPE VNVPAESRTGDQSGKPSEANAA*TC SNISPF\SFGAGSSQPGVSTNGSHLPP LKGLDIHRRNLCIFWLSWRGVRNV AKCL SARLAYPTVA\SVP HSIINGY KRVLA LSV\EPDYTFPLAEKVKAFL \ADPSAFVVAAPVG\APPAAPGGV VAAPAKVEAKEESESEDEDMGFGL FD |
| 1536 | 7033 | A | 1654 | 1 | 364 | |
| 1537 | 7034 | A | 1655 | 70 | 253 | |
| 1538 | 7035 | A | 1656 | 151 | 657 | APTTPGTGPGDPLDLVALAEQVQKA DEFIRANATNKLTVIA\DQLQ\HLPE QARKVLEE AHRDANLHHVACNIVK KPGDIYYLL*TG RVGQQYFSIISPKE LGDKFVHIDFLGAYKLQHDL SWTP V*GH*EGKMLKISMMGHVAKPVSG PASVHWNPTFQGTDSLEEWGF |
| 1539 | 7036 | A | 1657 | 345 | 547 | GFKPPDFFLCNENKWRKINTSSFSE Y*CLMHIHLLIFNTIFSS/LHTYIHKH THTHTPFSVFIMEGC |
| 1540 | 7037 | A | 1658 | 228 | 900 | PSQAGNTSPSGARSSFPKDMKLEN SSFEAINS QLT VETGDAHIIGRIESYS CKMAGDDKHMFKQFCQEGQPHVL EALSPPQTSGLSPSRLSKSQGGEEEG PLSDKCSRKTLFYLIATL NESFQA*L *LQHSPQPLSSAGSPALSWLG*MQS TAVCSQLCGEDFKDLKPQLWNAVG RGDLPGLKCDIYS\YNPYLSDP\FG EDGSLWSFNFFYNKRLKRNRL |
| 1541 | 7038 | A | 1659 | 35 | 1288 | |
| 1542 | 7039 | A | 1660 | 1 | 1641 | |
| 1543 | 7040 | A | 1661 | 212 | 369 | HPVTVYLLLGYLLFQLPCGSEFSTSE THGHSADRLG\AAFAVSRLEQDEYA PG |
| 1544 | 7041 | A | 1662 | 63 | 255 | VLMFSSSHG*GYQSS\RLQCKLQIVQ LIQDILLFFSF*IP E*LLS*LTPLKIFPL HQNGPSDFVS |
| 1545 | 7042 | A | 1663 | 169 | 391 | |
| 1546 | 7043 | A | 1664 | 85 | 1534 | KSSHCIKMGPQIFHKTSSELVLPATSC PSCPDQNEEDVSQTQYKECCG\GG WCSHSIFAVWHFI*RPDAT*FGLEQ RLTGLLASGPVSLREVV*LYSSLGT VISGK*KTSNVG*RGLALGSWAFSD KYSWFTMFTWACISGPTKAL\TTGV \GLIAF\GQCDVIVAGGVELMSDVPI RHSRKMIMLMLDLNKA KSMGQRLS LISKFRFNFLAPELPAVSEFSTSETM GHSADRLAAAFV SFL\DQDEYALR SHSLSKKAQDEGLLSDVVPFKVPGK DTVTKDNGIRPSSLEQMAKLPAPI KPYGTVTAANSSF/LLTDGASAMLI MAEEKALAMGYKPKAYL/RRDFM YVSQDPKDQLLLGPTYATPKVLEK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AGL\TMNDIDAFEFHEAFSG\QILAN F\KPMDSDFAE\NYMG*KKPRFGL PPLWRRFNNWG\GSL\LGHPFGTY GCR\LVMTAANRLRKKGGQYGL\V AACAPG\GQGSATDYVEAYPK |
| 1547 | 7044 | A | 1665 | 294 | 823 | |
| 1548 | 7045 | A | 1666 | 3 | 1171 | |
| 1549 | 7046 | A | 1667 | 1419 | 1801 | TMEIHPIEQLDPSDHLESTAAGQEA LFTYHSF*STFISFFETGPHFVTRLK CSSAIITHYSVELLGSSHPPTSASWV AGNTGVCPHVQLIFLFFVEMGSHY VARLVFNS\GLVIFLPWLPKVLGLQ V |
| 1550 | 7047 | B | 1668 | 68 | 471 | MVRKLIVPRAEAAEAGGLPELGGH RPQPARAARAAALTGCSGGEDYTR YNQLSRAVPVCSRLGAHARVRWEL CDFVTASSFCRRRLPTVLLKLRMAQ HLQGSIAL* |
| 1551 | 7048 | A | 1669 | 2 | 359 | |
| 1552 | 7049 | A | 1670 | 1 | 585 | PRGVIGHGPLGTSFIGKYGCGDYW VKAFLDRPSQPMQGPKNFE\VWD LVDVNT\DLMA\PVSAKKERKVSC MFIPDGRVSVSARIDRKGFCGEIS IHADFENTCSRIVVPKAAIVARHTY LANGQTKVLTQKLSSVRGNHISGT CASWRGKSLRVQKIRPSILGCNLR VEYSLIYVSVPGSKQVFIKAL |
| 1553 | 7050 | B | 1672 | 21 | 410 | MPSKVRCXSVQVFDAMKTATAVA HCKRGNGLIKLLPEVLLLGKERFAG VDTRVRVKGGGHVAQIYAIRQSISK ALVAYYQKYVDEASKKEIKDILIQY DRTLLVADPRRCESKKFGGPGARA RYQKSYR* |
| 1554 | 7051 | A | 1673 | 1 | 456 | MPS/KGPLQSVQVFGGRKKTATAVA H/CKRGNGLIKVNRPLEM/IEPRTL QYKVLGSGTGVS\GWR\TLGDRDVV ALESWGAGISNGMFRSCVGCQWA AGASSASRQERFAGVDIRVRVKGG GPWPRFMSKKFGGPGARARYQKST DKPIVTQNSLV |
| 1555 | 7052 | A | 1674 | 172 | 661 | LLEPVLLLGKERFAGVDIRVRVKGG GHVAQIYGESQELGAWRRWLWEG GLHSAPVPFNCVSFSQLSVSPIS\KAL VAYYQK\WSEHGSFP*GRWVCGDQ VKDSV*LSKSSSLLFLPDVDEASKK EIKDIL\QYDRTLLVADPRRCESKK FGGPGARARYQKSYR |
| 1556 | 7053 | A | 1675 | 27 | 554 | STLGAMPSK/GVPLQSVQVFGGRKK DSGQLLAH\CKRA\NGLIQG*TGGPL EMIEARARLQYK\LEP\VLLLGKE RFAG\VDIPCPV*KGGWSTWPQIYAI RQS\ISQKPLVAYYPEM*VSMGPSH E/YVDEAFQRREIKDILHPSY\DRNP AGLAGPFVRCE\SKKFGGPGA\RAR YQKSYR |
| 1557 | 7054 | A | 1676 | 192 | 836 | ALIMSFIFEWIYNGFSSVLQFLGLYK KSGKLVFL\GLDNAGKTTLLHMLK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DD\RLGQHVPTLHLTSEELTIAGM T\FTTFDLVGHE\QARRVWKN\YLPS QLMGFVFLVDCA\DHFSWNPKE LNALMTE*NNIPMCPILILGNK\IDR TDAISEEKLREIFGLYGTGPQER GEL*PLKELNARPM\EVFHVAVLLKEG KVYGRGFSAGLLPVLF |
| 1558 | 7055 | A | 1677 | 196 | 520 | DTVSRKNKSGKIFQLSSRV*YERSQ SGVKVYKCKTFGKAFTQ/HF*AHM RMYTGEKPYKY*ECGKFFLVLLL LMIQKYFHLIKIVRLYLIRKKV SCKQPSNKILQS |
| 1559 | 7056 | B | 1678 | 1 | 1521 | MGIRVTSVIVSRPVPHSEAVFCCWL LGATDVWIPEHPANPRLTFPLFP ESPGRHLREIKLQSARDASVKS AKNTRVIPKPQRVIHPGGQPTD KMDLDDLLDNPRIIAAIKKAKL KSVKEVLHFSGPDLKRLTNLSS PEVWHLLRTASLHLRGSSILTAL QLHQKQERFPTQHQRSLGCPVLD ALLRGGLPLDGITELAGRSSAGK TQLALQLCLAVQFPRQHGGLEAG AVYICTEDAFPHKRLQQLMAQQP RLRTDVPGELLQKLRFQSQIFIE HVADVDTLLEC VNKKVPVLLSRGM ARLVVIDSVAAPFRCEFD SQASAP RARHLQSLGAMLRELSSAFQSPVLCI NQVTEAMEEQGA AHGPLGFWDER VSPALGITWANQLLVRL LADRLREE EAALGCPARTLRVLSAPHLPPSSCS YTISAEGSWG TNCKQNTRLHISPET AGPAAHAACWPQQDTVRAGHSES WHASCCNPDTDMQGGTISTSVNQQ QEAQAKPPPTPL* |
| 1560 | 7057 | A | 1679 | 991 | 1367 | AVLVFNNGEANE GSGPRGP*GERS SRARPP/SGPGPWNCAPPRWCPPL RGWSSVSWD*TAQAKPVCKSP/AG GSSPGTGSPSAPSPPGAGTEPAWAG PAELPGVFSLNVPLSLSCLIF*SLAC LA |
| 1561 | 7058 | A | 1680 | 313 | 429 | CIESMVHGGENIFPAGHGGSHL*SQ HFGRPRQVDHLRSG |
| 1562 | 7059 | A | 1681 | 552 | 792 | GSASDYQSGIRTVGPRDWLCRRRA LDLDAARTQSVRAAEGKCAFLQMQ GPRVYTGPGRPRRADHLRSGV*DQ PGQHGETP |
| 1563 | 7060 | A | 1682 | 508 | 1085 | CQHFRPRRADHLRSIGVRAQPGQ HGETPSLLKILKLA/GHGGAPL*SQL LGRLRQENHLNPGGRGCGEPRSHH CTPAWETERDSISKKKTKTQVVICI* SLNLVREIKNKIGLTAE*ILQKNS ELEDVSIIEI*NEGQRDGKKMDRAFLRS MQQYQAVQYMCNQSPRRVGD RMGRINSQKKCKTYTMNTIKHC |
| 1564 | 7061 | C | 1683 | 46 | 516 | MLSDPPARIRTRKGPTETVSRIPRPN SPNGQGPVDSSPSGXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX* |
| 1565 | 7062 | A | 1684 | 2 | 100 | |
| 1566 | 7063 | A | 1685 | 2 | 814 | PGYKKGPQETGSRIPRPNPSPNPLRVL WTAHLVAMAPGSRTSL\LLAFALLC LALGFKEAGCPSQTP\LSRLF\DHG MVQGPSRVTS CAID\TYQGFEETYIP KDQKYSFLHDSQTSFCFS\DSIPTPS NMEGSATRNP\ILELLR\ASLLIE\SW LEPVRFLRSIVPPTTWVYEHLGTAI DYHLL\KDLEGGHPTV*WGRLEDG KPPDLGKILKQTYSKFDTNSHNHDA LLK\NYGLLYCFRKDM\DKVE\TFLR MVQCR\SVEGSCWLLGCPSSIL |
| 1567 | 7064 | A | 1686 | 3 | 452 | |
| 1568 | 7065 | A | 1687 | 3 | 516 | PTLLVPTDSERTHHGACLLPDKTNV \KAAWG\KVG AHAG\EYGAEALER MFLSFPT\TKTYFPHFDL\SHGF\CPGL RATGKKVADALTKRRG/HTWDDM PKRRCPP*SDLHAHKLARV\DPVQLS SS*SHLPCWVTPGPAHLPRPSSTPGG CKASLGQSFLGFL\KHRC\LNLPNNV |
| 1569 | 7066 | A | 1688 | 3 | 409 | SNFRS\NFGYNIPLKHLADRVAMYV HAYTLYSAVRPFGC/SGYWGCAIGK ARQAAKTEIEKLQMKEMTCRDIVK EVAKI\YIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREEAKEYAKE SLKEEDESDDDNM |
| 1570 | 7067 | A | 1689 | 2 | 437 | |
| 1571 | 7068 | A | 1690 | 126 | 409 | ILLWMDILICTDFGSVNYFNVWRL PKSYLSLFYSRIYIVHDEVKDKAFEL ELSWVG\ELTNGRHEIVPKDIREEA KEYAKESLKEEDESDDDNM |
| 1572 | 7069 | A | 1691 | 516 | 564 | |
| 1573 | 7070 | A | 1692 | 224 | 344 | ILLGFLVLASDHLQSKYAL*CPLR HLP\ELNPSLREGSVL |
| 1574 | 7071 | A | 1693 | 1 | 1237 | MGCRPVGQAGLELLTSARTCFVSD LKRGLKIQA\AKFNIDGNNECPIDTR KQLAENLVVIGGTSMLPGFLHRLLA EIRYLVEKPKYK\KALG\TKTFRIHTPP AKANCVAWLGARSL\LGYNRFLMF QPFRGEETVWSLLPKIQAYCCPFL KYDLSASTFSPDGRVFQVEYAMKA VENSSTAIGIRCKDG\VLGV\EK*VL SKLYERRVPNKKTF\LMFDR\HVGM A\VAG\LLADA\RLADIAREEASNF RSNFG\YTIPLKHLADRV\AHVWCHA \YTTLPVAVRPFGCQFPC*GPYSVN DGA\QLYHD*PHPGV\SIPVNWGCAI GQRPGQAWQRRKLEK\LQMKEMT C\RDIVKEVAKI\YIVHDEVKDKAFE LEPSW\VGELTK\GRHE\VPK\DIREE AEKYAKESLKEEDESDDDNV |
| 1575 | 7072 | A | 1694 | 1 | 1083 | |
| 1576 | 7073 | A | 1695 | 138 | 545 | RPGMWSTRSPNSTAWPLSLEPDPG MASASTTMHTTTIAEPDPGV\SGLP DGRMETPTPHP*LTMVVMAGCDV/ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AAVPIVLVSLLFVMLRYMYRHKGT YHTNEAKGTEFAESADAALQGDP ALAQDAGDSSRK\EYFI |
| 1577 | 7074 | A | 1696 | 2 | 498 | |
| 1578 | 7075 | A | 1697 | 41 | 510 | APSPRRPWGHFTEEDQGLLSTSLWG KGEMWKKCWEGRNPWERLPGCPT PWTPRGSEQLWQPCPSA/ILHPW ANPQSPRHHGK\KVLTSLGRCP*STL DDLKGTFAQLSELHCDKLHVDPEN FKLLGNVLVTVLAIHF\GKDFTPGG CRASWAEDG |
| 1579 | 7076 | A | 1701 | 153 | 744 | AVNLVPSKDRHLTQSRSQGGGVAN PNSGVYSARPSSPPQIALPAWGTG QPQTLQTSPEGEGFSVQTGAEVGVG RG*PRRRPPRARQGGKGVHSTLKKL KHRYRFHIADGLDRGQAPPLGRPLFL GPGWLRTH*GRAGK/QNPQTVGDH PGAGAPPSSPALAVSL*/H/CTGLC*I PSPACSPGSPSPRRGSHSPDAWV DP |
| 1580 | 7077 | A | 1702 | 35 | 569 | |
| 1581 | 7078 | A | 1703 | 509 | 2455 | LPAATVLFTSSPNFQIQPNRTNGD VTKKIHSLESSKISTLKGNLERGYF QPSWMTLRGVRLQLEEVPA DIVEIA RELEVEPEDVTEFLQSHDQTLAD QKLLLMAEQRKWFLEMETTPGGD AMNIVEITINNLEYNINFVDKGAAG FERIDSNFERSSTA EWVTVKQTQAH PSGGIQEGIVIIRDGSRPYTTPEHLPV RPNVEEEDSDIDESSPFLRNYKA AHSFIGRIRFKHSTLLREAFYIITSK EFFSAIRKLASSPEKKGKGGIIFTAINP FTRSINEIYKIQRRRGKERQLNDCV HRSDDANKGPESLGSAGSGQSHDV AQGHLQGLVLGQLFILAPLGKFHPE EDVKQATSNFENLQKQLARKMKLP IFIADAFTARA FRGNPAAVCLLENE LDEDMHQKIAREMNLSETAFIRKLH PTDNFAQKNMNSTLTFVTLSGELRA RRAEDGIVLDLPLYPAHPQDFHEVE DLIKTAIGNTLVQDICYSPDTQKLLV RLSDVYNRSFLGEPGKLNTENLLQV ENTGKVKGLILTLKGEPGGQTQAFD FYSRYFAPWVGVAEDPVTGSAHAV LSSYWSQHLGKKEMHAFQ/SFPPSE ESWEFPFVQT*RVDIRGCAPVVLEG TLTAYRWLCCDAAVS NHQVFSA |
| 1582 | 7079 | A | 1704 | 1 | 1503 | |
| 1583 | 7080 | A | 1705 | 1 | 635 | |
| 1584 | 7081 | A | 1706 | 1 | 804 | LQFSSALGGGRCRASASSPRRARRR GQRPRHPAPRRPQAARPSAAPRARR FLSQRPA AAAAAA QRAALMQAIKC VVVGKPKL*GKT\CLL\SYTTQCHF LGEYIPTVFDN\YSA\NVMVDGKTG EIWGLWDTAVQEDYDRVTPPYYP A/QADVFLF\CFPFVSPASFENVRAK WYLNVRHHCPN\TPAILVGTKLCLR DDKDTIEKLKEKKLTPITYPQGLA\ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MAKEIGAVKYL\EC SALTQRGLKTV FDEAIRAVLCPPPVKRKRKCLLL |
| 1585 | 7082 | A | 1707 | 1 | 848 | RPRVRAGAENMMFSAAARLSPWE GSPSFAENMNDWMPIAK\EYDPLKA GSIDGTDEDPHDRAVWRAMLARY VPNKGVIDPL\LTFLVARLNLQTK EG\K*KEV\FPRYGDIRRLRLVRDLV TGFSKG\YAFIEYKEERAVIKAYRD ADGLVIDQ\HEIFVDYELERTLKGW IPRRL\GGGL\GGKKESG\QLEFGGR DR\PFRRK\INLPVVKNDLYREGNRE\ RRERSRSRERHWDSRTRDRDHRG REKRWQEREPIRVWPDND\WRRER DFRDDRIGREKKERGK |
| 1586 | 7083 | A | 1708 | 3 | 3067 | |
| 1587 | 7084 | A | 1709 | 148 | 4435 | GIQRKYLKGSIMVSSGCRMRLWFI IVISFLPNTGFSRAALPFGLVRRELS CEGYSIDLRCPGSDVIMIESANYGRT DDKICDADPFQMENTDCYLPDAFKI MTQRCNNRTQCIVVTGSDVFPDPCP GTYKYLEVQYECVPYIFVCPGTLKA IVDSPCIYEAQKAGAWCKDPLQA ADKIYFMPWTPYRTDTLIEYASLED FQNSRQTTTYKLPNRVDGTGFVVY DGAVFFNKERTRNIVKFDLRTRIKS GEAIINYANYHDTSPYRWGGKTDID LAVDENGLWVIYATEQNNGMIVIS QLNPYTLRFEATWETVYDKRAASN AFMICGVLYVVRVSVYQDNESETGK NSIDIYINTRLNRGEYVDVPFPNQY QYIAAVDYNPRDNQLYVWNNNFIL RYSLEFGPPDPAQVPTTAVTITSSAE LFKTIISTTSTTSQKGPMSTTVAGSQ EGSKGTKPPPAVSTTKIPPITNIFPLP ERFCEALDSKGIKWPQTQRGMMVE RPCPKGTRGTASYLCMISTGTWNP GPDLSNCTSHWVNQLAQKIRSGEN AASLANELAKHTKGPVFAGDVSSS VRLMEQLVDILDAQLQELKPSEKDS AGRSYNKAIVDTVDNLLRPEALES WKHMNSSEQAHTATMLLDTLEEG AFVLADNLLPTRVSMPTENIVLEV AVLSTEGQIQDFKFPLGIKAGSSIQ LSANTVKQNSRNLAKLVFIYRSL GQFLSTENATIKLGADFIGRNSTIAV NSHVISVSINKESSRVYLTDPVLFIL PHIDPDNYFNANCSFWNYCERTMM GYWSTQGCKLVDTNKTRTTCACSH LTNFAILMAHREIAYKDGVHELLLT VITWVGIVISLVCLAICFTFCFFRGL QSDRNTIHKNLCLNLFIAEFIFLIGID KTKYAIACPIFAGLLHFFFLAAFAW MCLEGVQLYLMLVEVFESEYSRKK YYYVAGYLFPATVVGVSAAIDYKS YGTEKACWLHVDNYFIWSFIGPVTF IILLNIIFLVITLCKMVKHSNTLKPDS SRLENIKSWVLGAFALLCLLGLTW SFGLLFINE\ETIVDGHISFTNFCFP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GGVFHFPSFHCALPKGKVRKRIMA KCL/RRHLHTACGGP/LPT*ESPHSS VKASTHPEPSARYS\SGTQSRIRRM WNDTVRKQSESSFISGDINSTSTLNQ GHSLNNA\RDTSAMDTLPLNGNFN NSYSLHKGDYNDVQVVDCGLSLN DTAFEK\MISELVHNNLRGSSKTHN LELTLPVKPVIGGSSSEDDAIVADAS SL\MHSDNPG/VWELHHK\ELEAPLI PQRTSHLLYQPQKKVKSEGTDYSVS QLTAAEDHLQSPNRDSLYTSMPNL R\DSPYPESSPDMEEDLSPSRSENE DIYYKSMPNLGAGHQLQMCYQISR GNSDGYIIPINKEGCIPEGDVREGQM QLVTSL |
| 1588 | 7085 | B | 1710 | 98 | 264 | XQVVCKKYRGFTIPEAFRGVHRYLS NAYAREEFASCPDDEEIELAYEQV AKALK* |
| 1589 | 7086 | A | 1711 | 155 | 1217 | DPPSPVPAPPSSPRDGHFLVPDATM AEEQPQV\ELFVKAGSDGAKIGNCP FSQRLFMVLWLKGVTFNVTTVDTK RRTETVQKLCPPGGQLPFLLYGTEVH PDTTKIEEFLEAVL\CPPRYPKLAA LNPEVQHSWGWDIFAKFFLPNIQEF QTPALN*QSGRRGFLESP*KVLDNY LT\SPPSPEEVDETSC*KIEGVSQRK FLDGQRRPHPWLDLQTCCKVTH* VQVV\CKRK*PGNSPHPPKAFPGKC HRVP*SKMPYAPGKNPSHPVPDDE EIELRPMKVAKALQISPSLGLPSTP SIFSTKAPGGFHATPMGHTPKLASG QGILGDIEPAKGVVEEGMRERNGGP GSDF |
| 1590 | 7087 | A | 1712 | 39 | 256 | LSVKMEEGILPCSLYETTITDSKT*Q G*YI/EDFRLVFLINLNAYILKKMLV NHLR*NMRDNSETYRRIVRIV |
| 1591 | 7088 | A | 1713 | 1193 | 1436 | PQSDFLDTLPQTSP\I/*EVPTGLVC YSSRVNKRAAPPASIPVPACSPSPV SNPPHPVSNPPHVSAPLPCSSHQTQ QAP |
| 1592 | 7089 | A | 1715 | 2 | 533 | ARDSFLAAMASHR\LLLLCLAGL\VF VSEAGPTGTG\ESKCPLMVKVLD\A VRGSPAQMWP*HVFRKPR**PPW EAILPSGTRKTQLSLGELHGAHKLR EGICTNGIYKSGK*DTKFFTGKGTL GIFPHFPLRHCQEVGISTGQRTSGPR RLTPLAALLEPLTPISTTGCSFTNSQ GN |
| 1593 | 7090 | A | 1716 | 38 | 661 | APSPRRPWVISQRRTKATITSLWGK\ VNVE\ DAGGETLGR\LVVYPMDP RGFFDSFGNLSSASAIMGNPKVKA HG\KKVLT\SLGDAIK\HL\DDLKG/T PFAQA*SELHC*QACNVGS*GTFKL PGEILLVT/LFWAIPFSGKEFHPLRCQ VFLGQEQAEDGD\WS\GQCPCSF QITTELTGP*MQSFSRIWLYSCKQLQ IINLFLLRDHQ |
| 1594 | 7091 | A | 1717 | 32 | 487 | SRRHGSSLWGKVNVEDAGGETLGR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LLVVYPWTQRFFDSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG |
| 1595 | 7092 | A | 1718 | 41 | 597 | APSPRRPWVISQRRTKATITSLWGK \VNVEDAGGETLGRLLVVYPWT QRFFD\SFGNLSSASAIHGQPPKVQ GTWSKKVLTFLGEMP*KHLDDLK GHLLPKPEVNLHC\DKPAMWDPEN FKAPGEMLLVTRFWAIPFSAKEFHP WRLAGLPGQKDG*LGVGQCPCSFQ IPLKPLGP*IQ\SFQG |
| 1596 | 7093 | A | 1719 | 3 | 573 | HSLFGTSEVINKLLVPDAHGSFHRG GPRLLSTSLWKGECGKMEEKPL GRLLVVYPWTQRFFESFGNLVLLP SCPSMGQPPKVKAHGKRRCLSLG RCQ*STLDDLKGTFCPSLKRNLHC* QACNVGS*RTSKLLGENVAG*PVFG QFHFRANKFTPEGCKASWQKQKM AEDGDWSWPVPLFLPDYH |
| 1597 | 7094 | A | 1720 | 676 | 1283 | QRKILYTHNTTENKWEIINF*SF IFLFFLRRSFTLVAQAGVQ\WLDLGS LQPLPPRFKQFSLGLPSSWDYR/RC VPAHPANFCIF**RWGFTMLARLLS NS*PQGDPPASASQ\SAGITGVSA/H APVRASFFLSLTVSGVQWRDLGSLQ PLPSGFKGFSLSLPSSWDYGCPPPS PANFCIFSRHGFSPCWSGWSQTPDL K |
| 1598 | 7095 | A | 1721 | 41 | 669 | APSSRRPWVISQRRTKATITSLWGK \VNVEDAGGRKPLGKAPWLSTPWT \QRFFDSFGNLSSASA/LSMGKPPKS KAHGKKVLTSLGDA\TKHLDDLK GTFAQA*SATCTVDKLHVDPGGT FKLLGENVAG*PVFGQFHFRANKFT PGGCRASWQKQKMAEDGDWSGQ CPVLQIPLKLNCP*MQSFSRIRLLFL QAITNKSISAKRSP |
| 1599 | 7096 | A | 1722 | 2 | 307 | TPYLVGQVVAGAQAQLQFESHAGH LGPQLFNKFALPYIRDVAKQVKARL REAGLAPVPMIIFAKDGHFALEELA QAGYEVV/GDDFGPHRYIANLGHG LYPDM |
| 1600 | 7097 | A | 1723 | 20 | 473 | AVEFEANGLGPQGFPKNDIFL*A AWGEETDYTPVWCMRQAGRYLPE FRETRA AQDFSTCRSPEACCELTL QPLRRFPLDAAIIFSDILVVPQWTLM TYMVEGGGSSTMAQAKRWLYQRP QASHQLLRILTDALVPYLVGQVVA GAQAL |
| 1601 | 7098 | A | 1724 | 3 | 1170 | CKHSLGHTCYSPRGSSYRQLTMEA NGLGPQGFPELKNDFLRAAWGEE TDYTPVWCMRQAGRYLPEFRETRA AQDFSTCRSPEACCELTLQALGME VTMVPKGKPSFPEPLREEQDLERLR DPEVVASELGYVFQAITLTRQRLAG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RVPLIGFAGAPWTLMTYMVEGGGS STMAQAKRWLYQRPQASHQLLRIL TDALVPYLVGQVVAGAQAQLQFES HAGHLGPQLFNKFALPYIRDVAKQ VKARL\REAGLAPVPSIIFAKDGHF ALEELAQAGY\EVVGLD\WTVAPKK AREC\LGKTVTLQGNLDPCALYASE EEIGQLVKQNLDTFGPHRYIANLG HGLYPDMDPEHVGAFVDAGHKHS RLV*QNMWGPLWMLGINTHVWFD KTECIPLSRTPNPDDWLFSGP |
| 1602 | 7099 | B | 1725 | 92 | 846 | IIFAMDGHFALEELAQAGYEVVGLD WTVAPKKARECVGKTVTLQGNLDP CALYASEEEIGQLVKHMLDDFGPH RYIANLGHGLYPDMDPQHVGAFVD AVHKHLRLV* |
| 1603 | 7100 | A | 1726 | 1 | 804 | |
| 1604 | 7101 | A | 1727 | 178 | 1093 | TFLLPACLLAALLPLRHHVRGRAW VQGSILNEGVG*ALKD\LINEACWG Y*APAGVNLQSMGHRPTVSL\VQLT LRV*GASTPYRC\DRNLGHGR*NLT SMSKILKMAAGNED\ISLTLRAEDN AGYLGR*YFEGTKPGRKFSDYEMK LMDLDVEQLGIPEQE\YSCVVKMPS GEYA\RICRESQPILGDAVV\ISCAK DGSENFASGELGNET\IKLSQTSNV DKEEEA\VPIKMNEP\VQPNFCH*GY LNFFTKATPLSSTVDTPVCSADGTP LVGRSIAAGYGDHLKYLLGLPKDP RIEEGSLGHS |
| 1605 | 7102 | A | 1728 | 58 | 483 | AARDRLHLRRTTEQHVPEVEVQVK RRRTASLSNQCQLYPRRSQQQVVP VVDFQAE LRQAFLAETPRGTVA AIAATASIAGAPTQYPPGRGTPPPP RRQTTPPPGIMAPPPGMRPPIG/PPPI GFPLARGTPISMPPSGN |
| 1606 | 7103 | A | 1729 | 292 | 531 | FQAKTSLPLGFQKHQVLTVDIGFGG TAIMTVGKSSKMLQSLFPLQW/CFV KLCRVFVSFLFPHFALIIANNKCIEQ KKKKK |
| 1607 | 7104 | B | 1730 | 326 | 419 | XRLTCKRSLARSIASLNAPQTDASGI SGGPDA* |
| 1608 | 7105 | A | 1731 | 774 | 1763 | GNPRSYLLSIAFPLGLQKAFKVFNC GTLDGFWNSNHDLFGKS\SKLLQ\HI DYRMRCILQDGR\FIGTFKAFDKH MNLILCDCDEFKIK\PKNAKQPRA VEE/ESRVLGLVLLRG\ENLVSM TVE GPPPKDT\GIARVPLAGAAEGPGV GRAAGRGVPAG\VPISGPLAGLAG PCSRGSLGGP/SPQQVMTSTGKEAL* AAAAVA\ATASIAGAPNTVPTQGT GTPAPTPSGRATQPPGIMAPPP\GM RPPMGP\PMGLRPARGTP\IGMPAPG \MRPPPPG\IRGPPPPGMRPHKTL SIL FDPSQSLFPLQCVLVKLCRVSAELF CSLIIAIRC |
| 1609 | 7106 | A | 1732 | 32 | 487 | SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIM |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG |
| 1610 | 7107 | A | 1733 | 1 | 591 | NFALEAKNSARAISLVPDAHGVIS QRRTKATITSLWGK\VNVEDAGGE TLGRLLVVYPWTQRFFDQLLANLS SASAHHGQPPKVQGHMAKKVLTFL GEMPIKHLDDLKGHLLPKPEVNCT VDKPAMWDPENFKAPGEMLLVT/L FWAIPFSGKEFTP*RLQASWAERWV TWS\GQCPCSFQIPLKPLGP*IQ\SFQ G |
| 1611 | 7108 | A | 1734 | 1 | 477 | RRPSWLVA AVLNRNANMQIFVKTLT GQNHHLPLRYETQ*HPLKNVQKPKIS KNKGGYPHPD\QQRLDNLPKGQLE GWPALLSDYKHPRKESHPAPWCLR LR\GGIIEPFSPGPLPQKYLRQR*SC RQVLCFAFNPPCLSTGRKKKCGSH QTTLRPQEGRFK |
| 1612 | 7109 | C | 1735 | 9 | 254 | MEFHSCCPGWSAMARSQTAATAS QVQSDSPASASRVAGINRHALTHPA NFVFLVETRFLHVRQAGLELPPQPP KLLGLQV* |
| 1613 | 7110 | A | 1736 | 5 | 290 | FNLTHIESRPSRLKK/DEYE/FFTHLD KRSLPALTNIIKILRHDIGATVHEL SDKKKDTPWFPRTIQELDRFANQI LSYGAELDADHPVSPWPVG |
| 1614 | 7111 | A | 1737 | 68 | 312 | |
| 1615 | 7112 | A | 1738 | 317 | 916 | TSSPPSSLCFLSFSDICHELLGHVPLF SDRSFAQFSQEIGLASLGAPDEYIEK LATIYWFTVEFGLCKQGDSIKAYGA GLLSSFGELQYCLSEKPKLLPLELEK TGIQNYTVTEFQPLYVAESINDAK EKVGNSAATIPRPFVRYDPYTQRIE GLDNTQQAHDLG*FHLTVEIGILCS ALQKNKVKAMDRMVVCQAVE |
| 1616 | 7113 | A | 1739 | 389 | 1881 | NLQPHVLFANLPVPEALKSQRPHSR GASMSTAVLENPGLGRKLSDFGQIE TSY\EDNCNQKWVPISLDPPHLKER KLGALGPKYCALFEENDVNLT\HIE S\RPSRLK\KDEYGFFPPFGIKRSLPA LTNIIKILRHDIGATVHELSDKKKD TVPWFPRTIQ\ELDRFANQILSYGSG NWD\DHGPFKDPVYRARRKQFAD IAYNYRHGQPIPRVEYMEEKKTW GTVFKTLKSLYKTHACYEYNHIFPL LEKYCASHEDNIPQL\EDVSQFL\QT CTGFRLRPVAGLLSSRDFLGDLAFR VFHCTQYIRHGSKPMYTPEPDICHE LLGHVPLFSDRSFAQFSQEIGLASLG APDESIEKLAPIYWFTVEFGLCKQG DSIKAYGAGLLSSFGFQYCLSEKP KLLPL/ESLEKTAIQNYTVTEFQPLY YLAESFNDAQGEI*GTFAATIPRPF SV\RHDPHTPQRIGGSWDNTQQL\KI LA\DSI*Q*IGIPFAVALQNIK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1617 | 7114 | A | 1740 | 1 | 191 | MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWPQLST/FQQMWISKQEY DESGPSIVHRKCF |
| 1618 | 7115 | A | 1741 | 1 | 360 | SGACPAFLVDRNLRHHETTFFNLIMK CDVDIRKDLYANTVLSGG\TTMYPG IADRMQKEITAL/APPSTLRFRIAPP/ ERRKYSVWIGGSILASLSTFQQMC LGKQEYDESGPSIVQRKCF |
| 1619 | 7116 | A | 1742 | 13 | 1277 | INPPPLSRRCQLSHSVLPPLRRRVSL PVAMEEEIAALVIDNGSGMCKAGF AGDDAPRAVFPSIVGRPRHQGV MV GHGPRTDSYVGDEA/QRSKRGILT KYPIEHGIVTNWDDME\KIWHHTFY NELRV\APEKHPVL\LTEAPLNPKAN REKMTQ/ILCFETFNTPGHVPWPIQA VLSL*SLWAQPIGIVMDSG\DGVT TVPILRGATTLLHANLRLGPGGLARD LTDYLMKILT\ERGYSFTTHGPSGKT FRNIKGEACATSPLD\FEQ\EMGTAA SSSSLEKSYELPDGQVITIGNERFRC PEALFQPSFLGMESCGIHETTFFNSIM KCDVDIRKDLYANTVLSGGTTMDP GVADKIAEGRSTALAAPAP*KIRVIA PP\ERK\YSVWIGGSILASLSTFPARF WISKQEYDESGPSIVHRKCF |
| 1620 | 7117 | A | 1745 | 644 | 844 | ELSPTTFMPFSEGAEHLYLPPGQPG* GSESPGGCPA/PPYPSPYSPATPEP IEKSQPNPIRHRFPF |
| 1621 | 7118 | A | 1746 | 2 | 271 | |
| 1622 | 7119 | A | 1747 | 83 | 420 | DSSNPSCQSPTQLSKANTLGWHVV CELALPDQSSGTSASRGGLE*THLL VA*ALEPIVL*SGAGLPGL\GPVRP LG*AAVGPGAESLLPSVRSGSSLPQ RREGLSPDGPLP |
| 1623 | 7120 | A | 1748 | 154 | 1030 | SDISQAQLSCTGPPAIPGIPGIPGTPG PDGQPG\TPGIKGEKGLPG\LAGDHG EF\GEKGDPGIPG\NPGKKFGPKGP MGPKGGPGAPGTPGPKGDSGDYK ATQKIAFSATRTINVP/LLRRSQTNRF RPRCITNMNT\NYE\PRSGKFTLQGC PGLY*FNLSTPVS\RGNLCVN\LMRG RERAQKV\VTFCGLMAY\NTFQ\VT GGHGSSAEE/GPQKEGGGGKRPFF LQATDKN\SLTGAWEGANS\IFSGFL AFFQIWEGLTCGLASHPTPAPPARN AHYTPNNNHMTKPN\AHNRDW |
| 1624 | 7121 | A | 1749 | 3 | 607 | FCPRGQEFGEKNKLLSPRRPWVISQ RRTKATNTSLWGK\VKCGKNAGKE ETPGKGSLLVVL/HPWT\PRGSFEQLW QTCPSALCPSMGNPQSQGTMAKKV LTSLGRCP*STLD\DLKGHLLPKPEV NLHLLTSLHVG*RTFKLPGEMLLV T/LFWAIPFSAKEFHPLKVAGFPQK DG*LGVGQCPCSFQIPLKPLGP*IQ\S FQG |
| 1625 | 7122 | A | 1750 | 2 | 585 | AAAAPAGGNPEQRLDYERAAALGG PDGRAWGGRSPLPPAP*AQGAPGP RWPPPRAGSPAPSPAGCGGGKGGG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LVTPGRGGPRAAGREL/RAVRCPCP VRPRPPSKPALGGSLPQPEPAAAPG PSIR/PVLPPIQTGSPWRRPKSLRPVL GTRVGRTPPLPPP/PDPAGPPPLPLPG PHPSRPPPPTGPWRPARADGRV |
| 1626 | 7123 | A | 1751 | 25 | 1295 | KLCATKDLSYLA AAA SPTAFAYLG GLFSPKLPVTMAHRFPALTPAEQKK ELSEIAQSIVANGKGILAADESVGT MGNRLQRIK\VENTEENRRQFR\EIL FLLWDSSIQPGGIGGC*FLFPRR/YPL TQKGTARGKLFPGNIPSREKGD SW VGNQV*DQGRFLFCREP NKGNHH FKGLDGLF\ERFVQYKKDGVD FGK WRAVLR IADS\CPSSLAIHENANAL ARYASICQQNGLVPIVEPQVIPDGD HDLEHCQYVTEKVLAAVYKALND HHVYLEGTLLKPNMVTAGHACTK KYTPEQVG YGSP*QALHRTGPAAV PGVICFLSGGMSEEDATLNLNAYQTF A/TSTKSPWKLSFSYGRGLQAQCTG LPWGGKAANKGGNPRTA FMKRAH GLTCQAAQRDSMFTRVLLGAASHP SRL LHKPCL YPT |
| 1627 | 7124 | A | 1752 | 1 | 186 | IFSRDGA\HRVTQDGLDLLTS*SARL SLPKCSDYSREPPRPAQTPI LRHFH NSKHEKTME |
| 1628 | 7125 | A | 1754 | 74 | 595 | RGGQGLLSTSLWGK\VNVE\ DAGGE TPGKGSLVVYPMGPQRFFDSFGNL SSASAIHGQTPKV\AHGKKGADFP WDDAIKHL\DDLKGHLLPKPEVNLH C*QACNVGSLRTFKLPGENVAGLT VFGNPIFGKRISPLKVAGFP GQKD G* LGVGQCPCSFQ\PLKPLGP*IQ\SFQ G |
| 1629 | 7126 | A | 1755 | 21 | 457 | NPRVRGALTMELSES VQKGFQMLA DPRSFDSNAFTLLLRAAFQSLLDAQ ADEAVL\DNKNSLEILLGSIGRSLPHI TDVSWRLEYQIKTNQLHRMYRPAY LVTL SVQNTDSPSYPEISSSCSMEQL QDLGGKLDASKSLGKSTQL |
| 1630 | 7127 | A | 1756 | 1 | 455 | |
| 1631 | 7128 | A | 1757 | 3 | 468 | |
| 1632 | 7129 | A | 1758 | 50 | 895 | THASDGALTMELSES VQKGFQMLA DPRSFDSNAFTLLLRAAFQSLLDAQ ADEAVLDHPDLKHIDP\VV LKHC\ HAAAATYILEAGKHRA\DKSTLAST YL\EDCKILTEKRIELFFAREYQ\NNK NSLEILLGKY*GRSLPSYNRVFSW ALWIIQVKDQSTFHRMYRPAYLG DLKV VQNTGIPPS\YPREL VFSCQPW NQL\QDL\VGETLKDASKKPWK RAT SVVTLGKVNRSPPSSRRKTQKPPLP FSWNHRLCragCPFSVEKNFSLLNL YPFIHFGHFKNV |
| 1633 | 7130 | A | 1759 | 470 | 737 | RKSFFLAQTVLKWCCEKMSSPGKK LFPGEIWGVKGNKNKLWLPDPSIR HRFERVPSHKRPLPGWVRWLTPHPS TLGGQSAVDHLRSGVRDQPGQHGE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TPSVLKI*KLGRGGRQL*SQLFGRL RQENCLNTGGARGCSEPRSHHCTPA WATE*NSWDYSCLP RPANFYIFST DGVSPCWPGWSRTPDLK |
| 1634 | 7131 | A | 1760 | 1 | 297 | |
| 1635 | 7132 | A | 1761 | 1 | 162 | |
| 1636 | 7133 | A | 1762 | 54 | 504 | YTAIMSIMS YNGGAVMAMKGKNC VAIAADRRFGIQAQMVT TDFQKIFP MGDRLYIGLAGLATDVQTVAQRLK FRLNLYELKEGRQIKPYTLMSMVA NLLYEK/RDPDHLFETISQAMLNAV DRDAVSGMGVIVHIEKDKITRTL KARMD |
| 1637 | 7134 | A | 1763 | 51 | 748 | YTAIMSIMS YNGGAVMAMKGKNC VAIAADRRFGIQAARLLTTNFQKIFP MGDRLYIGLGPASPLDVQTS/VAQR LQVSGLNLY*V*REGIRQIQTFITLM EAWLANLFVMRKRFGLLTLRPVH LPGLGPERPFKALSIC/SL*DLIRVGP MGDLNDFCGSSGNLAPNQMLRECV ESLWGGPTWVPDSTVLKTIFPRPWL NAVGPWQCSGMGSSLFHIIEKDKI TTRTLKARMD |
| 1638 | 7135 | A | 1764 | 433 | 851 | KPQPFILCSKYNQMILLHLRAPGHA DASTQKQQLWL*NLLTSLGQRLFN FFETESH SVT*L/QCSGMISAYCNIC LPDSSNPPTSASRVAGTAKRQHHTQ LIFCIF/VVQTGFCHVGPGLGFTEAR AIHPPWV\PKVLGLQV |
| 1639 | 7136 | A | 1765 | 213 | 617 | KRFLV*KVASVLKGLHAI\VVSDRD GSTLLLKWANDNAPEHAF/RGPGFL \STFALATDQKQ TWDFSKNKSNC LLLTPYQGGFNFSFYLVWGEFS*A QAGSAQLQGLICSA*EKGTWFPLF* RN*GQVVEVSLI |
| 1640 | 7137 | A | 1766 | 2 | 140 | |
| 1641 | 7138 | A | 1767 | 157 | 371 | |
| 1642 | 7139 | A | 1768 | 3 | 135 | |
| 1643 | 7140 | A | 1769 | 1 | 1431 | MHKAGLLGLCARAWNSVRMASSG MTRRDPLANKVALVTASTDGIGFAI ARRLAQDGAHV VVSSRKQQNV DQ AVATLQGEGLSVTGT VCHVGKAED RERLVATAVKLHGGIDILVSNAAVN PFFGSIMDVTEEVWDKTL DINV KAP ALMTKAVVPEMEKRG GGSVVIVSSI AAFSPSPGFSPYNVSKTALLGLNNT LAIELAPRNIRVNC/LAPGLIKTSFSR MLGEPEDCAGIVSFLCSEDASYTTG ETVVNLSVMFTGGGVCRAASWKE GGTGTPRTPRES PRQREPGETSSTD T QENKVWNGLPANPQRPA AEGPVRR KTNKQKGIAS TSKDSINIRTGKDIH TKTPSIGHQHQRPKVDKTTKMERN QSKKAETSRNQNVSSLPKEYKSSPA REQNW MENKFDDLTDVSFRRSVIT NYTQLKEHVLTHCKEAKNLDKML NEWLTRMKNLEKSLNDLMELITTV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QELHEGYTSFNS |
| 1644 | 7141 | A | 1770 | 53 | 582 | RKETVSVSPQQSRHLIGVRSPKGLS EVALAGLIHAQGAATSVHCARAGK SVRLASSGMTRRDPLTNKVALVTA STD*ALHRLSLDLTTTQARQGLFSR SA\ALAQAIGATSQGPT/CQ*GKTQT SQAPFLYWLPVDYQAAKPYGGIDIL SSKAVVNPLFEA*RVSPPEARDLTL DIIG |
| 1645 | 7142 | A | 1771 | 44 | 1059 | AMHKTGLLGLCARAWNSVRMASS GMTRRDPLANKVALVTASTDGIGF AIARRLAQDGAHVVVSSRKQQNVD Q\AVATLQGEGLSVTGTVCHVGKA EDRGAAWWPPAVKLHGGIDILVSN AAVNPFFGSIMDVTEEV\WDKTLDA NVKGPKP*MTKAVVPEMEKRGGS \VIGLSIAAPSPSPGFSLYNVSKPAL LGLAQTLPIEL\APRNIRVNCLAPG\ LIKTSF\SRML\WMDKEKEESMKE\T LRIKKV*ASPEDCAGVVSFLCSEDAS LHSLGKTVVVGGGTPVPASEGTGK TAQRPKVGLLSFLVLFPAIQPNWPF PTSCSTLLFHPSNQFLPL |
| 1646 | 7143 | C | 1772 | 1 | 174 | MWIFIFNKYYQHVKSPTMSRTGKS ATCDGCGMAAHCSRCWGLSWGLG EALSYSKNVS* |
| 1647 | 7144 | A | 1773 | 154 | 765 | RAGLEELTAAMVRLNLCIVAVSQ NMGIGKNGDLPWPPLKNEFIYFQR MTTSSVEGKQNLVIMGKKTW\FSI PE/RRNRPFKG*EFNLVLSRELQGNL PQGAHFLFQKF*D/AMPLKLTEQPE LANKVDMVW\IVGGSS\VYKEAMN HLGHLKLFVTRIMQDFESDTFFSEID LEKYKLLPEYPGILSDVQEGKHIKY KFEVCEKDD |
| 1648 | 7145 | A | 1774 | 1 | 676 | DRPNSGRPRAALAAGSTFPVLACSS AMAPKGSSKQQSEEDLLLQDFSRN LSAKSSALFFGN\AFIVFAIPIWLYW RIWHMDLFKSAVLYSVMT*LSTYL VAFAYKNVKFVLKHKVAQKEGK DAVSK\EVTRKLFWKLDY*ERCSRE GRKD\ERILWK\KNEVADYEATNIF PIFYNNTLFLV\LVIVASFFILKNFQ PHSVSFSRNYILSISG\SSGLIALLFTG SK |
| 1649 | 7146 | A | 1775 | 99 | 362 | |
| 1650 | 7147 | A | 1776 | 3 | 403 | |
| 1651 | 7148 | A | 1777 | 184 | 360 | |
| 1652 | 7149 | A | 1778 | 1 | 885 | EFGTRWDFSMAVFADLDRAGSDL KALRGLVETA AHLGYSVVAINHIV DFKEKKQEIEKPAVSELFTTLPIVQ GKSRPIKILTRLTIIVSDP\SHCNGFER QLLRGARLYDVVAVF\PKGQEKSLF HIA\CTHLGCGDLV\CITVTEETTIFT SKRPPINVAIDRGLAFDLALIPLLSR TPTMRKVYNFSPAPPILMPNLAKGK NVNYLGGWQERAFREIR\GP\YDV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GKS*ACLFGPFF*K*TPRVRVSTNCR AA\LLHGETRKTAFGIISTVKKPRPS EGDEDCLPASKKAKCEG |
| 1653 | 7150 | A | 1779 | 175 | 534 | DCSLPSVCHFPHLPSPTHPPTHPPWG /CPSGGPEGLPIT*RHOVGSCPTAPPP VPAPSRQSDCGAVHSQDENTVNALI GGFLVLLHIMCNVVALTFYATIYED LCCTCNKYIEKAHTSVW |
| 1654 | 7151 | A | 1780 | 190 | 390 | TKRGAGEGNSKVVLGLQVGCQSQR GNHQGMFTWA/CCGKDSGGACSCSCL GV*CSWGQKSIRVSLLWGF |
| 1655 | 7152 | A | 1781 | 805 | 1325 | ASKLEGSPCGKGGVGLGGCFPKRPE PRNHPHFVLWYLPLPQTRLEPKPLP PQLPSVG*KGPGPSFGLSLTAGPLP LQERLVPTQLLPVGKPGPGPFPA TSSGKPKLKRPLCAKSTMP*THPPT VPKPPGQEAVENQAPMASEFPSPSP SVSGDLKPWGFRSFLCQGGAWS |
| 1656 | 7153 | A | 1782 | 1016 | 1560 | KDPELQASHFPCFSYCTPPAHFASLL DFAFSDPHLLGFLSSFLERSSI/CGKT DLSKTFSLD*SFGLNFSRLRESSYRP FGVQDAID*HPPAMFFSASQTLQGP SCGVPICAFIPAVPSTFQLPMFLWVR FLSLPSFSFPNPPVSSGPSLFPHTPFL TTP/LPHG*LFPSAPPALHHAATHFRT |
| 1657 | 7154 | C | 1783 | 68 | 223 | MSPSSVFFVXXXXXXXXXXXXXXXXXX XRASFIPFLDLXXXXFFLSFQMKSI DF* |
| 1658 | 7155 | A | 1784 | 1373 | 1651 | LSVLCHCVCVCVCV/CCD*KGLHSY LFPWTWKKIFFYLFK*NLLISSNHI*I NVKAYIVLYVN*ILKITKYMLLSTT |
| 1659 | 7156 | A | 1785 | 6 | 140 | |
| 1660 | 7157 | A | 1786 | 223 | 397 | QTPP*KSKQPFRSTSS*DQVPSQP*VPI PPINNPPIPPPFGEVYYFEPHILRKWV KGR |
| 1661 | 7158 | A | 1787 | 2287 | 2854 | |
| 1662 | 7159 | A | 1788 | 1 | 610 | SGRPFFFLSGGARATAQLAESWRG GQHLQSSSPPPPPASPGGPSSSDQRS PCSNAKARW/NTSIYSLVADGTC*D TALVGNKDPAPSIWAAIPGKTFLNIT PAEVGVL\VGKDWVKLLSLNGLDT GGPRNYNLLVPGDFHWLAGWGN* TVDL\QLKSIGGSPATFNIVVTMTAK TLGLLMGKEGIHGNFIDK*CYEMAS HLQRSQY |
| 1663 | 7160 | A | 1789 | 157 | 610 | GYRKKQLRGDRRWAIHRIRITLTSR NVKSLEK\VCA*L**RRRKKEKNLK S*KGP\VRMPTKTLRITTKKT\PCG*/ EGSKDRWDRFPD*GFHK\RLHLTLH SSFLRFV*GRFTSFSYLRPGFEVGSS PFADALSQISIHTIDDQLLKKKKKK KI |
| 1664 | 7161 | A | 1790 | 1367 | 1582 | METRWESPPPDNFNIAVTP*FCSNS D/CVLSVPDSSRLPRHFPPSHCTRKR PHLPTQQQPFRKCALQEKWFF |
| 1665 | 7162 | A | 1791 | 122 | 344 | ALGPLPLFFPPSPLPVQKG*YSNQKL EGAGPGQGGFQPVFP*LGGTSNFPAP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FRKSPSQVQAH*PGSDEDPRPL*EDPRPL |
| 1666 | 7163 | A | 1792 | 656 | 1068 | NQINFCLNGKYTYVCIDTLPLYMFN IHTLKHINTSVIISLEFAI*HKGQVEL HIKITYRSN*MWLGHNQRRN/LCPQ EGEEIPNEA*IFSIIKRQSWPGTVAH ACNLITLGG*DGRIS*DQVFKTSLINI VETPSLLKK |
| 1667 | 7164 | A | 1793 | 138 | 396 | |
| 1668 | 7165 | A | 1794 | 143 | 327 | CGVQLLPDRRRESRDIIIVEL*AAVA AAGGNPDGKKGGGGWEAGQRKER KESEDPDAEPDCV |
| 1669 | 7166 | A | 1795 | 23 | 483 | KAIVLLHIICTEVISIILFNDFIQDKRP CRLFTCCSLLRSASPVSSAANMP FSSTSSSTVSWLSLSSSLSSCFLSFR FGNSSCMSFSSIIPFVRPEDWKRMLL AK*GPLMALMLCALFFSSSSRLKPL FMSTTILSLKYGGGVQDVGWQ |
| 1670 | 7167 | A | 1796 | 429 | 1394 | TISFEADIIHMYKT*ETD*TIFLEPYD YLLQLPAGKQVRTQT/LSQAFNHW LKVPEAKLTDYLFEVDRKLFGLMPS LLNDIEDNSKLPTWAFVAHSIYGI PSVINSANYVYFLGLEKVLTDHPD AAKLFTTRQLELHHGQGLDIYWRD NYTCPT*EYKAMELQKTGGLFGLS KCLKHIVSDYQEYLKPLLNTLGLFF QIRDDYANLHSKEYSENKSFCELT EGKFSFPTIHAIWSRPESTQVQNILR QRTENIDIKKYCVHYLED\EGSFYET RNTLKELEAKAYKQIDARGGEPLS LVA\LVKHLK*RCSKEGKWNNV |
| 1671 | 7168 | A | 1797 | 145 | 172 | GGCLLESVDTSHGQSLLISASLNTK HPTGMHSTCWFHVELCGKGLGSRH TLKQHQSAP*SMPPA/PPAPCHIVPAQE PTS*VHPCWVFCVETG |
| 1672 | 7169 | A | 1798 | 197 | 378 | VLMSVLPALGYPPRSMWLYVRGLN ADTP*PPSTTFPLALPPSSTWNQ/PS* VHPLLGVCVET |
| 1673 | 7170 | A | 1799 | 32 | 377 | SSMPPTPGPSILSSLVPIPVSPFHPCPP VLYLWPAPI/Y*KLLPVPDLAHSPPS TPTLHVSHYPMVGITLTPVPLFFIPS NSLPNGGDPEPSSDQVEPVQPGLLS LPSSKSGGFCF |
| 1674 | 7171 | A | 1800 | 168 | 224 | |
| 1675 | 7172 | A | 1801 | 224 | 527 | CHQLRQELAIFTSFVILQLFSGHLDV YMQAWAQRPDKYEYDNK*FIEIKKI IQFTLISKRMK/YVGINLTR*VKDLH NENYKTLMEIEEDTSEWKDISCSW |
| 1676 | 7173 | A | 1802 | 22 | 430 | SPGCRRAESEKSQGSERGVGPSYRI WVGSGKLQSKGVVLWQAGAGVIR CSAGELLSQEKGFHKVMSSVKAGT SHLHFFCDSSVTSGHVDVYVQAWA QRPDYRYSVHCSGDGCTKVSEITTKN LFM*PKTTCTPKTTE |
| 1677 | 7174 | A | 1803 | 386 | 511 | |
| 1678 | 7175 | A | 1804 | 362 | 439 | |
| 1679 | 7176 | A | 1805 | 776 | 1376 | GAPWAFGGLPWVHGLAKEGVTAVI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AEHGLWNIGVHEGHGTLQLQHMH HYAVALRRHPFIQAQAQRGV LALG GGMGTRRE*VRARGQPRVHSNNCH TGQNRYSVPSEGLWT*YLL*GPK MTQDAEQAGRDGGDDGGLALVGE ALLEAHRDAIEQALPWGLRQLSLTV SQIGGHTVGPVHFPGLSHIGEEHGL RGQLSTV |
| 1680 | 7177 | A | 1806 | 420 | 508 | |
| 1681 | 7178 | A | 1807 | 735 | 841 | |
| 1682 | 7179 | A | 1808 | 796 | 1123 | IQWICHNTISAPKNYLEISPHINNKQ F*KKI*KHFPPA*RT*SKKYLGINVQ SLRSLYLEIYK/SLIKMIKN/DT*RYN PY**FGKINIVK*LYNPM*FRFNTVPI KMPIS |
| 1683 | 7180 | A | 1809 | 137 | 303 | |
| 1684 | 7181 | A | 1810 | 122 | 385 | YPALEHILKAQAIQSRCGCDSCLPSS APWDHPGPTTPSPGRRAAADPWHL SPIDGREHLR*VPVLPVTPPSPTLGH WVTDPSPGVGG |
| 1685 | 7182 | A | 1811 | 77 | 1181 | PLEKCYDLFSQNWSGFLPCFQEFQF QFKRILINRLKPDLEKSRKMGRK/R AEEYRQTFLTADV*RSPKKSRSRPRE SPKKAKKLEVIIGKPQGSSSF*QRIR KRERTPATRA*SQKREKARRRSRSI DRGFERMR\SDVRNRLTSPSRSRDR KGDRDRDREREKENERGRRDRD YDKERGNEREKERERSRERSKEQRS RGEVEEKKHREDKDDRRHRDDKR DSKKEKKHSRERSRERKHSRERSR NAGKRSRERSKEKSSKHKNESKEKS NKRSRSGSQGRDTSVEKSKKREHSP SKEKSRKRS*/ASKERSHKRDHSDS KDQSDKHDRRRSPKYRTREPRKTSI KNKDETV*KYFVKCGSH*ILLND |
| 1686 | 7183 | A | 1812 | 1 | 585 | PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPVEK\SAVTAL WGQA*TWMKVGGKALGK/RCWVV LPWDPKRSFEVLWGNLSQLPDAVN GANP*R*KASMAKEKVLGCPLVNG PWLT/HWTTLKGHPLPHTEVSLHCD K\LRGSLKNFRAPGATVLGLCCLA HSLLAKEFNPNKLQGLPIQEKLVGW VVG |
| 1687 | 7184 | A | 1813 | 505 | 671 | QKNKVYFFFETYEIYWPGTVAHAC NPSTLGS*G/GWIT*AQEFETSLANM LKPCLC |
| 1688 | 7185 | B | 1814 | 277 | 480 | GTGHFYGRTPSDTNCQEQYTHRKL CQIKSKADLVLMKNKSLTRVIRNI LAPQDQNHQQNPLNSQFLQ* |
| 1689 | 7186 | A | 1815 | 32 | 1386 | VLLGPKAERTNSRRNYQRRDYFSA PRSITSNQSAKSSSSRGVYSAYQAP DIHECCHFRSASFFLDKMATPAVPV SAPPATPTVPAAVPASAPASVPAPT PAPAAAPVPAAPASSSDPAAASAT TAAPGQTPASAQAPAQTPAPALPG PALPGFPGRVVRLLHPVILASIVD |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | \SYERRNEGACPS*SGTLFGKLVDK\ HSVE\VTN\CFSVPHNESEDEV\AVD MEFAK\NMYETGIKKVS\PNKLILG\ WYATGHDITEHSVL\IHEYYSREAP NPIHLT\VDTS\PGTGRMSIKA\YVST \LMGIPLGRT/LWGVMFTPLTVKY\ AYYDTERIRRLTLIMK\TCF*PPTRVI WTSQVDLQQEGGGIQLRNPGMPLS TSVANMPEGCTCLGKVSADNTIRK VGHFLMSL\VN\QVPENRKPMTFET MLNSNINDLFMV\TYLANLTQSR\IA LNEELVNL |
| 1690 | 7187 | A | 1816 | 273 | 748 | VIQNLFNKMDVGTGQVRVHACNP RHFRLRQEPKSGVQDQPDQHGET PSLKIQKLARR/GGVVHL*SQLLRR LKQENRLNPGGGGCSEPRSHHCTPV *VTQ*DSVPPAPRKKKMYVVLTKK FHIWHISFTLPNIKRSDSLNRKVT NFSCYCSKVS |
| 1691 | 7188 | A | 1817 | 1 | 406 | LCQLETYPPIQCTASDFPGPVTAS WAIQEAARSGQAKAGA/GSATLS/M AYAGARFVFS\LDAMNGKEGVVE CSFVKSQETECTYFSTPLLLGKKGIE KNLGIGKVSSFEK\MISDAIPELKAS IKKGEDFVKTLK |
| 1692 | 7189 | A | 1818 | 1 | 1222 | FRQRAGAGQCGGRWSHFRVTSSCA CYVDAPPAPAMLSALARA\PSACS/ LARSFSTSA\QNNAKVAVLGASGGI GQPLSLLLKNSPLVSRLTYDIAHTP \GSGPQDLS\HIETKSRK*KAYLGTW NSLPDCL\KGL*WW*VIPAGVPTKP GMDRD\DLFTTNATIVGTLTAACAQ HCPEAMICV\ANPVNST/ISPITSKK VFKKAWGQHPQKSSGVTTLNIVR AKTFVAELKGLDPAGVNVPIITGGH AGKTIPLISQVHAYDPVRGFECTPK VDFP\QDQLAALTG\RIQEAGTEVV KAKAGA\GSATLSQCRNAGARFVF S\LDANELEKERCLWECSLPLSPQE TECTYFS\TPLLLGKKGIEKKAKT\ LGIGKSL\PFEEK\MISDAIPELKA\SI KKGEDFVKTLK |
| 1693 | 7190 | C | 1819 | 876 | 1124 | MALGLRQRGIVSLAASITGPCPMSP APSPHGTQVLLPTKRHPQVCLSHTC VEMRQVTKRLSAFKVRNKPDRFY SALLCSTE* |
| 1694 | 7191 | A | 1821 | 103 | 483 | |
| 1695 | 7192 | B | 1822 | 1 | 798 | MAFLDNPTILAHIRQSHVTSDDTG MCEMVLIDHDVDLEKIHPPSMPGDS GSEIQGSNGETQGYVYAQSVDITSS WDFGIRRRSNTESPEPEQLRNLFIG GLSFETTNEKSRSHCEQWGTLPCDV VMKDSNTRSGGFGFV\TYATVEEV DAAMNARPHKRRKKYPLL\GKNTN DKQLDLGPEKGRKHALNCHRMKP ALFSVLCEIKEKTGGATQAFKENN QKAYKETYGVS\HITRHDMLQIPKL AQNEKSQVPSIRS\IQRLKII* |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1696 | 7193 | A | 1823 | 3 | 545 | |
| 1697 | 7194 | A | 1824 | 1 | 440 | VYLHLHSSQDRLLPMTVVTMASAR VQDLIGLICWQYTSEGRKPKLNDN VSA YCLHIAEDDGEWTHDFTTLD NEPIHKFGFSTLALVEKYSSPGLTSK ESLFVR\INA AHGFS\LIQVD\TQKVT MKEILLKAVKRRKGSQKVSGACD |
| 1698 | 7195 | A | 1825 | 293 | 2142 | GNWPTERMAFLDNPTIILAHIRQSH VTSDDTGMCEMVLIDHDVDLEKIH PPSMPGDSGSEIQGSNGETQGYVYA QSVDITSSWDFGIRRRSNTAQRLE LRKERQNQIKCKNIQWKIERNKQSK AQELKSLF*KKNLSKEKPPISGKQSI LSVRLEQCPLQLNNPFNEYSKFDGK GHVGTATATKKTDVYLPLHSSQDR LPMTVATMASARVQDLIGLIC*QYT SEGREPKLKDNDVSDYCLHIAEDDGE VDTDFPPLDSNEPIHKFGFSTLALVE KNSSPGLTSKESLFVRINA AHGFSLI QVDNTKVTMKDILLKAVKRKKGFQ NVSGPQYRLEKHSEPNVPADLDSTL ESHSAREFCLVRENSSRADGVFEED SQIDIATVQDMLSTLHYKSFPVSMI HRLRFTTDVQLGISGDKVEIDPVTN QKASTKFWIKQKPISIDSDLLCACDL AEEKSPSHALF*LYLASNHDKHS TFESDAATANEIVLKVNILAESRAS TARADYFAQKQRKLEQTVRAFSFQ KEKEIPGSIEQLAFQPQILVPVASEP ACPGPSALRSPPGVLSFGGEAHPL GPLGTGAGGLFGEGVGGPLRREAA GDIAMGRKFALAMGF |
| 1699 | 7196 | A | 1826 | 436 | 917 | RLSSKLLHGAYQCFKAKIENYLLSW LNRKFRISFKKEKFSKAVCLKNDIW LGTVARD CNPNTVRLKWEDHLSPG I*DQPGKQ*DL/PSLQKNKKLPRHGG VHTLWSQLLGRRLRWENHLSLGDQG CIEVSSRHCTRAWVTEQDPI*KQLG PQGVYHHA WVIFCFVEMQVSLFS RLVSNSWAQVILPLQPHSVGIAVTS HCTQPYVIL |
| 1700 | 7197 | A | 1827 | 46 | 573 | SQTPMGHFTEEDKATITSLWGKIV NVEDAGGETPGKGS LVVYPWTQ RFFDASFGNLSSASAIHGQTPKVKAH GKKVLTFLGTMP TKHL\DDLKGHL LPKPEVNCTFDKLACGILEELSSFLG KMLLG*PVFGNPIFGKRISPLEGARF FLGRKMGDLELASALVPSRLPLKPL GP |
| 1701 | 7198 | A | 1828 | 1 | 388 | |
| 1702 | 7199 | A | 1829 | 75 | 520 | TPERGSAYPRPLLCGAPPGEATVIM SDQEAKPSTEDLGDKKEGEYIKLV IGSGFSEIHFKVKMTTHLKKL*ES YCQRQG\VPM\NSLRFLFEGQRIAD\ NHTSNKNWGMEEEDVD*SFFREQT GGSFQQFRIFLFFFLSKSFFIF |
| 1703 | 7200 | B | 1830 | 78 | 236 | MSYIPGQPVTAVVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFSEDKT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DK* |
| 1704 | 7201 | A | 1831 | 67 | 587 | IRVEMSYIPGQPGTAVVQRGEIHL ROGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIALGLQ IGDKIMQVNGWDMTMVTHDQA RKRL\TKR\SEEVVRLLG*RGSRMQ K\AVQQSMLFLRQPPSPCDSCLPPLC TVTPLPHSGPHLASADRWAPASEGL |
| 1705 | 7202 | A | 1832 | 3 | 420 | HLSGTSEVINKLLVQTPMGHFTEE DKATITSLWGK\VNVEDAGGETLG RLLVVYPWTQRF\FDSFGNLSSASAI \MGNPKVKAHGKKVLTFLGEMPLK HL\DDLQGAPFAQA*SELALVDKPA MWDG*GTSKLLGEMLLG |
| 1706 | 7203 | A | 1833 | 3092 | 3227 | ERQ/WPGTVAHACNPSTLGG*GGG AGIT*GQEFKTSANTVNPSLL |
| 1707 | 7204 | A | 1836 | 3 | 1088 | SMAAVAAESACICRWRRSCSTGQF EELLRLKAKSLLVVHFWAPWAPQ CAQMNEVMAELAKELPQVSFVKL EAEGVPEVSEKYEISSVPTFL\FFKNS QK\NDRLGWVHMPQELTKKVQADM HLSGLLPTQALMEHL*RKILQPFGL EGNLTSLWLAFLWLFYWKGEPLSK EPR\CGFSK\QMVEILHKHNIQASSF DIFS\DEEVRQGLKAYSSWPTYPLA YGSSELIGGLDIKELEASEELDTICP KAPKLEERLKVLTNKA SVM LFMK GN\KQEA\CGFSKPNNGKYLNSTW C*NLETFRIILEDERKFGQGLKSLTP NWPNIPLSLYVKGEALVGGLDIVKE LKRKLGEFAAL*LRGEN |
| 1708 | 7205 | A | 1837 | 3 | 703 | VEFFSSQRAELYATPLTPAPGPNGGI PGWTLWLALPRPGNLRKGPGLSL QEVDEQPQHPLHVTYAGAAV/DDE LGKVLTPQVKNRPTSSISWDGLD/S KGKLYTLVLT\DPDAPKQKDPKY RE\WHHFLGWSTLKGQMTSATGTV LS\DYVGLGGLPKGTGLHR\YVWL \YEQ\DRPLK\CDPHPSATRS\GDHR GKIQRWASLPVKK**SSRAPGGWAP CYPQPEVGMNQCAPKL |
| 1709 | 7206 | A | 1838 | 717 | 1390 | ASTTTSSVHCARTYMGSVYNTPAR VRLRVGWRAADQLLLAASSTSAI VSTRALECAKMQNAEADATLVFI GYVVPALATLYAAGATLPRSAGKD TPPGTGDHGPAGALGTQAAGGHRV HAVWALDATLSDPAGAHGHHLAR EARGCTLPGGYCTL*RISPNSWSPA AL*HHFSTAT*TRASPASSNG**KSC PAG/APALLPGPHGGAAGAGVGGP ALLGET |
| 1710 | 7207 | A | 1839 | 1 | 310 | RTSPHSPRNILLLS/EPENADSLMLV DFEYSSYNYRGFDIGNHFCEWVYD YTHEEWPFYKARPTDYPTQEQLH FIRHYLAEAKKGETLSQEEQRKLEE DLLCM |
| 1711 | 7208 | A | 1840 | 3 | 375 | HYLAEAKKGETLSQEEQRKLEEDL LEMYSKDEMGNLRKLLLESTPSPV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VFCHNDIHSSS*LHPPTPWISPGASR AGPWREEQRAEGPGDWAEPPESET VQETGLFLSLSRSPWLAGQSPVLCM |
| 1712 | 7209 | A | 1841 | 94 | 429 | |
| 1713 | 7210 | B | 1842 | 96 | 979 | XVGEEPREVLLRLYGAILQGVDSL LESVMFAILAERSLGPQLYGVFPEG RLEQYIPVRAQSYPLLPKAPPPNPT PVPNVCLHIPHPNPITTLIASWVQSR PLKTQELREPVLSAAIATKMAQFHG MEMPFTKEPHWLFGTMER* |
| 1714 | 7211 | A | 1843 | 5 | 1463 | PEKPRPAGRGAERGRKEPSPSESG AHPGLGPRARAMAAEATAVAGS GAVGRCLAKNGLQQSKCPDTPKR RRASSLSRDAERRAYQWCREYLG AWRRVQTEELKVYPVSGGLSNLLF RCSLPDHLPSVGEEPREVLLRLYGAI LQGLDSLVLLESVMFAILAERSLGPQ LYGVFPEGRLQY/IPTSWVQSRPLK TQELREPVL/SQAIATKMAQFHGM EMPFTKEPHWLFGTMSRTLKQIQD RPPTGLPEMKLRGNVRLKDEMG NRKLLLESTPSPVVFCHNDIQEGNILL LSEPENADSLMLVDFEYSSYNYRG FDIGNHFCEWVYDLYSSEE/WPFH KKAGPPSPSPHQRRQVHFIRQLPLA RGK*KVESLPPRRSQKKNWKEADLL VRKSSRVFMFWQSHFLWGLWSILQ ASMSTNEFGYLDLCPSLRFQVLLPS KKGQA*PSVHSCILDSTLPLLGFLE PPGQGPWRGGTTSRRPWRLG |
| 1715 | 7212 | A | 1844 | 143 | 762 | CRQERAVAPARRAMERIPSAQPPTV CLPKAPGLEHGDLPGMYPALMYQ MYKSRRGLKRSEDSKETYPHRLI EKKRRDRINECIAQLKDLLPEHLKL TTLGHLEKAVVLELTALKHV KALTN LIDQQQLFKMHYA*LLIVF*L/SSFPV FILVLSRCLYL*SCYKYILYKYIKKE NVSDVYLYNYLIHTVRKNECIPVFE EKNNFFFL |
| 1716 | 7213 | A | 1845 | 203 | 1507 | CRQERAVAPARRAMERIPSAQPPA CLPKAPGLEHGDLPGMYPAHMYQ VYKSRRGIKRSEDSKETYPHRLIE KKRRDRINECIAQLKDLLPEHLKL TTLGHLEKAVVLELTALKHV KALTN NLNLSSSRQKIAL\QSGLQAGELSG RNVETGQEMFCSGFQTCAREVLQY LAKHENTRDLKVFASTHL\HRV VSELL\QGGTSRKPSDPASKVMDFR EKPSSPAKGSE\GPRKNCVPVIQRTF AHSSGEQSGSDTDTDSGYGGESEK GDLRSEQPCFKSDHGRRFTMGERIG AIKQEESEPPTKKNRMQLWDDAEGP FQLASDLNQLPPFGPTPQHQPFFCL PFYLI PPSS/ATAYLPMLEKC\WYPTS VPVLYPGLNASAAALSSFMNPKIS APLLMPQRLPSPLPAHPSVDSSVLL QALKPIPLNLETKD |
| 1717 | 7214 | A | 1846 | 628 | 1061 | AHRKSLYLCEACFPRSRASQETSGL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KEENWRLGRKTSKCRPGLSKKLGC ERKDRDCSG/CRKDEQQGPWEAPQ AARHSQKSRNARGRPFLEGGPGTE NR*QSFPPKNSREQGFNDPVG PQSV EPLEQPLFPWEWQWPALA QDREL |
| 1718 | 7215 | A | 1848 | 88 | 953 | FQAPQLCYDSAFMISSVPSPHILRVC EFPCFHAHLRVCEFPFHAHL CVCE FPCFHAHL CVCEFPFHAHL CVCE PCFHAHLRV SASVNFRFHAHL CVCE FPCFHAHLRVCEFPFHAHL PVSVN FCFHIHL CVCEFSFHAHLRVCEFP FHAHL CVSANFRVFTPTCASVNFRV FTPTCVCEFPFHAHLRV SASVCEFP CFHAHLQVYEFPCFHAHLRVCEFP FHAHLRVCEFPFHAHL CVCEFP HAHL CVCEFPFHAHL CVCEFP AHLRV SASVNFRFHAHL CVCEFP HAHLRVCEFPFHAHL PVSVNFCF IHL CVCEFSFHAHLRVCEFPFHA HLCVSAN/CPCFHTHLCVCEFP HLCL*ISVFSRPPASVCECL/CN/CPC FHAHLQ/CL*ISVFSCPPAGL*ISVFS CPPACL*ISVFSCPPVCL*ISVFSCPP ACVCEFLCFHAHL CVCDFPCFHAH QSATVLV |
| 1719 | 7216 | A | 1849 | 1 | 254 | |
| 1720 | 7217 | A | 1850 | 3 | 308 | |
| 1721 | 7218 | A | 1851 | 1 | 380 | IPTPLIGNFGPRGPRIRHERPQKRDD RREPSSFGRKRRQ*DGTL LCRRCGS/ KA\YHLQKSTCGKCGYPAKRKRKY NWSAKAKRRNTTGTGRMRHLKIV YRRFRAWDFREGTTPKPK*GSL LQH SSSS |
| 1722 | 7219 | A | 1852 | 41 | 544 | APSPRPWGHFTEED\KATNTSLWG K\VNVEDAGGETPGKGS LVVP\W TQRFDSFGNLSSAF\AHHGQTPKV KAHGK\KVL T\SLGDAIK\HLDDLKG TFAQA*VNLHL*QSCNVDPENFQA PGEMLLVTR/VLAIHF\GK\EFTPGGC KASWAEDG*LAVGQWPCSSRYH |
| 1723 | 7220 | A | 1853 | 145 | 705 | SWRNRTVSNGSAVSASSVHLCFAE CKALCGERILTDGSDVSRPTIAAGG CNGTVKYLL*QEV LKTAPL\HDGP SHVGIPRSCPKPLDKRQAHL CVLAS \NCDEPTMYVKLVEAL\CAEHQNP *LRVD\DNKKLG\EWG*GLLLKFDR GGGKPRKSWLG\CSCFS*FKDY\GK ESQAKDVIV\EYFKCKK |
| 1724 | 7221 | A | 1854 | 110 | 776 | SLASGPYL\THQQKVLGLYKRALRH LESWCVQRDKY\RYFACLMRARF EEHKK*KRIWAKATQL\KEARGKN FWYPVKHPKSQYILPLTSPLGGHPP Y*EDHD/CA YKVPRIGCL\DWHP E\KAMYP\DYFCQRRQWKENLRR GKA WGTEGLSSLQE\ETPAG\GPL TESFAPWPEKEGDLPPLW\WYIVT RPRERPMLE RERPHLSCLQVKYVT EHGTCP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1725 | 7222 | A | 1855 | 1 | 858 | |
| 1726 | 7223 | A | 1856 | 165 | 856 | PVSYHPRMCTGGCARCLGG\TLISL AFFGFL\ANILLFFPG\GKVIDDNDHL \SQEIW\FFGGILGKRCL**SFPALVF LGA*RNNDCCG\CCGNEGCGKRFA\ MFTSTIFAVGWILGELGYSFIISAISI NKGPNPSMAKK\TWGLPPSNDGD/ YILNDEGLNGTKCREPLQCGFPGN LDPLSSILLGRREGIQMV\LCANQV\ VNGPPWGTLCCGGTCQCCGCCGG\D GPVLNLRA |
| 1727 | 7224 | A | 1857 | 163 | 1322 | PGPYCGPVATMSLHGRRKEIYKYE APWTVYAMNWSVRPDKRFRWALG SFMEEHNNEGYLDGLDEERS*VNS KNILDRPYPTNKVMWIPDTKGVYP DLLATSGDYLRVWRVGETETRLEC LLNNNKN\SDFCAPLTSFDWNEVDP YLLGTSSIDTTCTIWGLETGQVLGR LNL\VSGHVKTQLIAHDK\EVYDIAF SRAGGGRDMFASVGADGSVRMFD LRHLEHSTIYEDPQHHPLLRLCWT KQDPNYLATMAM\DGMEVILDV RVPCTPVARLNNHRACVNGHLLW\ APHSS\CH\CTAAG*PPGFSSWD\Q QMPRAUEDP\LAYTAE\GEINN\Q\ WA\SNSAPNWESPIC\YNNCPWRYs ECsvGGAVPHEAGAFVFPASAPPPK |
| 1728 | 7225 | A | 1858 | 1 | 420 | REDRIQLWKPPYTDENKKVGLALK DRKNLLETRLHITGRELRSKIAETFG LQENYIKIVINKKQLQLGKTL EEQG VAHNVKAMVLELKQSEEDARKNF QLEEEEQNEAKLKEKQIQRTYRGL* ILAKRAAETVVDPEMTP |
| 1729 | 7226 | C | 1859 | 28 | 156 | MMYRLMSILTRHVSSLKSYILIHQK WTICCSWGLLPRKPGLV* |
| 1730 | 7227 | A | 1860 | 1 | 315 | |
| 1731 | 7228 | A | 1861 | 1 | 119 | |
| 1732 | 7229 | A | 1862 | 1 | 1477 | |
| 1733 | 7230 | A | 1863 | 3 | 1866 | PLQSGHSAGRGGSGVAQGW HKKK YLQAKM\TKFLREERIQLWKPPYTD ENKKVGLALKDLAKQYSDRLECCE NEVEKVIEEIRCKAIERGTGNDNYR TTGIATIEVFLPRLKK\DRKNLLET RLHITGRELRSKIAETFG LQENYIKI VINKKQLQLGKTL EEQGV AHNVKA MVLELKQSEEDARKNFQLEEEEQN EAKLKEKQIQRTKRGLEILAKRAAE TVVDPEMTPYLDIANQTGRSIRIPPS ERKALMLAMGYHEKGRAFLKRKE YGIALPCLLDADKYFCECCRELLDT VDNYAVLQLDIVWCYFRLEQLECL DDAEKKNLAQKCFKNCYGENHQ RLVHIKGNCGKEKVLFLRLYLQGI RNYHSGNDVEAYEYLN\RHVSSLKS YILIHQKWTICCSWGLLPRKHRLGL RACDGNVDHAATHITNRREELAQIR KEEKEKKRRRLENIRFLKGMGYST HAGQ\QILLSNPQMWWLNDSPET |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DNRQESS\SQENIDRLVYMGFDALV VAEPALRVFRGNVQLAAQTLAHNG GSLPPELPLSPEDSLSPPATSPSDSAG TSSASTDEDMETEAVNEILEDIPEHE EDYLDSTLEDEEHIAEYLSYVENRK SATKKN |
| 1734 | 7231 | A | 1864 | 1 | 727 | MVVWDADTQQVIPNGIQLAGLDKS HSGFALAPPTTLFPSGGGGGGGAKAT AAAGAGLASPGMKTNGGRCRIRAL CWSRREWRGAGEDTAAECPRPQPQ QHCLAPRFPVRLGTSPGQGWSGRG AGDLAKQYSDRLECCENEVEKVIEE IRCKAIERGTGNDNYRTTGIATIEVF LPPRLKKDRKNLLETRLHITGRELR SKIAETFGLOENYIKIVINKKQLQLG KTLEEQGVAHNVKAMVLELKQSE EDARKNFQL\QEEEQNEAKLIEERL QRTKRGLAEILAKRAAEPPVVPPEMT PYLDIANQTGRSIRIPPSERKALMLA MGYHEKGRAFLKRKEYGIALPCLL\ DADKYFCECCRELLDTVDNYAVLQ LDIVWCYFRLEQLECLDDAEKKLN LAQKCFKNCYGENHQRLVHIKGNC GKEKVLFLRLYLLQGIRNYHSGND VEAYEYLN\RHVSSLKSYILIHQKW TICCSWGLLPRKHRLGLRACDGNV DHAATHITNRREELAQIRKEEKEKK RRLENIRFLKGMGYSTHAAQQVL HAASGNLDEALKILLSNPQMWWLN DSNPETDNRQESPSQENIDRLVYMG FDALVA\EAALRVFRGKVPVAAQT PAYNGGSL/PFPELPLS\AEDSLSPAT \SPSDSAGTSSA\STDEDMETEAVNE ILEDIPEHEEDYLDSTLEDEEHIAEY LSYVENRKSSN*RCRIRALCWSRRE WRGAGEDTAAECPRPQPQQHCLAP RFPVRLGTSPGQGWSGRGAGDLAK QYSDRLECCENEVEKVIEEIRCKAIE RGTGNDNYRTTGIATIEVFPPRLK KDRKNLLETRLHITGRELRSKIAETF GLQENYIKIVINKKQLQLGKTLEEQ GVAHNVKADGCLN |
| 1735 | 7232 | A | 1865 | 1 | 513 | PRVRNLSREWLCDRHLREKMFSSV AHLARANPFDTPHLQLVHDGLGD LRSSSPGPTGQPRRPNLAAA AVEE QYSCDYGSGRFFILCGLGGIISCGTT HT\ALVPLD\LVKCRMKV\DPQKYK GIFNG\FSVTLKEDGVRGLAKGWAP TFL\GYSMQGLLQVLAIFYEVFKVLY |
| 1736 | 7233 | A | 1866 | 2 | 1296 | ALCEPQPFQSGGCVAILGRKMFSS VAHLARANPFNTPHLQLVHDGLGD LRSSSPGPTGKPRRPSQ/HMAAAPV EEQYSCDYGSGRFFILCGLGGIISCG TTHTALVPLDLVK\CRMQVDPQKY KGIFNGFSVTLKEDGV\RLAKGW APTFLGYSMQGLCKFGFYEVFKSL\ YSNMLGEVENTYL*RTSLYLAASAS\ AEFFADIALAPMEAAKVRIQTQPG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YANT*EGISFPKCIKEEGLTSILQGG LLPLWMRQIPYTMN*SSPCLERTVE A\LYKFV\VPK\PRRE*FKRQSRLVVT IW*QVTIARVFCANCFSPLPEFLG*P VLD*GKKVSQCFLWVLQRDLGFK\ GV\WKGLFA\RI\NIGTLT\ALQWFI YYSVKGYFR\LPRPPPEMQES\LK KKLGVNSVVRIKANCGLNLLVDPV FEESAKGTFIYLTV |
| 1737 | 7234 | A | 1867 | 127 | 433 | RPLESWIGLVRCNICRSPIAEAVFRK LVTQDNISKNNWRVDSAATSGYEIG NPPDYRGQSCMKRHGIPMSHVARQ \DLNRKSNRVKTCKAKIELLGSYDP QKQL |
| 1738 | 7235 | A | 1868 | 2 | 535 | |
| 1739 | 7236 | A | 1869 | 551 | 1299 | PADPPRPSYYRHRTPPQAHWSRLRR SRLRRRGSHTRCPVGVGAGLRRRA GARLAVRLRASACGTPRCLGASAR GKMAEQATKSVLFVCLGNICRSPIA EAVFRKLVTQDNISKNNWEGRQRG NFRWVIDSGAVSDWNVGRSPDPRA VSCLRNHGIHTAHKARQIT\KEVFP TFDYILCMDES\NLRDLNRKSNRVK TCKS*KFELPWEL*SPQKQLIED\PY YGE*LWTLETVYQQ\CVRICCRAFL\ EKAH |
| 1740 | 7237 | A | 1870 | 85 | 563 | SSF\DIVHVCNTPNVKKMVSGSSHK VIEQDLSIGDHPVTPVQSVYCKRS PKIPKIFVKVSKTNSETQIYLGWQV KIGFPNF*NPVAGILDRTKYRIFP*AP GIHKLKGYPREI*ASYV*KSPSTSMS TAALFPIAKPRAGP*MPTKGSWVK\ KIWYGQK |
| 1741 | 7238 | C | 1871 | 604 | 804 | MKRLRLRLRXINNLAKITQPLSKTAL NLSPTQGGSKSRAILEFQLSRPGVPN PTLNWPSLNPFREPE* |
| 1742 | 7239 | A | 1872 | 64 | 73 | AFL*RWGSPCCPRAGLK/PP*P/PSI CPRPPKPAGITRREPPGQAYFLII*F PSI*L |
| 1743 | 7240 | A | 1873 | 47 | 225 | NSHHVRGRPRCADSSSPSGDRGQPE AQPAPDSSAPEHAQEPGRAAVKRP DL*SHMTRRP |
| 1744 | 7241 | C | 1874 | 101 | 232 | MTMITPSSKLT\TKGNKSWSSSTAVA AALELVDPGCRNSARGF* |
| 1745 | 7242 | A | 1875 | 66 | 723 | AILIILLSSEGLWSSDQHRLVGVQDS PPQGLCCHFSAMATSEQSICQARA SVMVYDDTSKKWVPIKPG\QQGFSR INIYHNTASNTFRVVGVKFQDQQV VINYSIVKGMKYNQATPPFPQWRD ARQVYGLNFASKEEATTFSNAMLF ALNIMNSQEGGPSSQRQVQNGPSPD EMDIQRRQVMEQHQQQRQEFLERR TSATGPILPPGHPSSAASAPVSCSGP SPPPPPPVPPPTGA\TPPPPPPL\PAG GAQGSSHDES/SPCSGLAACH*LGPS LRRVPNGPEDASGGSSPSGTSKSDA NRASSGGGGGGLMEEMNKLLAKR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RKAASQSDKPAEKKEDESQMEDPS TSPSPGTRAASQPPNSSK\AGRKPW DRNNPLRNPLSSNLVRNPLLAKGPR KLRAPFSQQPHSRMKPAGS\VSDMA \LDAFDLD\RMKQEI*KEVVRELHK GERKEIID\AIRQEA*SGISRKKNLGH RAHPPTRTSFICSQRPRLM |
| 1746 | 7243 | A | 1876 | 1 | 668 | GERGVARHDRPRGTLREYKVVGRC LPTPK\CHTPPL\YR\MRIFAP*SMSSL SPRF\WYFVSQKKDEESLQWRFSY CAQVFEKSP\LRVK\NFGIWLRYDS RSG\THNMY\REY\RDLDHPQAPVHP SCLTRDNGVAPAPAA/HEAHFHFRFI ERLEENAGQQDCRRPGCSKQFPRIS RFKFPAAAPGSLRRQDKPRFTTKRP KTLKVQGPSSGVCQNKQTQETPR |
| 1747 | 7244 | A | 1877 | 1 | 1059 | |
| 1748 | 7245 | A | 1878 | 87 | 260 | |
| 1749 | 7246 | A | 1879 | 1 | 1254 | |
| 1750 | 7247 | A | 1880 | 160 | 615 | PSLNTYVTSPLSENFSAARYRNHSND LTCVHTELQNKTKLTVLEGDILDEP FLKRACQ\DVSV\IHTACIIDVFGVIT HRESIMNVNVKGRVAWGGDKARW GNEDQKEGQEGKRSLSIEHLLCSGP SDFADHYQLGELKAAIFS FIDEKTRT EQ |
| 1751 | 7248 | A | 1881 | 53 | 1338 | CPLQGHPRVTLES DLLPSIFCFLVSD SCYFGLATMGWSCLVTGAGGLLGQ RIVRLLVEEKELKEIRALDKAFRPEL REEFSKLQNK\TKLTVLEGDILDEPF LKESLARDRLRSIIHTACFHLMSFGV \THREFF\MNVQC*KVPSSC*EACVQ ASVPVFIYTSSIEVAGPNSYKEIIQNG HEEEPLENTWPAPYPRSKKLA\KKA VLAANGWNLK\NGGALYTCALRPM YIYGEGSRFLSVSINEALNNGILSS VGKFST\NPNVYV\GNVAWGHILAL RALQDPKKAPSIRGQFYISDDTPH QSYDNLNYTL\SKE\FGPPPLDSRWAS FPLSLMYWIGFLLGNR*GFL\LRPIY TYRPPFNRISSHCSN*ALFHLLFIKE GFSEILGVLRLPLTAGGGKAKAGKR VGSWVWVPFVDPAQGRNLEVPRIQ |
| 1752 | 7249 | A | 1882 | 3 | 575 | HSLFGTSEVINKLLVPDA\MGHFTTE DKATITSLWGK\VNVEDAGGEVTP GKGSLLVYP\WTQRF\FD\SFGNLSS ASA\MGKPPKSKAHG\KKVLTFLGT MPTKHLE*FSRGTF\CP\SLK*TCTC*Q ACMWDPGGTFKLPGENVAGLTVFG QSHFRQKNFTPEGARFFLGRKMGD LELASALVPSRLPLKPLGP |
| 1753 | 7250 | A | 1883 | 1 | 960 | GRPAPEDGGPLSLPNAAMARGPKK HLKRVAAPKHWM LDKLTGVFAPR PSTGPHKL\RECLPFIF\LRNRLKYA LTSDEVKKICMQRFIK\DGQVR\TD ITYPAGFMDVISIDKDGREFSVL/Y LIDTQGVRFCL*HRITP*GRAKVQSC AKMRKILLWAPKGIPSSWVT\HDAR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NHPATPDPPSSKVN*YHFRLDLETG KDYLISSKFDTW*PCVMVTGGAN LGRNWVLITNRERHPGIF*PLVHVK DANGNKLLATSDFSNIFWLLGKGN KPWISLAPRGKGIPPHLLEERDKRL AAKQSSWVKWGPWVTWSDLLVP |
| 1754 | 7251 | A | 1884 | 1 | 1218 | FFQNSARGAGAGWQLPWTRFVWT SGLLEINE\TLVIQQRGVRIYDGEEKI KFDAGTLLLSTHRLIWRDQKNHEC CMAILLSQIVFIEEQA\AGIGKSAKI VVHL\HPAPPNKEPGP\FQSSKNSYI KLSFKEHGQIEFYRRLSEEMTQRRW ENMPVSQSLQTNRGPPQGRIRAVGI VGTERKLEEKRKETDKNISEAFEDL SKLMIKAKEMVELSKSIANKIKDKQ GDITEDETIRFKSYL\LSMGIANPVT RETYGSGTQYHMAQLAKQLAWNIA RVPLEERGGIMSLTEVYCLVNRARG MELLSPEDLVNACKMLEALKLPLR LRVFDSGVMVIELQSHKEEEMVAS ALETVSEMGLTS*EFAKLVGMSVL LAKERLLLAEKMGHLCRDDSVGL RFYPNLFMTQS |
| 1755 | 7252 | C | 1885 | 179 | 361 | MPKVCFVHNFLKTSSERDLFALMN TVGKKHSIMSEKGRSKKFLHLIDSK KNEDPHLDGTL* |
| 1756 | 7253 | A | 1886 | 2 | 913 | RRLLLFGWARSGAVSLGSAGVSSS GFLTAPHSRRLTAAAAAAGGAWRF EAERHRGWGAEEEEQQPEGGA\CPG TERPCAMAYAYLFKYIIIGDTGGGR\ SCLLLQFTDKRFQPSAMTLTNGVEF GARMITIDGKQIKLQIWDTAGQES\ FRSITR\SYR\GAAGALLVYDITR\R DTSTHLTTWLEDA\RQHSHFQHGS LCLLGNKSDL\ESRKE/VSKKRKEGE SFLQPRNHGLHLPWKTSCKNCFPM* KEAFINTSKRNFIEKIQ\EGVFDINNE A\NGIKIGP\QHAATNATHAG\NQQG QQAGGGCC |
| 1757 | 7254 | A | 1893 | 138 | 426 | FIHSHCCIVFRLFIHFSLHPKVIHSPIN SLLRIFQF*AIMNSTV*NILIHVFW*V YTFFPAGINPKKGIARL*GVYIFSFSIY CQTVFQSDCKKAPF |
| 1758 | 7255 | A | 1894 | 45 | 1057 | FLVFLVETGFHHVAQAVLELLASSD PPALAPPKCWDYRCELLRLAEFCFL RTEFWYLLFFFFWRRSLALSPRLEC SGANL\THCNLR/LPGFKQFSCLSLSS SWDYRCMPPHLATFFVF/SVETGFH RVAQASLELLSSGSLPALA\FPKC\W DYRAKATV/WSPGVSSFILGL*TS* FHSLEPYLHAWKTTSHLPTKEALT W/VSHATAKHLWILVSILMEF*VA LIS/SFFLGPGGK*T*VTAPQCPSLGQ DTLS*FLHAACRSVPYPGLA/CGPS LWLTRVLLPTPP*QQHNP/DTLEKT SFPGPHWIL*/TQPSLSETPAPKVPP FPAFGSIPTHEEGLP |
| 1759 | 7256 | A | 1895 | 2 | 289 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1760 | 7257 | A | 1896 | 1 | 397 | |
| 1761 | 7258 | A | 1897 | 1 | 410 | STMISPVLLIFSSFLCHVAIAGRTCPK PDDLFPSTVVPLKTFYEPGEEITYSC KPGYVSRGGM\RKFCPLTGLWPIN TLKCTPRVCPFAGNLRKMGA\RLIT DFLNYSPTRFSSLLTWGFILEWAL DS\AKCIEGG |
| 1762 | 7259 | A | 1898 | 19 | 1215 | CQCDSSSTMIFSRCSLSSFLCHVAI AGRTCPKPDDLFPSTVVPLKTFYEP G\EEITYSCKPGYVSRGGIEESLSCPL VTGTVGPFNTSGNVT\PRVCPFAGIFR KMGGRTLITTF*NYPNTDPVFSLLTL GF*FWNGALDFWPSCTGGKGKWS P\ELPGLVAPI\CP\APSIP/TGFATLH VLLRPFRLGNNSPPIGDTAVFECLA HNMAMFG\NDTIT\CTTHGKLDLNY PECRGSKMPPFPHQDPDNGIW* TYP CQNPNTLFTRVKAPHLGLPHDGIFS GMGPRKE\EC*PQTWGKPGSWPLA PSW*KPSLVKGT\PKRPTVV/YPQ GERVKDSREKFKEWECLHG**KFLS FCKNKEKKCSYTEDAQCIDGTIEVP KCFK\EHSSLAFWKT\DA\DVKPC |
| 1763 | 7260 | A | 1899 | 58 | 446 | |
| 1764 | 7261 | A | 1900 | 1 | 954 | MGEVSGTSDCTDDQCRQVKKALEG GKAARGHRSKIKIRFFRPGGLGPGP AITAVAGMPRVYIGRLSYQAREHA VERLLNGHAKILEVDLKNYGFVE FDDLRLDADDAVYELNGKDLGGERV IVEHARGPRRDGSYGSGRSGYGYR RSGRDKYGPPTRTEDRLIVEN\LTR CSWQDLKDYM\QAGEVTYADAHK GRQKMKGVIEFVSYS\DMKRALEKL DGTEVNGRKIRLVEDKPGSRRRRSY SRSR\SHSRSRSRSRHSRKSRSRSGSS KSSH\SKSRSRSRSGSRSRSKSRSRSQ SRSRSKKEKSRSPSKDKSRSRSHSA\ GKSRSKSKDQAE\EFQNN\DNV\GK PKSRSPSRHKS\SKSRSRSQERRVEE GRKRGSF*QGQ/EAQEKSLRQSRSR\ SRSKAGSR*PVDRSRSKSKDKRKS RKSREESRSR\SRSRSKSERSRKRGS KRDSKAS\CKKKKKEDTDRSQSR PSRSV\SKEREHA/RSLESSQREGRG ESENAGTNQEDPGPGPRSN\SKSKP NLPIRMHR\SKIKSQASKTPISGPMSR SR\ASRSPSRSRSKSRSRSQSRSR KKEKSRSPSKDKSLQPQP |
| 1765 | 7262 | A | 1901 | 3 | 180 | |
| 1766 | 7263 | A | 1902 | 227 | 440 | GMHNV\CYVAVNE*FCGFIR*SLAE RRQIS*EFQLFKFTLCLELILARRAC RESMA\$PVAGSWSHFPEREF |
| 1767 | 7264 | A | 1903 | 2 | 438 | HEELDTSERKIEFDSASGTYTLYLN GDAHFEEPQSLWNVADLVHQSPPE EKAPLDLSCPQNLFTPK\QEIQWIRI GA\NVSNFTFAPSTIIFHLGHAVAM LGLMYVYWTQLNMFQTLKYLAIL GSVTFLAGNRMLAQQA\VKRTAH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1768 | 7265 | A | 1904 | 1 | 1660 | |
| 1769 | 7266 | A | 1905 | 156 | 2369 | PVLKTHPGPQSLPRVPGVPCGGLLE PLSRAEVSPRFGLRRDLLGGMAPPG SSTVFLALTIASTWALTPHYLTK HDVERLKASLDRPFTNLESAFYISV GLSSLGAQVPDAKKACTYIRSNLDP SNVDSLIFYAAQAISQGLSGCEISISN ETKDLLLA\AVSE\SSVYPRSYHAS WQL*SGLLGLSLWAVPKESTQVAL NWL VFKQKGKTVL\ATVQALQTAS HLSQQADLR SIVEEIEDLVARLDEL GGLYLQ\FEEGLETTAL\FVAATYKA \LMDH\VGTE\PSIKEDQVIQLMNAI FSKKNFES\LSEAFSVAASGVAAVLS HNRYPVPPVVVPEGSASDTHEQAI LRLQVTNVLSQPLTQATVKLEHAK SVASRATVLQKTSFTPVGIVFELNF MNVKFSGG*CDFLVEVEGDNRYIS\ NTVELRVQDPPTVEGITNVDLSTV\ DKDQSIAPQTTTRVTYPAKAKGTFH SAGQATRNFGLVLSSW*DVNTGAE LTPHQTFVRLHNQKTGPGSGCLFAE PGQQGTCYKFELDTSERKGLNLTSR SGTYTLYLIIG*CQL*RTQILWKCGL MWVVKFP*GKEASFDCLCSQEPFSL PKQGNFRHLFPGRP*GRRAPPPWCP NTFTAPESFFGPLL/LCFLRLLWIRD WVPKCLPTFTFCFLSTIIFHPWDML AYAGTSMYVY*TQAQPCSQTLEVP WPILGQCDRFLAGQSGMLAPARQV KRIAAEQSSRLAKYRTLRTAH |
| 1770 | 7267 | A | 1906 | 37 | 404 | PQLSRCRSECMYVNPTVVMTSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPVAVPCALGRGGRER WAAASFLYAPDPRPAHEVEHVVN AILFLLSDRSGMTTGSTLPVEGGFW AC |
| 1771 | 7268 | A | 1907 | 271 | 1086 | YTQCPGIEPVCVDLGDWEATERAL GSVGPVDLLVNNAAVALLQPFLEV TKEAFDR*ACEGGGTSGRGCPGGRS SPNL*PGSVPRPLDPLRVNLRAVIQV SQIVA\RGLIARGVPTGPS*NVSSQC FPAGQ*TNHSVLLLPTKGVPLDMLD QG*WAL\ELGPHKLSRCRSGVNA\V NPHSGG*RSMGPGPPWSDPHKAKI MLNRIPLGKFAGESEVEHVVNAIL FLLSDRSGMTTGSTLPVEGGFWAW LSSLHTPQAPWACFILTPNPSNKT |
| 1772 | 7269 | A | 1908 | 2 | 305 | ARESGSLVAPRSRPPWEHGLPGEHS *DAPRPHKSPTLPWLPHLHLSKEAL DTHQRSQHEECMPYKFTPTSEKR PQLMLPLPEQQCEQLCRFGSTPVTW A |
| 1773 | 7270 | A | 1909 | 2 | 529 | GTVAACGACYWLLGLMAVRASFE NNCEIGCFAKLTNTYCLVAIGGSEN FYSVFEGELSDTIPVVHASIAGCRIIG RMCVGTEEILADV LKVEVFRQTVA DQVLVGSYCVFSNQGGLVHPKTSIE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DQDELSSLLQVPLVAGTVNRGSEVI AAGMVVNDWCAFCGLDTTSTELSV VE |
| 1774 | 7271 | A | 1910 | 18 | 889 | GVQGTVAACGACYWLLGLMAVRA SFENN\CEIGCFAKLTNTYCLVAIGG SENFYSVFEGELSDTIPVVHASIAG CR\IGRMCVGN\RHGLL\VPNNTTD Q\EL\QHISATGLPRHSGRFRAGWKE RFLSLWGNFFNHLAIDYVGLGSNQ D\LDKGRQEEISGQMLFKGWEVFRQ TV\ADQVLVES\YCVFSNPGRWVP SPRPFQ*RPRNELSSISFKVPLVAGT C*TKGSEVICLLGMGGEMNWCA\FC GPGTPNPAQSCQVVEECLQS*NEAP ALAPIANRACGNSL\IDSLT |
| 1775 | 7272 | A | 1911 | 132 | 440 | |
| 1776 | 7273 | A | 1912 | 149 | 389 | FSWV*REIFSFLISLIFIYETFSKLIKIF QDHPLQKTYNYNVLMVMPKPQGGLP NTALLSLVLMAGTFFFAMMLRKFK NSS |
| 1777 | 7274 | A | 1913 | 3 | 153 | |
| 1778 | 7275 | A | 1914 | 94 | 593 | LVVFSSPSQSWERTECLGFLQIFQD HPLQKTYNYNVLMVMPKPQGGLPNT ALLSLVLMAGTFFFAMMLRKFKNS SYFPGKLRRVIGDFGVPIILIMVLV DFFIQDTYTQKLSVPDGFKVSNSA RGWV\HPLGLRSEFPIWMMFASAL PALLVFILIFLESQITT |
| 1779 | 7276 | A | 1915 | 115 | 3015 | TTGHSGPRHGGAAGGCSLASAVLP PGSGDLVLDLYLRWGKSPSQPS LSGHFPQDDYEDMMEENLEQEEYE DPDIPESQMEEPAAHDTEATATDYH TTSHPGTHKVYVELQELVID\ERIPD LQWMEAAPLR\QLDENLGENGAW GRPHLSHLTFWSLLELRRVFTKGT LLDLQETSLAGVANQLLDRFIFEDQI RPQDREELLRALLKHSHAGELEAL GGVKPAVLTRSGDPSQPLLQHSSL ETQLFCEQGDGGTEGHSPSGILEKSP PDSEATLVLVGRADFLEQPVLGFR LQEAEELEAVELVPPIRFLVLLGPE APHIDYTQLGRAAAATLMSEVFRID AYMAQSRGELLHSLEGFLDCSLVLP PTDAPSEQALLSLVPVQRELLRRRY QSSPAKPDSSFYKGLDLNGGPDDPL QQTGQLFGGLVRDIRRRYPYYLSDI TDAFSPQVLA AVIFIYFAALSPAITF GGLLGEKTRNQMGVSELLISTAVQ GILFALLGAQPLL VVGFSGPLLVFEE AFFSFCETNGL\EYIVGRVWIGFWLI LLVVLVVALRGVASLVRFISRYTQ EIFSFLISLIFIYETFSKLIKIFQDHPL QKTYNYNVLMVMPKPQGGLPNTALL SLVLMAGTFFFAMMLRKFKNSSYF PGKLRRVIGDFGVPIILIMVLVDFF IQDTYTQKTSQVPDGFKVSNSARG WVIHPLGLRSEFPIWMMFASALPC LLVFILIFLESQITTLIVSKPERKMK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GSGFHLDLLLVVGMGGVAALFGMP WLSATTVRSVTHANALTMGKAST PGAAVAQIQEVKAEQRISGLLVAVLV GLSILMEPILSRIPAVLFGIFLYMGV TSLSGIQLFDRILLFKPPKYHPDVP YVKRVKTWRMHLFTGIQIICLAVL WVVKSTPASLALPFVLILTVP LRRV LLPLIFRNVELOCLDADDAKATFDE EEGRDEYDEVAMPV |
| 1780 | 7277 | C | 1916 | 20 | 202 | MAAIKYLGISAILYYKYKCPRGQGN QPEELGTGSILCGNFSLGMLFPVQM YTVKKA YRAV* |
| 1781 | 7278 | A | 1917 | 1 | 493 | |
| 1782 | 7279 | A | 1918 | 214 | 612 | |
| 1783 | 7280 | A | 1919 | 287 | 847 | SDRPTMAPGVARGPTYWRLR\LG GAALLLLIPVAAAQEPPGAACSQN TNKTCEECLKNVSLWCNTNKACL DYPDTSVLPPASLCKLSSARWGVC WVNFDAIITMSVVG GTLLLGIA\NC CCCCRRKRSRKPDRSEEKAMR\ER EDR\WILQEERRAEMNTRHDEIRKK\Y YGLFKEENPYARFENN |
| 1784 | 7281 | A | 1920 | 61 | 515 | |
| 1785 | 7282 | A | 1921 | 1 | 2175 | |
| 1786 | 7283 | A | 1922 | 3159 | 3441 | |
| 1787 | 7284 | A | 1923 | 36 | 387 | |
| 1788 | 7285 | A | 1924 | 64 | 408 | |
| 1789 | 7286 | A | 1925 | 1 | 10514 | |
| 1790 | 7287 | A | 1926 | 64 | 601 | VNNILGLGHTFWALLASPKMEHKE VVL LLLFLKSGQGEPLDDYVNTQ GPSLFSVTKKQLGAGSREECAAKCE EDKEFPAGAFQYHSKEQQCVIMA ENRKSS\INRVRDAVLFGKGKCILF RVQDLGMERTTEGRCPKQKMASPC QKWEFHFPADLGQTFPFIFVFIYCK VVPLCL |
| 1791 | 7288 | A | 1927 | 173 | 491 | AGEARWESQSAHLKPEFGGPTGPN NAQSPPREADAQQVWREPPGPASK APHSPVGYSSPGHESHLPGDDPA KDGSCPP\PFPLGIEAPVPGPRKRIR TCCCMN |
| 1792 | 7289 | A | 1928 | 1 | 735 | |
| 1793 | 7290 | B | 1929 | 1 | 1026 | MRARRLPWALT\VAELGWD\TQGG DQTSPGGNDRMSMEAECSTTVSP LSCSIPTGCGQTREEVSARATPPPSL GASLLQTLTPDTHCTGVSATIMSML VVFLLLWPFSSSTLAKHKRIHTGE KPYKCEECKGAFSRSSSTLAKHKRIH TGEKPYKCKECKGAFRQSSTLTKH KJIHTEEKPYKCKECKDAFKRLSTL AKHKI\IHAGEKLYKCEECKGAFNRS SNLTIHKFIHTGEKPYKCEECKGAF NWSSSLTKHKRIHTREKPFKCKECKG KAFIWSSTLTRHKRIHTGEKPYKCE ECKGAFSRSSSTLTKHKTIHTGEKPY KCKECKGKLLSTPQPLLN\IK* |
| 1794 | 7291 | A | 1930 | 1 | 2832 | |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1795 | 7292 | A | 1931 | 98 | 3867 | PAGIGRATAKMPGTPGSLEMGLLTF RDVAIEFSPEEWQCLDTAQQNLYR NVMLENYRNLAFLGIALSKPDLITY LEQGKEPWNMKQHEMVDEPTGICP HFPQDFWPEQSMEDSFQKVLLRKY EKCGHENLQLRKGCKSVDECKVHK EGYNKLNQCLTTAQSKVFQCGKYL KVFYKFLNSNRHTIRHTGKKCFKCK KCVKSFCIRLHK\TQHKCVYTEKSC KCKECEKTLWSSTLTNHKEIHTED KPYKCEECGKAFKQLSTLTTHKIIC AKEKIYKCEECGKAFLWSSTLTRHK RIHTGEKPYKCEECGKAFFSHSSTLA KHKRIHTGEKPYKCEECGKAFFSHS ALAKHKRIHTGEKPYKCKECCGKAF SNSSTLANHKITHTEEKPYKCKECD KTFKRLSTLTCHKIHHAGEKLYKCE ECGKAFFNRSSNLTIHKFIHTGEKPY KCEECGKAFFNWSSSLTKHKRFHTR EKPFKCKECCGKGFIWSSTLTRHKRI HTGEKPYKCEECGKAFFQSSTLTKH KIIHTGEKPYKFEECGKAFFQSSTLN KHKIHSREKPYKCKECCGKAFFQFS TLTTHKIIHAGKKLYKCEECGKAFFN HSSSLSTHKIHTGEKSYKCEECGKA FLWSSTLRRHKRIHTGEKPYKCEE CGKAFFSHSS\ALAKHKRIHTGEKPY KCKECCGKAFFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTCHKIHH AGEKLYKCEECGKAFFNRSSNLTIHK FIHTGEKPYKCEECGKAFFNWSSSLT KHKRIHTREKPFKCKECCGKAFFWSS TLTRHKRIHTGEKPYKCEECGKAFFS RSSTLTCHKTIHTGEKPYKCKECCGK AFKHSSALAKHKIHHAGEKLYKCEE CGKAFFNQSSNLTIHKIHTKEKPSKS EECDKAFFWSSTLTEHKRIHTREKPY KCEECGKAFFSQPSHLTTHKRMHT GEKPYKCEECGKAFFSQSSTLTTHKII HTGEKPYKCEECGKAFFRSSTLTEH KIIHTGEKPYKCEECGKAFFSQSSTLT RHTRMHTGEKPYKCEECGKAFFNRS SKLTTHKIIHTGEKPYKCEECGKAFFI SSSTLNGHKRIHTREKPYKCEGCG\ KAFFSQSFN/TLTGHKRLHTGEKPYK CGECGKAFFKESSALTKHKIHTGEK PYKCEKCKAFFNQSSSLTNHKKIHT ITPKIHTREKPYKYKECCGKSFNRSST FTKHKVIHTGVKLYKCEECGKSFF WSSALTRHKIHTGQQPYKQEKFG KAFFNQFSHLTTR |
| 1796 | 7293 | A | 1932 | 590 | 891 | |
| 1797 | 7294 | A | 1933 | 1 | 1527 | |
| 1798 | 7295 | A | 1934 | 13 | 1668 | PESKMAGSRHRGLRARVRPLFCAL LLSLGRFVRGDGVGGDPAVALPHR RFEYKYSFLAGPHLVQSDGTVPFWA HAG\AISSSDQIRVAPSLKSQRGSV WTKTK\AAFENWEVEVTFRVTGRG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RIGADGLAIWYAENQGLEGPVFGS ADLWNGVGIFDSDNDGKKNPA IVIIGNNGQIHVDHNDGASQALAS CQRDFRNKPYPVARAKITY\YQNTL\ TVMINNGVFTPDKNDEYFCAKVEN MIIPAQGYFGISAATGGLADDHDVL SFLTFLTEPGKEPPTPDKEISEKEK EKYQEEFEHFQQELDKKKEEFQKG HPDL\QWQPAEEIFESVRDRELRLQ VFEGQNRHLEIKQLNRQLDMILDE QRRYVSSLTEEISKRGAGMPGQHG QITQQELDTVVKTQHEILRQVNEM KNSMS\EPVRLVSGMQHPGS\AGGV YG\TTQHFID\KEHLH\VKR\IDIDL VQRNMP\SNEKPKCELPFPSCSLST VHFQ\IFVVVQTVLFIGYIMYRSQQ EAAAKKILLTTIFLCTSSICVQNDVV LREFKYLNCFIV |
| 1799 | 7296 | C | 1935 | 238 | 360 | MGGLGLSLRSLSSASPAXFRPAHAP VGAAGLGPASPQGGL* |
| 1800 | 7297 | A | 1936 | 1 | 1656 | |
| 1801 | 7298 | A | 1937 | 83 | 260 | |
| 1802 | 7299 | A | 1938 | 1 | 678 | |
| 1803 | 7300 | A | 1939 | 1 | 1097 | |
| 1804 | 7301 | A | 1940 | 1 | 1706 | MQLLLAECMGQSGPPGAVCHCQR VWQARAVRRSKRPVPSTTQGLKSV GAWRGSGRQLHLQPQYRIHWVKP AGLLSLVGTMENICVWPSDCKYTN RHSVSSSRLLDSLKRDIYAGKPQPI KSERRNPPSYAMAAAQLRDSEETG GSEFVFAEKTLRKCVKCPQVELENV AFAKDAEESRDAQRLGHWPCIME TLNASGTFAIRLLKILCQDNPSHN FCSPVSISSALAMVLLGAKGNTATQ MAQALSLNTEEDIHRAFQSLLTEVN KAGTQYLLRTANRLFGEKTCQFLST FKESCLQFYHAELKELSFIRAAEESR KHINTWV\SKKTEGKIEELLPGSSID AETRLVLVNAIYFKGKWNEPDET YTREMPFKINQEEQRPVQMMYQE ATFKLA\HVGGLRAQLLELPYARK ELSL\VLLPDDGVELSTVEKSLTFE KLTAWTKPDCMKSTEVEVLLPKFK LQEDYDMESVLRHLGIVDAFQQGK ADLSAMSAERDLCLSKFVHKSFE VNEEGTEAAAASSL\WVVAECCME SGPRFCADHPFLFFIRHDRANSILFC GRFSSP |
| 1805 | 7302 | A | 1941 | 3 | 428 | ETLERIKNDPKLEEVNLNNIRKIPI TLKAYAEALKENSIVKKFSIVGTRS NDPVAYALAEMLENKELKTLNVE SNFISGAGILRPGEALPYNTYLVEM RSDNQSQPPGNKVEMEIVSMLAEKN ATLLRVR*HFSQQDAR |
| 1806 | 7303 | A | 1942 | 1 | 1258 | ALARPLPAGAPRPPASICPPAPVP QPASAPAPQLCVRVLLSTEIQETQTS SSTMSYRRELEKYRDLDEDEILGAL TEEELRTLENELDELDPDNALLPAG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LRQKDQTTKAPTGPFKREELLDHLE KQAKEFKDREDLVPYTGEKRGKV WVPKQKPLDPVLESVTLEPELEEAL ANASDAELCDIAAILGMHTLMSNQ QYYQALSSSSIMNKEGLNSVIKPTQ YKPVPDEEPNSTDVEETLERIKNND PKLEEVNLLNNIRNIPIPTLKAYAEAL KENSIVKKFSIVGTRSGDG\VAAYAL AEMLKENKVLKTLNVESNFISGAWI LRLVEALPYNTSLVEMKIDNQSQPL GNKVEMEIVSMVEKDPHHFLKFGL PPYPSKEPRLR\ASTAM\MTIALVR ERRLAAPDLGPSFPKCRSGV |
| 1807 | 7304 | A | 1943 | 2 | 382 | EIAHQIEEQQMGEIVTEQQT IVTEQQTGQKIQIVTALDHNTQGKQ FILTNHDGSTPSKVILARQDSTPGK\ VFLTPDAAGVNQLFFTPDLSAQ HLQDVIMGAVTCEGCKGFFKRSIRK N |
| 1808 | 7305 | A | 1944 | 240 | 454 | |
| 1809 | 7306 | A | 1945 | 1 | 1851 | |
| 1810 | 7307 | A | 1946 | 128 | 512 | TAPLAAGRRPGDALGPRPLAVGVK GTPWPPPPTRSLVSPPSVSYRRFCAL LTPASGADATVPRLPLVDWGALRE ERLKKADGMWDRDSRRRELSVFG ACALATGRSGERRS*RSQGGVEGSE GRAAAL |
| 1811 | 7308 | A | 1947 | 1 | 705 | |
| 1812 | 7309 | A | 1948 | 124 | 1583 | IMATIEEIAHQIEEQQMGEIVTEQQT GQKIQIVTALDHNTQGKQFILTNHD GSTPSKVILARQDSTPGKVFLTPD AAGVNQLFFTPDLSAQHLQLLTD NSPDQGPKNVFDLCVVC GDKASGR HYGAVTCEGCKGFFKRSIRKNLVYS CRGSKD\CIINKHHRNRCQYCRLQR CIAFGMKQDSVQCERKPIEVSREKS SNCAASTEKIYIRKDLRSPLTATPTF VTDSESTRSTGLLDSGMFMNIHPSG VKTESAVLMTSDKAESCQGDLSL ANVVTSLANLGKTKDLSQNSNEMS MIESLSNDDTSLCEFQEMQTNGDVS RAFDTLAKALNPGESTACQSSVAG MEGSVHLITGDSSINYTEKEGPLLS SHVAFRLTMPSPMPEYLVNHYIGES ASRLFLSMHWALSIPSFQALG\QEK QP*SLVKAYWNEFLTGLAQCWQV MNVATILATFVNCLHNSLQQDAKV IAALIHFTTRAITDL |
| 1813 | 7310 | A | 1949 | 6 | 2028 | KILRTLTPQKYPRTESSLRRESRSHM PTAFLNLSCRSAPQSTRGSRGTVAS APDAGGSRAQKRREIMATIEEIAHPI IEQQMGEIVTEQQTGQKIQIVTALD HKTQGKQVILTNHDGSTPSKVILAR QDSTPGKVFLTPDAAGVNQLFFTT PDLSAQHLQLLTDNSPDQGPKNV DLCVVC GDKASGRHYGAVTCEGC KGFFKRSIRKNLVYSCRGSKDCIIN KHHRNRCQYCRLQRCIAFGMRQDS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VQCERNPLEVSREKSSNCAASTEKI YIRKDLRSPLTATPTFVTDSESTRST GLLDSGMFMNIHPSGVKTESAVLM TSDKAESCQGDLSLANVVTSLANL GKTKDLSQNSNEMSMIESLSNDDTS LCEFQEMQTNGDVSRFDLAKAL NPGESTACQSSVAGMEGSVHLITGD SSINYTDKEGPLLSDSHVAFRLTMP SPMPEYLVNHYIGESASRLLFLSMH WALSIPSFQSGRGKEN\SISLVESLLG IELFTLGLAQCWQVMNVATILATF VNCLHNSLQQDKMSTDRRKLLME HIFKLQEFCSNMVKLCIDGYDYAYL KAIVLFSPDHPSLENMEQIEKFQEK AYVEFQDYITKTYPPDDTYRLSRLLL RLPALRLDGCTITEELFFKGLIGNIR IDSVIPHILKMEPADYNSPIGHSI |
| 1814 | 7311 | C | 1950 | 65 | 286 | MDYCNTFLPSNPETVFGDIMPRVVK PDLGTALSRGFTHEINKTYLSHLKL GSQKTHFWFIISFYAHLTLIYP* |
| 1815 | 7312 | A | 1951 | 15 | 82 | |
| 1816 | 7313 | A | 1952 | 2 | 1934 | CVQAATSLSVGICPLPGPGSPWPY PGVSVNVWIFKQIDDEGDLRLINK EVLGVVVISSKDSVQHQGVSLTME GTVNLQLSAKSVGVFEAFYNSVKA QLRRSVQATGLEERPALPERLQQEG SEEAGGLSGAEALPRRARGSPIQII NSTIEMVKPGKFPSPGKTEIPFEFPLH LKGNKVLVYETYHGVFVNIQYTLRC DMKRSLAKDLTKTCEFIVHSAPQK GKFTSPVDFTITPETLQNVKEHSHQ TEAGQQRAFRFRSALRGGRLTAR ADNSSSNVAQGSQKSGHPCSRPSS VLPQQRQVCRVKRALLPKFLL/RRT SQLNKLCHHAATNGRAGGGELGSR HQKRGAAAGARGDPGQSRP*P*L* KTRGRRGSKSKSVAVP*Q*PRV*GK VCRISYARDATEIQNIQIADGDVCR GLSVPIYMFVPRLFTCPTLETTFNFKV GKWHSPSPHGPMPGRAAQROGLL WVTELRTCPSVPQCQGLPQAIQLR ACCPAAQQNLVKELLCRTGDTPT GSPGACGTSTVTWGNTQTHISVDM GRPQPQVGTDSKAPSTAELPQCGA QHRVPSAHTMPFPPLLTLGKEMVL VCRQDQOGSPISAEESVEKESCLLK EFEVNIIVLLHPDHLITENFPLKLCR I |
| 1817 | 7314 | A | 1953 | 262 | 1274 | ATAGREGKGRGPQPSGEAPLVSLGS RAATSGGCCGELEMGTGLDIKSKR ANKVYHAGEVLGVVVISSKDSVQ HQGVSLTMEGTVNLQLSAKSVGVF EAFYNSVKPIQIINSTIEMVKPGKFP GKTEIPFEFPLHLKGNKVLVYETYH GVFVNIQYTLRC\DMKRSLAKDLT KTCEFIVHSAPQKGKFTSPVDFTIT PETLQNVKERALLPKFLLRRTS\QLN KLCHHAATNGRAGGGELGSR\HQK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RGAAAGARGDVRVCR\SYARDAPE IQN\QIADGDVCRGLSVPIYMFPR LFTCPTLETTNFKVEFEVNIVVLLHP DHLITENFPLKLCRI |
| 1818 | 7315 | A | 1954 | 2 | 236 | DRCLMLKQGSEAWLTSISIEPPAPPV YQAPCQSCPEPPGAHEPSDSPHHTP VHPPPE\TRTPVLPQPRVPPRSM S |
| 1819 | 7316 | A | 1955 | 760 | 925 | HLEYLPTYANSSYS\WPSSVAHTCN PSTLGGRRGGRTGGQEFKTSVANIT KPCLY |
| 1820 | 7317 | A | 1956 | 32 | 487 | SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG |
| 1821 | 7318 | A | 1957 | 41 | 638 | APSPRRPWGHFTEEDQGLLSTSLWG KVNVEKCWKEKTPGKGSLLVYP\ WT\QRFFD\SFGNLSSAFAHHGQTP KVKAHGK\KVLTLGRCCQSTLDD LKGTFQAQLSELHCDKLHVDPENFK LLGNVLVTVL\AIHFGKDFTPGGC RASWQKMGD*SGQCPVLQ\IPLSS L\PMMQSFSRIRLLFLQAITNNKSISA KRSP |
| 1822 | 7319 | A | 1958 | 3 | 227 | |
| 1823 | 7320 | C | 1959 | 171 | 366 | MHTPSVEKPSCGSQLFVYIRKFWKK RNLVKVLNMTTSSVTEDEVPLYPEW CMLWRYPASRPNVRKP* |
| 1824 | 7321 | C | 1960 | 332 | 421 | MEEKIFSQPGMVAPTCNPSTLGGQG RWIT* |
| 1825 | 7322 | A | 1961 | 322 | 1145 | RFSKSPDSDGAQLVSPSGSRTRQQV ELAATPTQCSTLLSPWASDGTGCHG AAGRSSGRLRPTGALRWVPLHFPS PARGDSQARSLPTRAASADSSLPG CGRREVCGSRAPAGG/PPLAPAPPA APVPASAAAQPPAPAWAYEQVWA GRGALRSPSASSGEAADD SYGVVA GRWGRPVDQSR LGTAGEGIAGRES WGSVTSWVLGSHMVKFLV AELGI CETQDWRRGSEGGAGEFGAVAIHC IGTWVADNAVTCPLLNTTQLEIPFG VQFWML |
| 1826 | 7323 | A | 1962 | 30 | 2814 | LPRAKVEGAPRAPSPQDPGVPPRAP SPRSPSPALRALPAPLSPRSPLDEPM ARPRRAREPLL VALLPLAWLAQAG LARAAGSVRLAGGLTLGGLFPVHA RGAAGRACGPLKKEQGVHRLEAM LYALDRVNADPELLPGVRLGARLL DTCSRDTYALEQALS FVQALIRGRG DGDEVGVRCPGGVPPLRPAPPERV VAVVGASASSVSIMVANVLR LFAIP QISYASTAPELSDS\TRYDFFSRVPP DSYQAQAMVDIVRALGWN YVSTL ASEGNYGESGVEAFVQISREAGGVC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | IAQSIKIPREPKPGEFSKVIRRLMETP NARGIIIFANEDDIRRVLEAARQANL TGHFLWVGSDSWGAKTSPILSLEDV AVGAITILPKRASIDGFDQYFMTRSL ENNRRNIWF AEFWEENFNCKLTSSG TQSDSTRKCTGEERIGRDSTYEQE GKVQFVIDAVYAIAHALHSMHQAL CPGHTGLCPAMEPTDGRMLLQYIR AVRFNGSAGTPVMFNENGDAAPGRY DIFQYQATNGSASSGGYQAVGQWA ETLRDVEALQWSGDPHEVPSSLCS LPCGPGERKKMVKGVPCCWHCEA CDGYRFQVDEFTCEACPGDMRPTP NHTGCRPTPVVRLSWSSPWAAPLL LAVLGIVATTTTVVATFVRYNNTPIV RASGRELSYVLLTGIFLIYAITFLMV AEPGAAVCAARRLFLGLGTTLSYSA LLTKTNRIYRIFEQGKRSVTPPPFISP TSQLVITFSLTSLQVVGMIWLGAR PPHSVIDYEEQRTVDPEQARGVLKC DMSDLSLIGCLGYSLLMVTCTVY AIKARGVPETFNEAKPIGFTMYTTCI IWLAFVPIFFGTAQSAEKIYIQTTLT VSLSLASVSLGMLYVPKTYVILFH PEQNVQKRKRSCLKATSTVAAPPKG EDAEAHK |
| 1827 | 7324 | C | 1963 | 334 | 387 | MKCYIYIMTLVLLIV* |
| 1828 | 7325 | A | 1964 | 1 | 489 | |
| 1829 | 7326 | A | 1965 | 152 | 717 | VESIEDVGNHRTDHGADMISIH YEE ENAFILDTLKKQWKGPDILLGMV YDTDDASFKWVDNSNMTFDKWD \QDDEAEDLVDTC AFLHIKTGEWKK GNCEVSSVEGTLCKTAIPYKRK YLS DNHILISALVIASVTILTVLGAIWFL YKKHSDSRFTTVFLTGPQLPAYMEN CVLVVGEENEYPVQFD |
| 1830 | 7327 | A | 1966 | 3 | 614 | LLFFPSAKMALETGPKDLRHLRACL LCSLV/KGTIDQFEYDGCDCYAYL QMKGNR\EM\VYDCTSSSFDGIAM MSPED\SWVSK\WQAKSSNFKPAGV YA\VSVTGRLAPKGIR/VRELKSR\G VALQIPGDTANKDLAKMQGCQHLC SPPCLCHIISCSWNLNEQNFQILPTLQ FRLSSTVERAAHHFILLSSLDYRWG GRDLGWVD |
| 1831 | 7328 | A | 1967 | 66 | 407 | |
| 1832 | 7329 | A | 1968 | 2 | 1272 | CPWPESTGQSGVTSSKARPSLAERW AGPAKKKRKGVEHGPAAREAGLM KRLSS/LGDL LTSPEIEVLFTDIKVR THCPKSLPGTETVQIIESSFFLNILG GKKKKQSWEQEGCHLKDFGDLST PVPKDDLNNLIVNPRSVGLANQEL AEVVSRAVSDGYSCVTLGGDHSLAI GTISGHARHCPDLCVWVDAHAD NTPLTTSSGNLHGQPVSFLLRELQD KVPQLPGFSWIKPCISSASIVYIGLR DVDPPEHFILKNYDIQYFSMRDIDR LGIQKVMERTFDLLIGKRQRPILHSF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DIDAFDPTLAPATGTPVVGGLTYRE GMYIAEEIHNTGQRNTTENFDTSSQ TLTEGLLSALDLVEVNPQLATSEEE AKTTANLAVDVIASSFGQTREGGHI VYDQLPTPSSPDESENQARVRI |
| 1833 | 7330 | A | 1969 | 212 | 460 | |
| 1834 | 7331 | A | 1970 | 1 | 1223 | TVVECLSPA WHEESSGGRWRSLPA SNRAEPLPWRFSVLRIMSLRGSLSR LL\QTRVRSILKKS VHSVHVIGAPFS QGQKRKGVEHGPA AIREAGLMKRL SSLGCHLKDF/GQDLSFTPVPKDDL YNNLIVNPRSVGLANQELAEVVS AV/SQDGYSCVTLGGDHSLAIGTISG HARHCPDLCVWVDAHADINTPLT TSSGNLHGQPVSFLLRELQ\DKVPQ LPGFSWD/IKPCISSARIVYIGLRD VYPPEHFILKGTMDIQYF\SMEEILDR LGIQEGHNGTDFDL\LIGKRQRPIHLS YDIDAFDPTTHAPAHRTPVVGDITYR EAMYIAEKIH\NTGLLSALDLVEVN PQLATSEEEAKTTANLAVDVIGLPS LWVQTREGGAYWSYDPTFPTP\SSP DESENQARVRI |
| 1835 | 7332 | C | 1971 | 162 | 425 | MVGPSLHAGXXXVYIPRFLYIRSWL PCIFFSGGVTVGNIQRQLAMGVPEK PIVIESSKPXILEXGRFLEENLXLVD YXKGLSFFLK* |
| 1836 | 7333 | A | 1972 | 89 | 308 | |
| 1837 | 7334 | A | 1973 | 2 | 454 | |
| 1838 | 7335 | A | 1974 | 570 | 1418 | PMPRLHDHFWSCSCAHSARRRGPP RAIAAGLAAKVGEMHIVFVSGPSLM AVLSASDADPAPRGRSAVKSGPYP GSPYPNTWHHSLMQKSLVLFVGE VLALVLNLLQIQRNVTLPFEEVIATI FSSAWWVPP\CCGTAPADVGLLYPC IDSHLGEPHKFKERMGQVSMRCIAV FVGINHASAKLDFANNVQLSLTLAA LSLGLWWTFDRSRSGLGIGITIAFL ATL\ITQFLVYNGVYQYTSPDFLYIR SWLPC\IFFSGSVTVGNIGRQLGYG VFLEKPHSD |
| 1839 | 7336 | A | 1975 | 1 | 287 | KFQERGIIQIKYPP/RAFTLSHTHTRH AHIQAPTVTNQT/DFP/RPRR*ESSS SSEGANSFLKIMT*RQSSSPKEKDV RPATSTTSCSMLLSILFIG |
| 1840 | 7337 | A | 1976 | 1 | 166 | |
| 1841 | 7338 | A | 1977 | 37 | 448 | GGCTCPCSRWQGSPPQAPAGLPPPL ASGPAPSASASPQPSGGPIPLH/VR*E SSSSSEGANSVCSSRSCSLAETFS*S AHCLE*NLTPSPSFYETPLSVVSLA LVVSSGGRPVLGPCAESPGHRGWV ASPWSSGWSP |
| 1842 | 7339 | A | 1978 | 45 | 249 | |
| 1843 | 7340 | A | 1979 | 77 | 3801 | KGGVFAHDLVPLPFQGTDSPPRAP PGRGVPLPPGALTMNTRD\TPRVAE TSHHLKIFLPKKLLECLPRCPLLPE RLRWNTNEEIASYLITFEKHDEWLS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | CAPKTRPQNGSIILYNRKKVKYRKD GYLWKKRKDGKTTREDHMKLKVQ GMECLYGCYVHSSIVPTFHRRCYW LLQNPDIVLVHYLNVPALEDCGKG CSPIFCSISSDRREW LKWSREELLGQ LKPMFHGIKWSCGNGTEEF SVEHL VQQILDTHPTKPAPRTHACLCSGGL GSGSLTHKCSSTKHRIISPKVEPRAL TLTSIPHPHPPEPPPLIAPLPPELPA HTSPSSSSSSSSSGFAEPLERPSPTS RGGSSRGGTAILLLTGLEQRAGGLT PTRHLAPQADPRPSMSLA VVVGTEP SAPPAPPSPAFDPDRFLNSPQRGQTY GGGQGVSPDFPEAEAAHTPCSALP AAALEPQAAARGPPPQSVAGGRRG NCFIQDDDSGEELKGHGAAPPISP PPSPPPSPAPLEPSSRVGRGEALFGG PVGASELEPFLSSFPDLMGELISDE APSIPAPTPQLSPALSTITDFSPESY PEGGVKVLITGPWTEAAEHYSCVF DHIAVPASLVQPGVLR CYCPAHEV GLVSLQVAGREGPLSASVLF EYRAR RFLSLPSTQLDWLSLDDNQFRMSIL ERLEQMEKRMAEIAAAGQVPCQGP DAPPVQDEGQGP GFEARVVVLVES MIPRSTWKGPERLAHGSPFRGMSLL HLAAAQGYARLIETLSQWRSVETG SLDLEQEVDPLNVDHFSCTPLMWA CALGHLEAAVLLFRWNRQALSIPDS LGRPLPSVAHSRGHVRLARCLEELQ RQEPSVEPPFALSPPSSSPDTGLSSVS SPSELSDGTF SVTSAYSSAPDGSPPP APLPASEMTMEDMAPGQLSSGVPE APLLLMDYEATNPKGPLSSLPALPP ASDDGAAPEDADSPQAVDVIPVDM ISLAKQIIEATPERIKREDFVGLPEAG ASMRERTGAVGLSETMSWLASYLE NVDHFPSSSTPPSELPFERGRLAVPSA PSWAEFLSASTSGKMESDFALLTSL DHEQRELYEAARVIQTA FRKYKGR RLKEQQEVAAAVIQRCYRKYKQLT WIALKFALYKKMTQAAILIQSKFRS YYEQKRFQQSRRAAVLIQQHYRSY RRRPGPPHRTSATLPARNKGSFLTK KQDQAARKIMRFLRRCRHRMRELK QNQELEGLPQPGLAT |
| 1844 | 7341 | A | 1980 | 1 | 4333 | MQVQDDGVNLIPFAKCSR VVSRSPP PRLPSQSLRPMPQRYGDVFWKNLN QRPTPTWLEEQHIPMLRATGCSQL GLYPPEQLPPPEMLWRRKKRRPCLE GMQQQGLGGVPARVRAVTYHLED LRRRQSIINDTDSPPRPLRPGVTLPP GALTMNTKDTTEVAENTRPLKIFLP KKLLECLPRCPLPPERLRWNTNEEI ASYLITFEKHDEWLSCAPKTRPQNG SIILYNRKKVKYRKDGYLWKKRKD GKTTREDHMKLKVQGMECLYGCY VHSSIVPTFHRRCYWLLQNPDIVLV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HYLNVPALEDCGKGCSPIFCSISSDR REWLKWSREELLGQLKPMFHGIKW SCGNGTEEFSVEHLVQQILDTHPTK PAPRTHACLCSGGLGSGSLTHKCSS TKHRIISPKVEPRALTLTSIPHAHPPE PPPLIAPLPPELPAHTSPSSSSSSSS GFAEPLEIRPSPTSRGGSSRGGTAIL LLTGLEQRAGGLTPTRHLAPQADPR PSMSLAVVVGTEPSAPPAPPSPAFDP DRFLNSPORGQTYGGGQGVSPDFPE AEAHTPCSALEPAAALEPQAAAR GPPPQSVAGGRRGNCFIQDDDSGE ELKGHGAAPPISPPSPPPSPAPLEP SSRVGRGEALFGGPVGASELEPFSL SSFPDLMGELISDEAPSIPAPTPQLSP ALSTTTDFSPESYPEGGVKVLITGP WTEAAEHYSCVFDHIAVPASLVQP GVLRCYCPALPLPYTQKSALLGDLK DHQSDRLAALLSTSVFSPSLYSSIQH VSHEVGLVSLQVAGREGPLSASVLF EYRARRFLSLPSTQLDWLSLDDNQF RMSILERLEQMEKRMAEIAAAGQV PCQGPDAPPVQDEGQGPGEARVV VLVESMIPRSTWKGPRLAHGSPFR GMSLLHLAAAQGYARLIETLSQWR SVETGSLDLEQVDPLNVDHFSCTP LMWACALGHLEAAVLLFRWNRQ ALSNPDSLGRPLPSVAHSRGHVRLA RCLEELQRQEPSVEPPFALSPPSSSP DTGLSSVSSPSEL\TDGTFSVTAAYS SAPDGSPPPAPLPASEMTMEDMAPG QLSSGGPEAPLLLMDYEATNSKGPL SSLPALPPASDDGGGPEDADSPQAV DVIPADMISLAKQIEATPERIKREDF VGLPEAGASMRERTGAVGLSETMS WLASYL\ENVDFHPSSTPPSEL\PER \GRLGLSLTAPSWAEFLSCIPPVGKI GKLIFALLTL\SD\QEQRLEYAARVI QTAFRKYKGRRLKEQQEVAAAVIQ RCYRKYKQFALYKKMTQAAILIQS KFRSYYEQKRFQQSRAAVLIQQH YRSYRRRPGPPHRTSATLPARNKGS FLTKKQDQAARKIMRFLRRCRHRH SALPFKTHRPLSVTPKMADLLGSILS SMEKPPSLGDQETRRKAREQAARL KETTRARETTESGVS |
| 1845 | 7342 | A | 1982 | 1 | 145 | |
| 1846 | 7343 | A | 1983 | 1 | 419 | |
| 1847 | 7344 | A | 1984 | 3 | 532 | PRASRSRPTGLREAAGSGPREAPRR SGCKSPGLGTVAMLRPKALTQVLS QANTGGVQSTLLLNNEGSLLA\YS GLRGTTDAPGSPAIA\SNIWAA\YG PETGTQAFNEDNLQ\IILHGTCMGG AVLGHSPELANLSCLLYCIAKEDRG AFGNCFKAKGPGLLGGSYLEEPLTQ VAAS |
| 1848 | 7345 | A | 1985 | 2 | 555 | |
| 1849 | 7346 | A | 1986 | 90 | 323 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1850 | 7347 | A | 1987 | 1 | 4695 | |
| 1851 | 7348 | A | 1988 | 81 | 523 | SCLCRDRACLTSLPVSFQVQGVGSK GWRDVTTFSSGKAEGPLDSPSEGH YQNSGLDHFQNSNIDQSFWETFGSA EPTKTRKSPSSDS\WTCADTSTER\R SSDSWEVWGLASTNR\NSNSDGV GGEGTKKAVPPAVPTDDGWDNQNW |
| 1852 | 7349 | A | 1989 | 1187 | 1720 | QNQSRDKMRDLREGQMEPPKSELI GWGGGETSRWVRGGASPPPALSP LFLITWSGHKDLKDLKVRGLRGLE APRVNVWETEANQAGLQPLGPPAT IGLRPRERPGRVGRGGPAWPLG EFGIPGVGLRARHQHELRRWRPGR ASPRPERKAAWKGPQGPAGPADG RAARSRG |
| 1853 | 7350 | A | 1990 | 738 | 1086 | GTASENLGCKILKHRQQMLRKVYP VVLHILSYRGSHSSRKKNWGRLENI LKTFFFLGGGGDGSCWQRPGWELQ WALFSGSLQSPPGFKQFSCLSLLS SWEYRCTPPCLANFCIFQ |
| 1854 | 7351 | A | 1991 | 1 | 340 | LGEGGRTAVEALPGPSLDHWYRSA GEEKDGP/VYCAAQHLRGRSLPKA WPPPPSSLPVLTDEQKSR/YPGHEAH DQGG\WDARQSIIRKVDPETGRTR WGAFGLTYTTGSGSVG |
| 1855 | 7352 | A | 1992 | 1 | 142 | |
| 1856 | 7353 | A | 1993 | 58 | 328 | LKKKGKEKAEAAQQVEALPGPSLDQ WHRSAEEEDGPVLTDEQKSR/YPG HEAHDQGG\WDARQSIIRKCGGPLR RGAPGLLKGDGEGPKRKS |
| 1857 | 7354 | A | 1994 | 120 | 416 | LFFGESSRLTVLEDLKNVFPQVAV FEPKAEIFHTQKAPLVFLATGFYPD HVELSWVNGKEVHSGVSTDPQP LMEQAALNDSRYCLSSRLRVSATF |
| 1858 | 7355 | A | 1995 | 1 | 977 | VKLPSCPDPAMGTSLLCWMALCLL GADHADTGVSQNPRHNITKRGQNV TFRCDPISEHNRLYWYRQTLGQGPE FLTYFQNEAQLEKSRLSDRFSER PKGSFSTLEIQRTEQGDSAMYLCA SIGAGLPSSNQPHFGDGTRLSILED LNKVPPEVAVFEPSEAEISHTQKAT LVCLATGIFPDHVELSWVNGKEV HSGVSTDPQPLKEQPALNDSRYCLS SRLRVSATFWQNPRNHFRQVQFY GLSENDEWTQDRAKPVTVQVSAEA WGRADCGFTSV\SYQQGVLSATIL YEILLGKATLYAVLVSAVLMMAMV KRKDF |
| 1859 | 7356 | A | 1996 | 2 | 883 | FVSQLSPEKVVCGHHLKMLSLLLLL LGLGSVFSAVISQKPSRDICQRTSV KIECRSLDFQATTMFWYRQFPKKS MLMATSNEGSKATYEQGVEKDKFL INHASLTLSTLTVTSAHPEDSSFYICS ARESTSDPKNEQYFGPAGTRLTVLE DLKNVFPPEVAVFEPSEAEISHTQK ATLVCLATGAFPDHVELSWVNG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KEAHSGVSTDPQPLKEQPALNDSRY CLSSRLRVSA TFW\QNPRNHFRQV QFYGLSENDEWTQDRAKPVTOIVS AEA WGRAGEWGLGRCLEER |
| 1860 | 7357 | A | 1997 | 195 | 1133 | PQHGGHFPRKIKSCSWQARPLEDEA TLGQCGVEALT TLEVTRPACLEVKS MVPWPVLEKVRGQTPKVAKHGEK KKKKTGRAKRRMQYNRRFVNVVP TFGKKKGTTFTKIFVGGLPYHTTDA SLRKYFEGFGDIEEA VVITDRQTGK SRGYGFVTMADRAAAERACKDPNP IIDGRKANVNLA YLGAKPWCLQTG FAIGVQQLHPTLIQRTYGLTPNYMY PPAIVQATVVIPAAPVPSLSSPYIEYT PASPAYAQYPPATYDQYPYAASPA TVRSFVGYSYPAAVPQALSAAAPA GTTFLQYQAPHVQPD RMH |
| 1861 | 7358 | B | 1998 | 60 | 378 | NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIH FISPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX* |
| 1862 | 7359 | A | 1999 | 1 | 437 | DPRATEGMVVADKTCQKSTGRLPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISK NKLD FLRP YTVPNKKGTRLGRYRCEKGTTAVL TEKITPLEIEVLEETVQTMDTS |
| 1863 | 7360 | A | 2000 | 2290 | 2481 | |
| 1864 | 7361 | A | 2001 | 3 | 860 | FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKL\PRPKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIH FISPNIYCCGAGTAA DTAMTYQLISSNLKLHSLSTGRLP RV\VTANRMLKQMLFRYQGYIGAA LV LGGVDVTGPHLY\SIYPHGSTDK VP\YVTHGFLAPLA\AMAVFEDKFR PD\MEEEEAKNLVSEDSPPQFP PPS WRIFNDLGSGSNIDLCVISK\NKLDF LRP\YTVPNKKGTRLGWRYRCEKG VTAVLTEKIPLLWST |
| 1865 | 7362 | A | 2002 | 1 | 340 | RQGTIVAISIQGKMSIPFRSAYAAS KHATQAFFDCLRAEME QYEIEVTVI SPGRSC/VEVAQDVLAAGKKKKD VILADLLPSLAVYLRTLAPGLFFSL MASRAR*ERKSKNS |
| 1866 | 7363 | A | 2003 | 56 | 385 | RPWTSSPPQPSCPCSAAWASSASS GCCSGCAGRPTCGMLWW*SQAPA QGRSPVEVAQDVLA AVGKKKKDVI LADLLPSLAVYLRTLAPGLFFSLMA SRARKERKSKNS |
| 1867 | 7364 | A | 2004 | 2 | 409 | |
| 1868 | 7365 | A | 2005 | 1 | 1092 | |
| 1869 | 7366 | A | 2006 | 50 | 1101 | LTMVSPATMKSLPKVKAMDFITST AILPLLFGCLGV\FGL\FRLLQWVR GKAYLRNAV VVITGATSGLGKECA KV FYAAGAKLVLCGRNGGALEELN |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RELTAS\HATKVQTHKPLLGGPSDL TDSGAIVAAAAEESFSCF\GYGRHY FVNNAGISYRGTTMDT\TVDVDR VMETNYFGPVALTKALLPSMIKRR QGHIVAISSIQGKMSIPFRSGICQPS KHATQ\AFFDCLAVPEMEQY\IEIV TVISPG\YIHTNLS\VNAITADGSRYG VMDTT\TSPGPESPVEGGPRMFLAC LWGKKKKDVT\ADLPALPLAVY\ LRTLAP\GLLPSSLPCLPRAQKRAGN PKNSLV |
| 1870 | 7367 | A | 2007 | 75 | 461 | |
| 1871 | 7368 | A | 2008 | 3 | 426 | DAWVCLSPAFILLELCAARV*EGLP NRVHRTEEVNHVDFYAFSYYDLA GGAGPIDAEKGGSLVVGDFEIAATKY VCRTLETQSQSSPFSCMDLTYVSL LQEVGFPRSKVLKLTRKIDNVYTT WAPGAIFHYIDSLNRQKS |
| 1872 | 7369 | A | 2009 | 3 | 421 | QALGNRGVVSRGWRPGWRRPGRG SPKDRLPPAPRKRALVSVGVAERA VHETPTLTHETFKALKPGLSAYADD VEKSAQGIRELLDVAKQDIPDF*K ATPLILK/ATAGLRLLEPKKAQR*LA \KGKEVFKAWLFFEGNDW |
| 1873 | 7370 | A | 2010 | 337 | 769 | PLALCLAPAASLHELCAAKVSEVLH NRVHRTEEVKHVDFHAFSYYDLA AGVGLIDAEKGGSLVVGDFEIAAK YVGVTVSVKGRVSSPVCRTLETQP QSSPFSCMDLTYVSLLLQEFGFPRS KVLKLTRKIDNVETSWALGAIF |
| 1874 | 7371 | A | 2011 | 2 | 486 | |
| 1875 | 7372 | A | 2012 | 176 | 1643 | MKKGIRYETSRKTNYIFQQPQHGP WQTRMRKISNHGSLRVAKVAYPLG LCVGVFIYVAYIKWHRANATQAFF SITRAAPGARWGQQAHSPLGTAAD GHEVFYGIMFDAGSTGTRVHVFQF TRPPRETPTL/TAHETFKALKPGLSA YADDVEKSAQGIRELLDVAKQDIPF DFWKA TPLVLKATAGLRLLPGEKA QKLLQKVKEVFKASPFLVGDDCVSI MNGTNE\GVSAWITINFLTGSLKTPR RSNVGMLDLGGGSTQIVFLTHVEG TLQASPPRYLTALRMFNRTYKLYC YSYLGLGLMSARLAILGGVEGQPA KD GKELVSPCLSPSFKGEWEHAEVT YRVSGQKAAASLHELCAARVSEVL QNRVHRTEEVKHVDFYAFSYY\YD LAAGVG\LIDAEKGGSLVVGDFE\A AAKYV/CVRTLGETQPAQSSPFSCMD LTYVSLLLQEFGFPRSKVLKLTRKID NVETSWALGAIFHYIDSLNRQKSPA S |
| 1876 | 7373 | A | 2013 | 21 | 119 | PGWPQTPDFKRS/PPLWPPKVLGLQ V*ATAPGPK |
| 1877 | 7374 | A | 2014 | 1420 | 1627 | IGLNPSSVPSTFFSYSPQFTEGVPP/P GMERP/PFPWEQRPTGWSFFSPCPQ TPSPPTSEHGTPPNWPKC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1878 | 7375 | A | 2015 | 447 | 775 | QIPKEHLHHP/PQTSNRSRPLR/P/GN RPNPESPTGSPPQECCSCLAPRGSA WGDPNPLQRTPGAGKVAGGPFPPP TQSSPPGKALCINLKKGFAAIKLLD NVLQPSSALGFL |
| 1879 | 7376 | C | 2016 | 49 | 519 | MYGKGKSNSSAVPSDXQAREKLAL YVYEYLLHVGAQKSAQTFLSEIRW EKNITLGEPPGFLHSWWCVFWDLY CAAPERRETCEHSSEAKAFHDYPFM SPRYPGGPRPPLRIPNQALGGVPGS QPLLPSGMDPTRQQGHPNMGGPMQ RMTPPRGMVP* |
| 1880 | 7377 | A | 2017 | 1 | 1155 | |
| 1881 | 7378 | A | 2018 | 56 | 1416 | WVDRCVTVGAALGTSMYGKG\KS NSSAVPSDSQAREKLALYVYEYLL HVGAQKSAQTFLSEIRWEK\NITLG EPPG\FLHSWWCVFWDLYCAAPER RETCEHSSEAKAFHDYSAAAA\PS VLG\NIPPGRWACQLGPVTTGRSFQ PFMFTFGYPG\GPRSPLR\PNQALG G\VPGGQPLLPSGMDST\RQQ\GHPN MGGAMQR\MTPPRGM\VP LGPQFLT PWLSLQNYGGA\MRPPLNALGGPG MPGMEQGSRCGRP\PNPTNA\NSL PFSSAFSWNLLGPPG\GGGPPG\TPA MPSSSRFQPTSGDNMYTLMNAVPP GP\NRPNFPMGP\GSDGPMGGGLGG MESHMNGSLGS\GDMASISKNSPN NMSLSIQ\GIPK\DDGAMGANFLN PFQSESYSPSKPYKCVFPFGLFMKP TVSQPFPELRTEENYSSTSVPVKQR NLSHTKPTFLFPALSPLL |
| 1882 | 7379 | B | 2019 | 162 | 349 | LEELEEEELDLVLLRAFCLLLSW DVEAEQFLEV SFLFFFLFSDPRPRD RLRLLERLREPT* |
| 1883 | 7380 | A | 2020 | 2 | 353 | SSSDGRKKRGKYKDKRRKKKKKR KKLKKKGKEKAEAAQVEALPGPSL DQWHR SAGEEEDGPVLTDEQKSR/ YPGHEAHDQGG\WDARQSIIRKVV DPETGRTRWGAFLTYTTGSGSVG |
| 1884 | 7381 | A | 2021 | 1 | 142 | |
| 1885 | 7382 | A | 2022 | 404 | 946 | PVCACPRPEQGTKVYLFPSWLSSLT FSLHHREKQAEGRGEEEDASSASS SSSSSSSSASSSSSSSDGRKKRGK YKDKRRKKKKKRKKLKKKGKEKA EAQQVEALPGPSLDQWHR SAGEEE DGPVLTDEQKSR/YPGHE\THDQGG\ WDARQSIIRKCGGPLRRGAPGLLKG DGEGPKRKS |
| 1886 | 7383 | A | 2023 | 3 | 634 | |
| 1887 | 7384 | A | 2024 | 131 | 546 | VAGTPGRHPHTRLIFPVFCRGGVFL CFPGWSFFFFKPSDLDSFHLEMIHPR CESWKMPGALPM/YCSP/CCLLVLL KDQGGQASTGVRRRKESWLPAPHS STVQVTQEGWREQSRELKTECQL GWFLFLLQPYSRSRFY |
| 1888 | 7385 | A | 2025 | 363 | 578 | RPYPCLSPPRSSTNPLSS**LNKIPS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LPSSWEKW*IPPKNNCLSLNPSPPS LAPSLDDIKEGLSWKKKKK |
| 1889 | 7386 | A | 2026 | 166 | 191 | KNVIHQSKNCVFKLLDQIHNFPLS TLLHVIVDLFLGLFGVPE/CSDP*RLP GTPPYQPAPARQPAPADHRQWPVPQ RGPEASG |
| 1890 | 7387 | C | 2027 | 358 | 405 | MSSREGARDGGEGRLS* |
| 1891 | 7388 | C | 2028 | 306 | 347 | MSPGRGPGMEGRG* |
| 1892 | 7389 | A | 2029 | 2 | 358 | QCGGIRFWRAPVFLVLSWSPQDGIT GEEPDTSHDPRHLHQASSCPPAHPLP PTQSCSSCQGWLCPPQGCPPGGPRT A/CIVPWPSFVASAATQERGQCPPL DPLSPNQTRALHLSGTSGK |
| 1893 | 7390 | B | 2030 | 1043 | 1146 | MPSSVSWGILLLAGLCLVPVSLAE DPQGDAAQKTDTSHHQDQDHPTFNK ITPNLAEFASFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEASPVISGASKRA KKQINGKMGETLLKSKDPRKEDFT LDQVTTVKGAYDEAFRACLTSSHX * |
| 1894 | 7391 | A | 2031 | 2 | 402 | SQTQREPTMVLSPADKTNVKA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR |
| 1895 | 7392 | A | 2032 | 9 | 509 | NSARATDSERTHHGARLLPDKTNV KA\AWGKVGAHAGEYGAEALERM FLSFPT\TKTYFPHFDL\SHGFAQVK GATAKKVA\DALTKAVA\HVDGHA QTALSALSGPATAHKL\RVGPGSTF KLL\SHLPCWLT\GRPPSPAEFQPLA VARLPWNKVPGLLVEAPLLEPSK |
| 1896 | 7393 | A | 2035 | 413 | 674 | CRSDRWAKEHRGKRGQDSSKDVM ARLMEAPKQTAQYFFIFYFFETKSY SVTQAGVQWLDLGSQRPPPGP\SD SPASASRAWPQTAH |
| 1897 | 7394 | A | 2036 | 2525 | 2734 | LTNGTESTPPPRPTPSRCSRQRCPE VGPPFCSPFCVPAHFKLLPWTFQG TVISSPQIISSSVCAFF |
| 1898 | 7395 | A | 2037 | 168 | 392 | NKSFFPPSSSFDLSILNTFSFPLTLSSL RSGPTHHTHTHAN/THHTHTHTHT HTPSSDPQAHPHTLTDNWVSTL |
| 1899 | 7396 | A | 2038 | 216 | 528 | AGEKLGLGAGDTSWRVVWPAACT PGRVERVGWCRV\GPADPSGGLTPG VACGASWQGPFSWAKDLQGPGSW WPVWPPTRPFLDLGSSGLLIWVHK WPWGVVCVYV |
| 1900 | 7397 | A | 2039 | 37 | 424 | RWNFLATTPSAVFRVWEAQMLTCE RWPTLSGRRQTYLLLPFAP*PQTGC WSPDGSRLFTVLGEPLIYSLSPER CGEGKGALEVQSQQRLWQICLRQ QYRHQMVRRLGERLTPWSGTPVG NVWLCL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1901 | 7398 | A | 2040 | 1 | 442 | PEFRVDDFVLRYPAYESSPGTELRECLG/WPFRPGVCRLQTSCEPWNLPLQLTKDPLKTPGRLDHGTRTAFIH HREQVWKRCINIWRDVGLFGVLNE IANSEKEVFEWVKTAGSWALALCR WASSLHGSLFPHLSLRNEDLIAEF |
| 1902 | 7399 | A | 2041 | 722 | 1395 | CLCLGLWACQS\CILIWTL\DPSTSLF\TRPSSG\CAQVLSPGHTPVTSLAW APSGGRLLSASPVDAAIRVWDVSTE TCVPLPWFRGGGVNLLWSPDGSKI LATTPSAVFRVWEAQMWDLWRRW PTLSGRCQTGCWSPDGSRLLFVTLG EPLIYSLSPERCGEKGVALEVQSQ QRLWQICLRQQ/YTRHQMVRRLGLG ERLTPWSGTPVGNVWLCFMKGKA QGLPGW |
| 1903 | 7400 | A | 2042 | 1 | 418 | MPEQEPTAEQLS*IAAENEDEHSV NYKPRAQKSIQEIQELDKDDESLRK YKRALLGRVAVSADPNVPNVVAP GRVRLLPQALSATTPGRPSLTQPGT NKGPSAHIAESRLCLPRPIPLRVV SARLRQRRLSLLLF |
| 1904 | 7401 | A | 2043 | 1 | 525 | LSQQASLESF*KHFFCLKEVVEYRIK ISFRVNREIVSGMKYIQHTYRKGVK IDKTDYIVGSYWPRAEYEFLTPKS PRWTASPTPSVLQSGAPLGHQYLLP PSVPSSGHWPGVCSPLLVPPLLGR PSLTLPGTNKGPSAHIAESRLCLPR PIPLRVVSARLRQRRLSLLLF |
| 1905 | 7402 | A | 2044 | 354 | 487 | |
| 1906 | 7403 | B | 2045 | 61 | 516 | KSIQEIQELDKDDESLRKYKEALLG RVAVSADPNVPNVVVTGLTLVCSS APGPLELDLTGDLESFKKQSFVLKE GVEYRIKISFRVNREIVSGMKYIQHT YRKGVKIDKTDYMGVSGYPRAEY EFLPRPIPLRVVSARLRQRRLSLLLF* |
| 1907 | 7404 | A | 2046 | 11 | 328 | |
| 1908 | 7405 | A | 2047 | 1 | 507 | LTFVCSFRPVPLYDLRSNLDKSNQ SFLFKEAVDYRIKISFRFHPKYISLI*\YIQHTYSK/GVKIDKTDYMLGSY/GP RAEYEFLTPVEEAPKGMLARGSYS IKSRFTDDDKTDHLSWEWNLTISIY CLRPCRWPATGLAPVPPGSQCHHPR QAFDPARNKQGTKCTHC |
| 1909 | 7406 | A | 2048 | 1 | 327 | TAEQLAQIAAENEDEHSVNYK/PP AQKSIQEIQELDKDDESLRKYKEAL LAPLAVSADPNVPNVVVTGLTLVC SS/APGPLELDLTGDLESFKKQSFVL KEGVECTVGP |
| 1910 | 7407 | A | 2049 | 1 | 452 | |
| 1911 | 7408 | A | 2050 | 3 | 868 | SHFVLDVIPGVGHLTLPQRMPLSRN RGGGEERRCPPWSPFGAPLQPTLLL RSAPPLGIQVQGLSPSRPQVSRPRLS LSMAEQEPTAEQLAQIAAENEDEH SVNYKPPAQKSIQEIQELDKDDESL RKYKEALLGRRWPF\$ADPNVPNVV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VTGLTLVCS\SAPGPLELDTGDL\ESFKKQFVLCLKEGVEYRIKISFRFNP RDNCPGMKYIQHTYRKGVKIDKTD YMGVSYG\PRAEGSFELTPVE\EAP\KGM LARGSYSIKSRFTDDDKTDHL SWEWNLTIKKDWKD |
| 1912 | 7409 | A | 2051 | 1 | 618 | TLLVPQDSERTHPWLLSPADK\TNV KGPPGGKVGAAHVRSMCAEALER MFLSFPTTKTYFPHFDLSHG\SAQV\KGHG\KKVADALTNVAHVDDMP NALSALSDLHAHKLRVDPV\NFKL LKPLACLVDPGPAHLPAEFQPLAV ATSSLGQSFLGFLWANLKFELQIPV KLGS LGWAMLSLPLWAFPPAPPPLS CTRTPVVFEIKS |
| 1913 | 7410 | A | 2052 | 3 | 398 | |
| 1914 | 7411 | A | 2053 | 1773 | 3913 | FEQNTKLDQAQQAPEDHYPISLLLP SHMAIGLLMAQEGHCKDSSAMGEE AHHPLTPATPPFPPLSPDWGHMQPD FFVPVAVPAVFRGPPQLQCHGRRLF LNSPCAQKSSSGLVVEPGLSRTLLE MVKLTSMRGQFLEAQIPTGISLTLQ YQLYQKQTNKNMSYSFVLFLKWV ALGQGRAGYPSLEDADSRRFNCS RSFLITVIGITLTVEIVTSGMMKGTR VRWSGAGNEGMMGLEEGRNERSV KEAPPRAVEAQPKDRTWDVGKG QGTEGEGRGLEVEGQQHQGSEPGTI PFSVSWGVLLLAGLCCLPSSLVED PQEDAAQKTDTSHTDQGDWEDLA CQKISYNVTDLAFDLYKSWLIYHN QHVLVTPTSVAMAFAMLSLGTKA DTRTEILEGLNVNLTETPEAKIHECF QQVLQALSRLPDTRLQLTTGSSLFVN KSMKLVDTFLEDTKKLYHSEASSIN FRDTEEAKEQINNYVEKRTGRKVV DLVKHLKKDTSALVDYISFHGKW KDKFKAERIMVEGFHVDDKTIRVP MINHLGRFDIHRDRELSSWVLAQH YVGNATAFFILPDPKKMWQLEEK LYSHLENIQRAFDIRSINLHFPKLSIS GTYKLKRVPRNLGITKIFSNEADLS GVSQEAPLKLSKAVHVAVLTI DEK GTEATGAPHLEEKAWSKYQTMFN RPFLVIIKEYITNFPLFIGKVVNPTQK |
| 1915 | 7412 | A | 2054 | 3 | 409 | PGPVVVSNNSSAHGSQRTSGPESSM KIYCCPEMVEYQKKGKSLDSEPSVP SAAKPPSPEKTAPVASTPSSTPIALS PPTKVPEPNENVGDAVQTKLIMLV DDFY YGRDGGKVAQLTNFPKVATS FRCPHCTKRLY |
| 1916 | 7413 | C | 2055 | 235 | 366 | MRIPETKPLTRNGSEVKELAHSSPQ DNQNDQMSFFIVLLPRNG* |
| 1917 | 7414 | A | 2056 | 3 | 484 | STTPTATQPTSLWQLAVQSPGQSNQ TTNPKLGKASEEEMAEPGLGWWVE NR*LSLGHR\APSFPSPA VSIA SFVT VKRPGVTGENSNEVAKLVNTLNTIP SLGQSPGPVVVSNNSSAHGSQRTSG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PESSMKGTTIT*KTLSSQSFKNINKVF VVSELYTQK |
| 1918 | 7415 | A | 2057 | 2 | 4256 | FVHGSMADTDLFMECEEELEPWQ KISDVIEDSVVEDYNSVDKTTTVSV SQQPVSAPVPIAAHASVAGHLSTST TVSSSGAQNSDSTKKTLVTLIANN AGNPLVQQGGQPLILTQNPAPGLGT MVTQPVLRPVQVMQNAHVTSPPV ASQPIFITTQGFVRNVRPVQNAMN QVGIVLVNQGGQTVRPITLVAPGT QFVKPTVGVPQVFSQMTVPVRPGST MPVRPTTNTFTTVIPATLTIRSTVPQ SQSQQTKSTPSTSTTPTATQPTSLGQ LAVQSPGQSNQTTNPKLAPSFPSPP AVSIASFVTVKRPGVTGENSNEVAK LVNTLNTIPSLGQSPGPVVVSNNSS AHGSQRTSGPESSMKVTSSIPVFDL QDGGRKICPRCNAQFRVTEALRGH MCYCCPEMVEYQKKGKSLDSEPSV PSAAKPPSPEKTAPVASTPSSSTIPAL SPPTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCTKRLKNNIRFMNHMKHHV ELDQQNGEVDGHTICQHCYRQFSTP FQLQCHLENVHSPYESTTKCKICEW AFESEPLFLQHMKDTHKPGEMPYV CQVCQYRSSLYSEVDVHFRMIHED TRHLLCPYCLKVFKNGNAFQQHYM RHQKRNVYHCNKCRLQFLFAKDKI EHLQHHKTFRKPKQLEGLKPGTK VTIRASRGQPRTPVPVSSNDTPPSALQ EAAPLTSSMDPLPVFLYPPVQRSIQK RAVRKMSVMGRQTCLECSFEIPDFP NHFTYVHCSLCRYSTCCSRAYAN HMINNHVPRKSPKYLALFKNSVSGI KLACTSCTFVTSVGDAMAKHLVFN PSHRSSSILPRGLTWIAHSRHGQTRD RVHDRNVKNMYPSPSPTNKAATV KSAGATPAEPEELLTPLAPALPSPAS TATPPPTPTHQPALALPPLATEGAEC LNVDDQDEGSPVTQEPELASGGGG SGGVGKKEQLSVKKLRVVLFAACC NTEQAAEHFRNPQRRIRRWLRRFQ ASQGENLEGKYLSEAEKLAEWV LTQREQQLPVNEETLFQKATKIGRS LEGGFKISYEWAVRFMLRHHLTPH ARRAVAHTLAPKDVAENAGLFIDFV QRQIHNDLPLSMIVAIDEISLFLDT EVLSSDDRKENALQTVGTGEPWCD VVLAILADGTVLPTLVFYRGQMDQ PANMPDSILLEAKESGYSDDEIME LWSTRVWQKHTACQRSKGMLVMD CHRTHLSEEVLAMLSASSTLPAVVP AGCSSKIQLDVCIKRTVKNFLHKK WKEQAREMADTACDSDVLLQLVL VWLGEVLGVIGDCPKLVQRSFLVA SVLPGPDGNINSPTRNADMQKELIA SLEEQLKLSGEHFESSTPRPRSSPEE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TIEPESLHQLFEGESENE\$FYGFEEA DLDLMEI |
| 1919 | 7416 | A | 2058 | 3 | 824 | |
| 1920 | 7417 | A | 2059 | 1 | 1077 | MLSGVGGFVLGLLFLGAGLFIYFRN QKAEESFVSALSIDLSGGGNMALLS MVCLKFPGG\$SCMAALTVTLMVLS SPLALAG\DTR\PPVRLRKTEDEPLG CVLSGLRVGPDSVFPGGRFCNRIVL VPPARFLEQVKHECHFFNGTERVRF LDRYFYHQEEYVRFDSDVGEYRAV TELGRPDAEYWNSQKDLLEQKRAA VDTYCRHNYGVGESFTVQRRVYPE VTVYPAKTQPLQHHNLLVCSVNGF YPGSIEVRWFRNGQEEKTGVVSTGL IQNGDWFQTLVMLETVPRSGEVY TCQVEHPSLTSPLTVEWRARSESAQ SKMLSGVGGFVLGLLFLGAGLFIYF RNQKGHSGLQPTGFLS |
| 1921 | 7418 | A | 2060 | 2 | 867 | GRVGLPAALAPGPVLFSSMVCLRLP GGSCMAVLTVTLMVLSSPLALAGD TRPRFLEYSTSECHFFNGTERVRYL DRYFHNQEENVRFDSVDVGEFRAVT ELGRPDAEYWNSQKDLLEQKRAA VDNYCRHNYGVVESFTVQRRVHPK VTVYPSRTQPLQHHNLLVCSVSGF YPGSIEVRWFRNGQEEKTGVVSTG LIHNGDWFHTLVMLETVPRSGEV YTCQVEAPRA*QAPLTVE\WRARS ESAQSKMLSGVGGFVLGLLFLGAG LFIYFRNQKGHSGLQPRGFLS |
| 1922 | 7419 | A | 2061 | 3 | 940 | RNFRVDPRVRREEGFIVLPERDLPA SLAPGPVLVSSMVSLKLPGGSCMTA RTVSLMVLSSPLALAGDTRPRFLW QPKRECHFFNGTERVRFLDRYFYN QEE\$VRFDSDVGEYRAVTELGRP AEY\WNSQKDLLE\QRRAA\VDTYC RHNYGVGESFPVQRR\VEPKVTY PSKTQPLQHHNLL/VFC\$VSGFYPGS IEVRWFLNGQEEKAGV\VPQALIQN GDWTFQTW\VMLETVPRSGEGLHC QSE\HPGVTSLLTVEWRARSESAQS KMLSGVGGFVLG\LLLPLGPGLFIY FRNQKGHSGLQPTGFPELKCR |
| 1923 | 7420 | A | 2062 | 25 | 384 | EFHRLRENPPMVAVSCPTKTNVKG PPGGKVGAAHVRSMCAEALERMFL SFPT\TKTYFPHFDLASHG\SAQVKGP RQRRWPNALTKRRGAPLDDMP/NT ALSALSDLHAHKL\$RVDPVQLSSS |
| 1924 | 7421 | A | 2065 | 47 | 353 | AGRVRLWDCVEVDLTELGAGQSV EASRHAWEVRRNRCHWAPQLFLS FAPGWGG\GEGRVGDGGAVGWFPS PQPPSSPPGVMPCPH\$DRRGTEPGRD LVPAQ |
| 1925 | 7422 | A | 2066 | 3 | 692 | KRLPKMAEVQVLVL\DGRAHSSLG\ RLAGHRGLNQVLLGRK\VVVV\RCE G\NISGNFYRNEVKVPWLFPSKRIM NTNPSRRPLTTSGAPSR\FWRTVRG MLPHKTQAEAKAA\LDRL\KVFDGI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PPPYGQEKSGMVVPAALKVVR\LK PTRKFCLIFFSFGGAL\AHQ\VGWK YQAVTAP\LEE\KRKREKPRFH YRK KENSIMRL\RKQAREETWRKKIDKY TEVLKTHGLLV |
| 1926 | 7423 | A | 2067 | 1 | 2091 | |
| 1927 | 7424 | A | 2068 | 384 | 4189 | ERTSPAMITSELPVLQDSTNEATAH SDAGSELEETEVEKGRIRGRPP STNKKPRKSPCEKSKIEAGIRGAGR GRANGHPQQNGEGEPVTLFEVVKL GKSAMQSVVDDWIESYKQDRDIAL LDLINFQICSGCRGTVRIEMFRNM QNAEIIRKMTEEFDEDSGDYPLTMP GPQWKKFRSNFCEFIGVLIRQCQYSI IYDEYMMDTVISLLTGLSDSQVRAF RHTSTLAAMKLMTALVNVALNLSI HQDNTQRQYEAERNKMIGKRANER LELLQKRKELQENQDEIENMMNSI FKGIFVHRY\RDAAIEIRAICIEIGV WMKMYSDAFLNDSYLYVGVWTLH DRQGEVRLKCLKALQSLYTNRELF KLELFTNRFKDRIVSMTLDKEYDVA VEAIRLVTLILHGSEEALSNEDECENV YHLVYSAHRPVAVAAGEFLHKKLF SRHDPQAEALAKRRGRNSPNGNLI RMLVLFLESELHEHAAYLVDSLW ESSQELLKDWECMTELLLEEPVQGE EAMSDRQESALIELMVCTIRQAAEA HPPVGRGTGKRVLTAKERKTQIDD RNKLTEHFIITLPMLLSKYSADAEK VANLLQIPQYFDLEIYSTGRMEKHL DALLKQIKFVVEKHVESDVLEACS KTYSILCSEETYIQNRVDIARSQID EFVDRFNHNSVEDLLQEGEEADDDDI YNVLSTLKRLTSFQNAHDLTKWDL FGNCYRLLKTGIEHGAMPEQIVVQA LQCSHYSILWQLVKITDGSPSKEDL LVLRKTVKSFLAVCQQCLSNVNT P VKEQAFMLLCDLLMIFSHQLMTGG REGLOPLVFNPDTGLQSELLSFVMD HVFIDQDEENQSMEGDEEDEANKIE ALHKRRNLLAAFSKLITYDIVDMHA AADIFKHMYKYNDYGDIIKETLSK TRQIDKIQCAKTLILSLQQLFNELVQ EQGPNLDRTSAHVSGIKELARRFAL TFGLDQIKTREAVATLHKDGIEFAF KYQNQKGQEYPPPNLAFLEVLSEFS SKLLRQDKKTVHSYLEKFLTEQMM ERREDVWLPLISYRNSLVTTGGEDDR MSVNSGSSSSKTSSVRNKKGRPPLH KKRVEDESLDNTWLNRTDTMIQTP GPLPAPQLTYTVLRENSRPMGDQI QEPSEHGSEPYFLHNPQMQISWLG HPKLEHLNPKDITGMNYMKVITGA RHAALCLMEEDAEPFEDVMMSSR SQLEDNMNEEFEDTM\VIDLPPSRN RRERAELRP\DF\SDAAIIEDDSGFG MPMF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1928 | 7425 | A | 2069 | 1 | 2661 | |
| 1929 | 7426 | A | 2070 | 1 | 1454 | |
| 1930 | 7427 | A | 2071 | 1 | 2364 | |
| 1931 | 7428 | A | 2072 | 1 | 1368 | |
| 1932 | 7429 | A | 2073 | 114 | 1473 | VKGDRFGALRFNDPCPAGIKLPMTFF TELEKTTLKFIWNQKRARIAKSILSQ KNKAGGSTLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTGPSEITPHT YNYLIFDKPEKNKQWGNDSLFNKW CWENWLAICRKLKLDPFLTPYTRIN SRWIKDLNVRPKTIKTLEENLGITIQ DIGMGKDFMSKTPKAMATKDKIDK WDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIHKSGNNRCWRG CGEIGTLLHCWWDWKL VQPLWKS VWRFLRDLELEIPFDPAPLLGIYPN DYKSCCYKDTCTRMFIVALFTIAKT WNQPKCPTMIDWIKKMWHIYTME YYAAIKNDEFM/SFVGTWMKLEIIL SKLLQEQQTK |
| 1933 | 7430 | B | 2074 | 1 | 1890 | MDKFLDITYTLPRLNQEEVESLNRPI TGSEIVAINSLPTKKSPGPDGFTAEF YQRYKEELVPFLLKLFQSIEKEGILP NSFYEASILIPKPGRDITTKIENFRPIS LMNIDAKILNKILANRIQQHIKKLIH HDQVGFTPGMQGWFNICKSINIIQHI NRTKDKNHMIISIDAEKAFDKIQQH FMLKTLNKL GIDGTYLKMIRTIYDK PTANIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVMELLARAIQEKEIKGI QLGKEEVKLSLFADDMIRIKYLGIO LIRDMKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTLNFI WNQKRARTAKSILSQKNKARGIML PDFKLYYKATVTKTAWCWYQNRD IDQWNRTPESEITPHIYNYLIFDKPD KNKQWGKDSLFNKWCWENWLAIC RKLKLPFLTPYTTINSRWIKDLNV RPKTIKTLEENLGNTIQDIGMGKDF MSKTPKAMATKAKIDKWDLIKLS FCTAKETTISVNRQPTKWEKIFATY SSDTGLISRIYNELKQIYKKKTNNPI NKWAKDMNRHFSKEDIYAAQKHM KNAHHHPSEKCKSKHNEIPSHTS* |
| 1934 | 7431 | A | 2075 | 1 | 2676 | MKAEIKMFFEINENKDTTYQNLWD AFKAVCRGKFIALNAHNRKQERPFI DTLTSQLEKEKQEQTTHSKASRRQE MTKIRAELEKEIQKTLQKINESRSW FFERJNKIDRPLARLIKKKREKNQID AIKNDKGDITTDPTIEIQTIREYYKH LYANKLENLEEMDKFLDITYTLPRL NQEEVESLNRPI TGPEIVAINSLPTK RSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYEASILIPKPG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RDTTKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPGMQG WFNIRKSINVVQHINRTKHKNHMI SIDA EKAFDKIQQPFMLKTLNKLSD GTY LKIIRATYDKPTANIILNGQNLE AFPLKTGTRQGHPLSPLLFNIVLEVL ARAIRQEKEIKAQNLLKLISNFRKVS VYKINVQKSQAFLYTNNRQTESQIM RELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNIPCS WIGRINIVKMAILPKVIYRFNAIPIKL PTTFFTELEKTILKFIWNQKRAHIAK TILSQKNKAGGIMLPDFKLYYKATV TKTAWYWYQKRDIDQWNRIELSEII PHIYNHLIFDKPDKNKKWGKDSVF NKRCWENWLAICRKLKLDFTLTPY TKINSRWIKDLHVRPKAIKLEENL GITIQDIGMGKDFTSKTPKAMATKA KIDKWDLIKLKSFKTAKETTIRVNR QPTKWEKIFAIYSSDKGLISRIYKEL KQIYKKKTNNPIKKWAKDMNRHFS KEDIYAANRHMKKCSSSLAIREMQI KTTMRYHLTPVRKAIIKSGNNRC WRGCGEIGTLLHCWWDCKLVQPL WKT VWQFLRDLELEIPFYPAIPLLGI YPKDY |
| 1935 | 7432 | A | 2076 | 1 | 3045 | MDKFLNTYTLPRLKQEEVESLNRPI TGSDIEAIINSLPTKKISPGPDGFTA FCQRYKEE/LEKEGILPNSFYEASIIL PKPASDTTKKENFRPISLMNINAKIL NKILAKQIRQHIKKLIHHDQVGFIPG MHGLFNICKSVNIIQHINRTNDKNH MIISIDA EKPFDKIQQHFM LKTLNKL AQNLLKLIGNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMNEFPFTIASKR IKYLG IQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCS\WEKTTLKFI W/NQKRAHIAKSIISQKNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWGKDSL FNKWCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLKSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYA AKKHMKK CSSSLVIREIQIKTTMRYHLTPVRMA IIKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS VWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVILLHVFWDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLPCSSAC RRPVGLQLVMINSNGNFQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDPLLTA PL GSTPQAAVCRGPRGRELRAAPADS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HLFQRDLWPFNKVIVHGEKGSNQT SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENCGFSD PSDPQNLQKGEGCPSLVRASTAPPQ EKATEQPLLCKTTESPFGMTVGPCT DETLDHGAPSKHVPGTAHNELALL DLRVIKSAGSAAVHHKLKVLHWRS SLSNNKGTGRLYEQVA |
| 1936 | 7433 | A | 2077 | 1 | 2142 | |
| 1937 | 7434 | A | 2078 | 1 | 1551 | MRFKEKIHLEHNIKEPSEAASADGGA VASYPDLAKIVDEGRYKAEVMQLR CGWRAPASDCVHSVAVVGVDVSL EVLARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPTVSAQNLLKLIS NFSRVSGYKINVOKSQAFLYTNK QTESQIMSELPFTIASKTIKYLGIQLT RDVKDLFKENYKPLLNKIKEDTNK WKNIPCSWIGRINIVKMAILPKVIYR FNAIHIKLPMTFFTELEKTTLKFIWN QKGVHIAKSILSKKNKAGGIMLPHF KLYYKATVTKTAWYQYQNRDIDQWN CNRTEPSEIIPHIYNHLMFDKPKDNK KWGKDSL FNKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNVRPK PIKTLEENLGITIQDIGMGKDFMSKT PKAIATKAKIDKWDLIKKSFCTAK ETTIGVNRQPTTELEKIFAIYSSDKGLI SRIYKELKQIYKKK\NNPIKKWVKD MNRHFSKEDIYAVNRHMKKCSSSL VIREMQIKTTMRYYLTPV |
| 1938 | 7435 | A | 2079 | 1 | 1458 | GLSGDLLGAHQLPDVLCGVQPLPD LLLPPQNLLALQSLQDDLLWALDP AAAAPWAMDRGAATQWAVGPVV SDPWVMEAVASLPSAMDLDAAQ TWLLGAASLLVTDQPMQPSADQL AEFPDLLSKVSQSLRIKYLGIKLT VNDLFDKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIYRFN AIPKLPMTFFTELENTTLKFIWNQK RACIAKSILSKKNKAGSIMLPDFKL YHKATVTKTAWYQYQNRDIDQWN GTEPSEIMSHIYNLIFDKPEKNKQR GKDSLFSKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKIKT LEENLVNTIQDIGMGKDFMSKTPKA MATKAKIDKWDLIKKSFCTAKET TIRVNRQPTTEWEKIFAIYSSDKGLIS RIYKELQQIYRKKTNPIKKWAKD MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPV |
| 1939 | 7436 | A | 2080 | 1 | 2028 | |
| 1940 | 7437 | A | 2081 | 2 | 1547 | |
| 1941 | 7438 | A | 2082 | 3 | 1945 | |
| 1942 | 7439 | A | 2083 | 1 | 2124 | |
| 1943 | 7440 | A | 2084 | 1 | 2250 | |
| 1944 | 7441 | A | 2085 | 2 | 2483 | GKYYKLSSGTAPTCVSLGWGLARG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DSAAPALGSRTSACAPCSHGTWKL SLEPSDRLSPCDRSSEEAHTHAPHRL LALVASLPWSRLPLLAPQSHSEAEA TSQPTGVENHHQKTRYVKAGGPVI CRSLPESRGFLWASEGRKCMIGSW AAMGRLRKSTISSRFGPQTLAGTGR PQAIPVLKKHSDAVLLGVCFLKLLH QHHQELGENADSQTLPTQTHWEFILS EDYNKMTPVKNYQVLEVLARAMR QEKQIKSIQLGKEEVKLSVFADDMI VYLENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQIISEL PFTIPSKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCSWV GRINIMKMAILPRVIYIFNAISIKLPM TFFTELEKTTLKFIWNQKRARIAKTI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRGVDQWNRIEPSEII PHIHNLIFDKPDKNKKWGKDSLFT KWCWENWLAICRKLKLDPLTPYT KINSTWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKETTIRVNRQ PTEWEKIFTIYPSDKGLIPRIYKELK QYKKKSNPIKKWAKDINRHFSK EDIYAANRHMKKCSSSLVIREMQN KITIR/YHLTPVRMAIKKSGNNRDM DEAGNHHSEQTIARTENQAPYLLTH RWELNNENTWTQVEEHHTLGPIVG VICRKVFPNGSGPSKPSGLHFSQPLP QVTSVVAKITIVPWEMKLIAMGVQ DELNIAFHKNHLLMNDTTIHMTPIYI QPAPKS |
| 1945 | 7442 | A | 2086 | 1 | 2622 | |
| 1946 | 7443 | A | 2087 | 853 | 2831 | YPESTMNSNKFTRKKQTTPSKSG*R I*TDTSQKKTFMQPKDT*KNAQHH WSLEKCKSKPQ*DTISHQLEWRSK SQDRKD*QSTLLAILIKKKGQKNQI DT/IKNDKEGITTDPREIQTIREYYK HLYTNKVENLEEMDKFLDTYTLPT LKQKKEVKTLNRPITGSEIEAINSLP T/KKSPGPDRFTAIFYR/DIRSSGQG NQARERNKGYSIRKRGSIQVPVCR* HHCIFRKPHHLSPKSS*ADKQLQQS LRIQNQSAKITSIPHQ*QTNREPNE *TPIHNCFKENKMPRNPTYKGCEGS LQGELQTTAQ*NKRGHKRMEEHSM LMDRKNQYRENGHTAQGNL*IQCH PHQATNDDFFHRIGKNYFKVHMEPK KSPHRQVNPKEQSWRHHTT*LQ TILQGYNSQNSMVLVPKQRHRPME QNRAPGNNTIHLQLSDL*QI*QKQE MGKGFPI**MVLGKLANHM*KAET GSLPHILYKN*FKMD*RLKC*T*NH KNPRRKPRQYHSGHRHGQGLHD*N TKSNGNKSQN*QMGSN*TKELLHST RNYHQSEQATYRMGENFCNLLI*Q RANIQNLRQT*TNLQDKNKQPHQK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VGKGYEQTLLKRRHLCSQKTHEKM LIITGHQRNANQNHNEIPSHTS*NGD H/SNQVRKQQVLERMWRN |
| 1947 | 7444 | A | 2088 | 1 | 4954 | MVFSIDAQKAFDKIQHRFMLKTLN KLGIDGTYLKIIIRAIYNKPTGNIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLAIRAIRQEKEIKGIQLGKEEVK LSLFADDIIVYLENPIVSAQNLLKLI GNFSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYLGIQL TRDVKNLFKENYKPLLNEIKEDTDK WKNIPCSWIGRIHIVKMATLPKVIY RLHAIHIKLPMTFFTELEKTTLKFIW NKKRARIKSIKLSQKNKGGGITPPDF KLYYKATVTKTARYWYQNRDIDQ WKTREPSEIIPHIYNHLIFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLNPF LTPYTKINSRWIKDLNIRPKT IKTLEENLGNTIQDKGVGKDFMSQT PKAMATKAKIDKWDLIKLSFCTA KETTIRVNRQPTWEKIFAIYSSDKG LISRIYKELKQIDKKKANNPINKWA KDMNRHFSKEDIYAANRHMKKSSS SLAIREMQIKTTMRYHLTPVRMVII KKSGNNSEGLNPGYKGFPTIWAFL PVAQSKDSGLASLNSDPDIPSMLEC SLKAPQLYRSKNVGOVFISSASQAF TKKARIYARLRVSQALKTLCKSSCH DGWSFERLARIQEVSLPISPDILCSE AYHYGTPQWLVAATGTAQTFL NOKSQYQKQEQTTHSKASRMQEIT KIRAEKIEITRKTLOKIDESRSWFF ERINKTDRPLARLTQKREKNQIDA IKNGKGDITDPTGIQITIREYYKHL YAKKLENLEEMDKFLDTYTLPRLN QEEVDSLNRPIGTAEIVAINSLPTKK SPGPDGFTAIFYQRHKEELVPFLK LFQSIEKEGILPNSFYEASILIPKGR DTTKKENLRPISLMNIDAKILSKILA NRIQQHIKKLIHHDQVCFIPGMQGW FNIRKSINVIQHINRAKDKNHMISID AEKAFDKIQQTFMLKTLNKLIGDGT YFKIIRAIYEKPTANIILNGQKLEAFP LKTGTRQGCPLSPLLFNIVLEVLAIR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKIYKIDVQKSQAFLYTNNNDKQ ESQIMSELPFTTASRIKYLGIQLTR DVKDLFK\ENHKPLLNEIKEDTNKW KNIFIPCLWVGRINIVKMAILPKGIY RFNAIPIKLPMTFFTELEK\TTLKFIW NQRARITKSILSQKNKAGGITLPDF KLYYKATLTKTAWYWYQHRDINQ WNRTEPSEIIPHIYNHLIFDKPDKNK KWGKHSLFNKWCWESWLDICRKL KLDPYTKFTPYTKINSRWIKGLNVR PKTIKTLEDKPIQVFNTIQDIGMGKD FMSKTPKAMATKAKIDKWDLIKLK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SFCTGKETTIRVNRQPTWEKIFAIY SSDKELISRIYKELKQIYKKK\TNNPI KKWAKDMNRHFSKEDIYAANKHM KK\CSSSLAIREMQIQTMMRYHLTPV RMANKKSGNNRCWRGCGEVGTL HCWWDCNLVQPLWKS VWRFLRDL ELEIPFDP AIPLLGIYPKDYKSCCYK DTCTRMFIVALFTIAKTWNQPKCPT MMDWIKKMWHIYTM EYYAAIKND EFMSFVG TWMKLEIILSKLSQE QKT KHRIFSLIGGN |
| 1948 | 7445 | A | 2089 | 93 | 225 | |
| 1949 | 7446 | A | 2090 | 133 | 849 | PVWPKWSGWPLL MRSFAPARIATV VIGGVVAMAAVPMVLSAMGFTSV GIAASSIAAKMMSTAAIANGGGVA AGSLVAILQSVAWLYSSSHQEPLRK STDPKATELTRAGMEASALTSSAV TSVAKVVRVAS/GSCVVL P/LARIAT VVIGGVVAMAAVPMVLSAMGFTS VGIAASSIAAKMMSTAAIANGGGV AAGSLVAILQSVAWLYSSSHQEPLR KSTDPKATELTRAGMEASALTSSA VTSVAKVVRVASGS AVVLPLAALS PNISLLRPLLGALEASSFMLGSLTGT LFCNLEMGNRLRKWRGSQCGSTHR MFFWFPARIATSCDWRSCGPMAGC ANGCSSAMGLQLRAGIALVLP |
| 1950 | 7447 | A | 2091 | 161 | 1344 | TCPVLR YHSTMSSHKGSAVAQNG APASNREADTVELAELGPLLEEK GK RVIANPPK\AEEEQTCPVPQ\EEEE VRVL\TLPLQAH HAMEKMEEFVYK VWEGRW RVIPYDVL PD\WLKGND\ YLLHGH RPPMPSFRACFKSIFR\HTE TGN\WTHLA/LGFV LFLFLGILTML RPNMYFMAPLQ/EKKVVF GMFFLG AVLCLSFSWLFHTAYCHFGGVFSTF PQRELFKGLLLNMGELWSPGLYY SFYCSPQPARLIYLSIVCVLGISANV AQWDRFATPKHRQTRAGVFLG\LG LSG\VVPTMHFTNRWRALSKATTV GQ\MGWFFLMAVMYITGKLAFNAA RIPERFFPGKFDIWFQSHQ\FHVL\ VVAAAFVHFYGS/VSNLQEFPLTGL EGGL |
| 1951 | 7448 | A | 2092 | 2 | 1419 | RLRDPYRSSLRCRRGASRTSSAARS RSRSPAVEGCNRSPGAPQPAPRARR RPSRGAPGRAMVKVA\FNSALAQK EAKKDEPKSGEEALIIPPDAVAVDC KDPDDVVLVGQRRACGWRMCFGL AFMLAGVILGGAYLYKYFALQPDD VYYCGIKYIK\DDVILN/ESPSADAP AALYQTIEENIK\IFEERRSLNFISVP VPEFVADSDPAKIVQDFN\RKLTAYL DFNL\DKCYVIP\NTSMCYATPKTL LELLIN\KAGNLFALSPYLD SMRHM GYLLDR\ENIDHLGF\FTYRLCHDK\ ETYKLATRRKLFKGIQ\KREGQQLF SAISGIFENKFAVETLICSW |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1952 | 7449 | A | 2093 | 1 | 669 | |
| 1953 | 7450 | A | 2094 | 267 | 550 | GRTMMFGAKRRQEWEKVRKPED PEECPEEVYDPRSLYERLQEQKDRK QQELRGTVSNCKNMVRGLDEDET TFLDEVSRQQELIEKQPKRRRT |
| 1954 | 7451 | A | 2095 | 1 | 418 | |
| 1955 | 7452 | A | 2096 | 272 | 383 | |
| 1956 | 7453 | A | 2097 | 118 | 379 | RSGGGRGRRGPVHLHLKHPMLKRP DFLYRKPFSSRGWEHGPPSRKSHLL/ GAPPPFPKFFCHLC*APSPFRVLSPY QKRIHLVPPTQLH |
| 1957 | 7454 | A | 2098 | 1 | 276 | |
| 1958 | 7455 | A | 2099 | 1 | 341 | |
| 1959 | 7456 | A | 2100 | 1 | 450 | ACPYLALNSSMFCPDLILPTCLISST GFVGEKFLQGFKSLSPGSLWLSEG LDYFLSVPGDQYDVCAICLDEYED GDKLRVLPCHAYHSRCVDPWLTQ TRKTCPICK\QPVHRGPGDEDQ\EE\ ETQGQEEGYEGE\PRDQ\ASERTPF LG |
| 1960 | 7457 | A | 2101 | 238 | 525 | |
| 1961 | 7458 | B | 2102 | 178 | 373 | XLPQPLRGPLAHS DPERPAPFASSLF IGVLGKTKRKKLKGKEEGDERGS KGTNPALRKDPTFGF* |
| 1962 | 7459 | A | 2103 | 634 | 1940 | SGVDISFFELVFLPRRPHVAGKWDL GGGWDPGIPKGGAGRAQNSASAPC YQDARPPQPLSSRCHAPLQPFPLPV VVA AVLWGSGPDPGASFRATS\DH NCQHGIFADLPALF\GATLSLEGPQG L LGEPHPDNACSPIAPPPAPVNGS VFIALLRFD CNFDLKV LNAQKAG YGAAVIHNVNSNELLKMVWNSEEI QQQIWIPSVFIGERSSEYLALFVYE KGARVLLVPDNTFPLGYYLIPFTGIV GLLVLAMGAVMIARCIQHR\KR\LQ RNRLTK\EQLNQIPTQTNQKRDQ\Y DVCAICLIEYEDGDK\LR\VFPGAHA YH\NRCVDPWLTQTR\KT\CPICK\Q PVHR\GPGDEDQ\EEETQGQK\EGDE GE\PR\DH PASERTPLL G\SSPTLPTS\ FGFLRPKFPLV FSLGPSTDPPLSPPS SPCYPGLITPHTYTTFG |
| 1963 | 7460 | A | 2104 | 25 | 527 | EFHRLRENPPMVA VSCPTKTNVKA\ AWG\KVGAAHVRSMCAEALERMF LSFPT\TKTYFPHFDL\SHG\SAQVKG ATGKKVADALTNAVANVDDMPN VAVRPEATLHAHKL RVDPVNF\KL LKPLACLVDPGAHLPRPSFTPGGA TSSLGQSFLGFLKHRCLNLPNYR |
| 1964 | 7461 | A | 2105 | 262 | 364 | |
| 1965 | 7462 | A | 2106 | 3 | 1265 | PRPGLRAPDAPGSAPRERAQPRDPR AGQVRRLGDKARPRAQLRRESG GAESVTRPLRAASPAPPPRAARAA MSEKPKLGRRAPSASLSARCRAPR CCSCRARRPRIPQQCPRSVFACSSP ESLLVGVALSPGIALGAGSCVECTE SAREQASGVTPKGRALRGLAPVSST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AVLPGRPSRPRYSPTSPHRVPAIASP SVRPPLSFVSPQSCPQCAPTPTHRAP CAPTASIASPGVRPPLPIAPPGVRPR LPITPPMEGVKTENDHINLKVAGQD GSVVQFKIKRHTPLSKLMKAYCER QGLSMRQIRF\RFDDGQPNQWKLDDL STAGDWKDEDTVDVFPSSKTGRCA GEQPWQGTVSRGPVPKPGPSILALL LNGEHGDHADHKGVCNRSRTFTT MIFLSLMYFKLQLKTISAGMNL |
| 1966 | 7463 | A | 2107 | 4 | 408 | |
| 1967 | 7464 | A | 2108 | 1 | 465 | PACGYVPALSSASKSRSALGFPLPR CPRGRVDPELAALWPLLQCCCQLL QMGCFFPLGLGPAI*SPHPHQSHSLGI DRS*FQNAQSPPGFCVSCGPLREVS VCLP*PG*ARCCLGCSFGSGHSRLG NTAQ TANQCILPQASSTLCC*LHPQ NLVCP |
| 1968 | 7465 | A | 2109 | 126 | 488 | |
| 1969 | 7466 | A | 2110 | 1 | 5586 | |
| 1970 | 7467 | A | 2111 | 68 | 310 | TDLPTQNMVFTFSSNWG/TVRQVLS /YSCTRETLOHRELDKTRARGPE*GS VVLTSPLWSPCRKCATGTYHGSPH CQSSGGGR |
| 1971 | 7468 | A | 2112 | 2 | 630 | FFFFSDLLNFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*KPVNSSPSSVFVFCVASP AYRRSSSSFSRISFSVSGICPWWSR DGEVGTTFPSQFAKGRKGLIRRGGP QHPLRLSPGPIEEQK*GLVSPKARLG ISPCQLCPGFWSYL\DSVPSPPGGSC SGCTVPGSSHNVSPVSHPSGPACGV RTALSSA |
| 1972 | 7469 | A | 2113 | 331 | 754 | NFLKTNNVWSKWITHVLSQFWYQG FJLFCLGSIVKCTEIDSSICTE\PSHTK QHMLGGKNQTLNS/DPQGVKCSG* EAM*PRGGISQGDNDMGEMNGTT TTKTFCFIFMPGEDQGCSSCVSTRTT RKSQVQKSRGTISR YFHK |
| 1973 | 7470 | B | 2114 | 110 | 225 | XLGRPQLAGSLRSRFPISGMRGEFFT QDCQRNAGREELQGRLSIQSFSPILA LGPDDSCETKTGMDKLS* |
| 1974 | 7471 | A | 2115 | 83 | 287 | SLLLKCSGVIVLRRPLGYGQVMK* PGAA Y*GRTG*SHPFSTDWSTDG VRKSIWCHRNCRWESPS |
| 1975 | 7472 | A | 2116 | 167 | 397 | EPLLALLKSGEVAPARQEATGLGEA KCSCAMGLSGPKTQPQEGCEERRL QSKR*SSGDPGWGDEGHWP TPNRS CLL |
| 1976 | 7473 | A | 2117 | 1 | 540 | FCHLQIYYFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*NTSNSSPSSVFVICVTSP AIRRKLLNLSLGLSLLKFLGSVPGGT AGMGKSVPLSPSQVCCGFRSFNHQ AGHAPGCTVPGSSP*CVSRVQHPSG PCMWVTYPALSLSFNKSQCPWVFP LPTMPPG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1977 | 7474 | A | 2118 | 1 | 3121 | RQEAELARMGFDLQNVWIVSHINS NYKLCPSYPQKLLVPVWITDKELN VASFRSWKRIPVVVYRHLRNGAAI ARCSQPEISWWGWRNADDEYL VTS IAKACALDPGTRATGGSLSTGNNDT SEACDADFSSLTACSGVESTAAPQ KLLILDARSYTA AVANRAKGGGCE CEEYYPNCEVVFMMGMANIHAIRNSF QYLRAVCSQMPDPSNWLSALESTK WLQHLSVMLKAAVLVANTVDREG RPVLVHCSDGWDRTPQIVALAKILL DPYYRTLEGFQVLVESDWLDFGHK FGDRCGHQENVEDQNEQCPVFLQW LDSVHQLLKQFPCLFEFNEAFLVKL VQHTYSCLYGTFLLANNPCEREKRNI YKRTC SVWALLRAGNKNFHNFLYT PSSDMVLHPVCHVRALHLWTA VYL PASSPCTLGEENMDLYLSPVAQSQE FSGRSLDRLPKTRSMDDL SACTS SPLTRTSSDPNLNNHCQEV RVGLEP WHSNPEGSETSFVDSGVGGPQQT GEVGLPPPLPSSQKDYL SNKPFKSH KSCSPSYKLLNTAVPREMKSN TSDP EIKVLEETKGPAPDPSAQDELGRTL DGIGEPPEHCPETEAVSALSKVISNK CDGVCNFPESQNSPTGTPQQAQPD SMLGVPSKCVLDHSLSTVCNPPSAA CQTPLDPSTDFLNQDSSGSVASISH QEQLSSVPDLTHGEEDIGKRGNNRN GQLENPRFGKMPLELVRKPISQSQI SEFSFLGSNWDSFQGMVTSFPSGEA TPRRLLSYGCCSKRPNSKQMRATGP CFGGQWAQREGVKSPVCSSHSNGH CTGPGGKNQMWLSSH PKQVSSTKP VPLNCPSVPPLYLDDDG LFPPTDVI QHRLRQIEAGYKQEVEQLRRQ\ VRE FQ\ MRLDIRHWCAPPAEPPMDYEDD FTCLKESDGS DTEDFGSDHSEDCLS EASWEPVDKKETE VTRWVPDHMA SH\ CYNCDCEFWLAKRRHHCRNCG NVFCAGCCHLKLPIPDQQLYDPVLV CNSCYEHIQVSRARELMSQQLKKPI ATASS |
| 1978 | 7475 | A | 2123 | 3 | 259 | FPHRAGPILSSFQVPQRWLVGGFGR NCIAGGESVWDR TNKYTRN* AQE WGMFWSLDGHLGESIIRGRSNTG ALSCPWPLGHL P |
| 1979 | 7476 | A | 2124 | 1171 | 1784 | KLYSLSVLYKGEAKV VLLKPA\YDV SSFSFF\QRPTVQE FMTFTSQLIVER S/SRKGTRASVKEQDYLCHVYVRN DSL AG/VVVIADNEYPSRGGPFTLL\ EKVLDEFSQAKSHRIDWPVGIPWL TIHYPALDGHL SRYQNPREADPMT KVQAELDETKIILHNTPWESLLERG EKLLDLVSKSEVLGTQSKAFYKTA RKQNSCCAIM |
| 1980 | 7477 | A | 2125 | 2 | 262 | RGNWVFLHTTEFSLTRSLISFN SCFI TRLECSGAITAHCSLDLLGSS/QSPTS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PSRVAGTTGVCHHTQLIYLKQFFLE MRSPFVAQLV |
| 1981 | 7478 | A | 2126 | 36 | 376 | PFDPAVLTAKA AVRALVASRLAAA SAFTSLSPGGRTSPSQRALHLSVPRP AARVALVLVHLSRGGAEVQIFAPD VPQMHVIDHTKGQPSGESRCGGGI GTCFLSTSHGAFF |
| 1982 | 7479 | A | 2127 | 3 | 724 | LAAASAFTPLCPVCRTSPSQRALHL CVPRPAGRVSLVLSGCGVYNGTDIH EASAILVHLSRGGAEVQIFAPDVPH MHVNDHTKGQPSGESMNVLTES ERIRRGKITDLANLSAANHDA AIFP GGFGAAKNLSTFAVDGKDCKVNKE VERVLKEFHQAGKPIGHSLKDLP GH CPGRPLKWSLRKRCLRAPEGGPC CSRVTAGVKVSPMVSTSGSRPCQRS VPWMSAQREPMALSSVTD |
| 1983 | 7480 | A | 2128 | 172 | 1020 | PSDPAVLTA MA AVRALVASRLAAA SAFTSLSPGGRTSPSQRALHLSVPRP AARVALVLSGCGVYDGT EIH EASA ILEHLSRGRAEDHIFAPDVPHMHVI DHTKGQPSGESRNVLTESARIARG KITDLANLSAANHDA AIFP/GEGFG AAKNLSTFCRWTGKICKVNKEVER VLKEFHQAGKPIGLCCIA PVLA AK VLKGVEVTVGHEQE EGKWPYAG TAEAILALGAKHCVK(EVVEAH)VD QKNKVVTTPAFM CETA LHYIHDGV GAMVRKVLELTGK |
| 1984 | 7481 | A | 2129 | 1 | 416 | IQYRSDLELHSITMKKGGVLFLLGII LLVLIAAHGTPVVRKGRCSCHITNQ GTIHLQSLKDLKPFGPS PSCQKIDIIA TLKNGIQTCLNPDSADVKELIKKW EKQVSQKKKQKNGKKHQKKKVLK VRKSQRSRQKKT |
| 1985 | 7482 | A | 2130 | 2 | 81 | |
| 1986 | 7483 | A | 2131 | 2 | 130 | |
| 1987 | 7484 | A | 2132 | 1 | 524 | RPRIRHEPQTQREPTMVLSPA\DKTK AQRPPRLKLGATPGEYGGEP LERM VLFPPPTPKPYFPHF\DL SHGSAQVK GATAKKVA\DALTKAVAHVDGHA QTALSALSDLHGAQAFGWDPVNF QASLSHL PCLGEPWAGPPSPA EFHP LAVARLPWGQSFLGFL LKHRCLNL PNYR |
| 1988 | 7485 | A | 2133 | 388 | 654 | GLFFVLQFFFLFCFVFLRSHSVSQAG VHWC RHGSAAST/SPGSSDPPTLAS\ KVLGVTDMSHCTWAESYFFTKMGS SPVVACACSSSYLGG |
| 1989 | 7486 | A | 2134 | 384 | 622 | INAPPRCPQLCTSEVCAME/CPQRV PAGPCPGCPRGNLLIHAPSNRPGTTS QINDPQPFLRICFWGSPKTPSHRHKS FFF |
| 1990 | 7487 | C | 2135 | 44 | 340 | MKCSQPXRCHFQSD FQKCAPCPRA QTHWLEPPGRVQTISSMRNAQKGF ADSIRLWRLPASGVGWVVSPEGAG DPSHLLDPPGHSAPYSPAPRQLSRV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | P* |
| 1991 | 7488 | C | 2136 | 2413 | 2829 | MFPRRACATCPNLKRACVCAPLRP RFGTSRVWCACLLPSPEPTGSVNVI FYVPLPSGLLSTSAPGSRASGVGV LEGARGSFSSPWTLPGHFWSLFPSS LGSLSRCPLGKGDQEALVQGALGW GQRAWTPAQCSVDNG* |
| 1992 | 7489 | A | 2137 | 69 | 332 | YQVLKTDKNMSRISFFPFLRKGLAL SPRMECSGAITAHCSLRISQSQ/DDP/ AHVSLSSWGLQGTCHHTQLIFLFF VGDEGLCCPGVRS |
| 1993 | 7490 | B | 2144 | 73 | 358 | XVPGSRGPETKLWDDFSMSQATKR KHVVKEVLGEHIVPSDQQQIVRVLR TPGNNLHEVETAQGQRFLVSMPSK YRKNIWIKRGDFLIVDPIEEGEK* |
| 1994 | 7491 | A | 2145 | 80 | 201 | |
| 1995 | 7492 | A | 2146 | 498 | 748 | FLPRRGDNDSDYPQ/WTAKACRRRRT CW*T*TWIRSGQRKMWSCGRRL TTCMPRTRTAARLMACGSGSWRR SGPSCGCRLSP |
| 1996 | 7493 | A | 2147 | 1 | 1764 | MTTSQKHRDFVAEPMGEKPVGSLA GIGEVLGKKLEERGFDKAYVVLGQ FLVLKKDEDLFREWLKDTCGANAK QSRDCFGCLRE/WCAKSRPAAEVSE LKADSKEGPQAQGPEQERTGL |
| 1997 | 7494 | A | 2148 | 842 | 1186 | FLPRRGDNDSDYPQ/WTAKACRRRRT CW*T*TWIRSGQRKMWSCGRRL TTCMPRTRA WTTWRSKNLALSCP SMTKSLKSGHIPSASRAARLMA CGSGSWRRSGPSCGCRLSP |
| 1998 | 7495 | A | 2149 | 526 | 1158 | SCGLSLIKMTTSQKHRDFVAEPMGE KPVGSLAGIGEVLGKKLEERGFDKG L/YVVLGQFLADIEKMKTSFREWLK DTCGANAK\QSRDCFRMPFEKWCE ALLVDALLGKFSIPPAPQSRSLASRS RDSSPCPSYEGKD/CYCARTHL\RRYF RGSFGEFSPLNHFQLFFGILRSWHAF PRPFFPWPVSWVTVYQLFLEWDFP GPIPHPHPHFQSV |
| 1999 | 7496 | A | 2150 | 150 | 446 | HEGLLLKLRILSDVYFLLFFETRSCF VAHAGVQWHHYNLSL/T/PPGTPMF PPLLASQVAGSTGMNHQAQIKKTF FGENMILLCCSGWLSGIFVLYSLY |
| 2000 | 7497 | C | 2151 | 203 | 427 | MNFVRSIWMAQSTILLTARGXATLI IAISFLAPXLAQSVHAVSSFQSQQAD LLNGQCGFQQSSEPQPHVHTTSS* |
| 2001 | 7498 | A | 2152 | 1 | 1065 | |
| 2002 | 7499 | A | 2153 | 597 | 1292 | QTFSNTIFLLTRHKQHSMILVPMNT PGVKIIRPLSVFGYTDNFHGGHFEIH FNQVR\VPATNLILGEGRGFEISQG RLGPG\RIHHCMRTVG\WAERLLQI MCERATQRIAFKKKLYAHEVVAH WIAESRIAIEKIRLLTLKAAHSMDTL GSAGAKKEIAMIKVAAPRAVSKIVD WAIQVCGGAGVSQDYPLANMYAI TRVLRADGPDEVHLSAIATMELRD QAKRLTAKI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2003 | 7500 | A | 2154 | 1694 | 1886 | ASDSRVAPAGIS/PSAPFPTQLSPRRS PPSPPPPPQSPGLGIFSPKASPVGILHL FKTLFCILNV |
| 2004 | 7501 | A | 2155 | 1002 | 1480 | MLLLKTTERFEVSVCMACTYV\SNL GKKQRSVSFLASGLMRVSTGPELRL HHSFVLTGDVGRRICRLLVGLFTKG DTSSKR\HFPSPGP\CFLLCDLAR\V GSSPKINRVPHFTRTQTSTQRSCTVF VWQRCSLVGPFQVTVFTM\YFHSL RSISRFS |
| 2005 | 7502 | A | 2156 | 1 | 1623 | RLPFVDVDARVYADAPAKLLLPPL AFWELAVRLRGAEAAASERQVYSVA VKLLLHPAFQSCLLLTLLGLWRTT PEAHASSLGAPASAAFLQDLIHR GEGDSLTLQQLKALLNHLVDVGVR GNVTQHVQGHRNLSTCFSSGDLFT AHNF\SEQLRIGSSELHEFCPTILQQL DSRACTSENQENEENEQTEGRPSA VEVWGYGLLCVTVISLCSLLGASV VPFMKKTLYKRLLLYFRALAIGTLL LKRLFQLIPGAVWFQPLEDYYVSKS AVVFGGFYLFFFTEKILKILLKQKNE HHHGHSHYASESLPSKKDQEEGVM EKLQNGDLDHMIPQHCSSELDGKA PMVDEKVIVGSLSVQDLQASQSAC YWLKGVRYSDIGTLAWMITL\SDGL HNFIDGLAIGASFTVSVFQGISVAI LCEEFPHELGDVFIL\NAGMSIQQA LFFNFLSACCCYLGLAFGILAGSHFS ANWIFALAGGMFLYISLADMFP NEVCQEDERKGSILIPFIQNLGLLTG FTIMVVLTMYSGQIQIG |
| 2006 | 7503 | A | 2157 | 1 | 604 | MGTRWEPGWAPGLAPAAQARSS GRAAPAAGSERARERERDGGSVGG GGSSAIPSERAADAHGEDSGAYR WERANRPFNNCCCLAFYLGMEEA RWLYAGLFCVYGASLIAIATHVPLF GSQIKAE/DPSGDSAPAAHLPPQPAQ /PHLPQAQLMLTGSQLAGHPLGMR WSMATQHAGCVSQRCLFPMTVG CSQGNILWSL |
| 2007 | 7504 | A | 2158 | 22 | 1358 | VHFSMGAPEIRMSKPLEAEKQGLDS PSEHTDTERNGPDTNHQNPQNKTSP FSVSPTGPSTKIKAEPSGDSAPAAP LPPQPAQPHLPQAQLMLTGSQLAG DIQQLLQLQLVLVPSHHLQPPAQF LLPQAQSQPGLLPTPNLFQLPQQT QGALLTSQPRAGLPTQPPKCLEPPS HPEEPSDLEEELEQFARTFKQRRILG FTQGDVGLAMGKLYGNDFSQTTIF RFEALNLSFKNMCKLKPLLEKWLN DAETMSVDSSLPSPIQLSSPSLGFDG LPGRRRKKRTSIETNVRFALEKSFL ANQKPTSEEILLIAEQLHMEKEVIRV WFCNRRQKEKRINPCSAAPMLPSPG KPASYSPPHMTVPQGGAGTLPLSQAS SSLSTTVTTYLSCGDAPPQPDWR GWGRGRGCAPPQFHPLCHSPTPGH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HQQHKPQPLKAATRLSACQA |
| 2008 | 7505 | A | 2159 | 3 | 452 | |
| 2009 | 7506 | A | 2160 | 9 | 633 | NSARATDSERTHHGARLLPDKTNV KAAWGVGAHAGEYGAEALERMF LSFPT\TKTYFPFDLSQRSAQVKG ATGKKVADALTNAVA\HVD\DMPO TALSGPEATLHGAQSFQVDPVQLSS SLSHWPAWLTGPAHLPRPSFNPW RLQRLPWGQSFLGFLVEEPLLEPSKI PVKAWKPSGWPCFLCPFGASPOGPP SLSWNPYPRWSFE |
| 2010 | 7507 | B | 2161 | 55 | 372 | MERFLMDGFQPPQLSTYALTLYKH TATVDGKTILVADINVTQKSFNFAK KFSPLLYFVSAADGTNNVVKLFNDAI RLAVSYKQNSQDFMDEIFQELENFS LEQEEEN* |
| 2011 | 7508 | A | 2162 | 552 | 1809 | QLRGRGASRKWSALRRELGRRAWF ESAQSPDWRQGPKGPTSRVPLSSP HSEPHPEMAEDKTKPSELDQGKYD ADDNVKIICLGDSAVGKSKLMERFL MDGLYPSRFEVLLVPVGLPTLMYQ CPTAHPFVPAAQEGGLDFWDTAGQ DTLSSPPTPHPSMELVPVCSQPQQLS TYALTLYKHTATVDGKTILVDFWD TAGQERFQSMHASYYHKAHACIMV FDIQRKVTYRNLSTWYTELREFRPEI PCIVVANKIDDRPMSYLLSTADINV TQKSFNFAKKFSLPLYFVSAADGTN VVKVWLTAEVASKLFNDAILAVS YKQNSQDFMDEIFQELEVGVQVHISG GMEETAPLQG*GLQPSRVTLA*VCP TKCIRAAVEQMGGQASPATLFTNF SLEQEEEDVPDQEQSSSIETPSEEA |
| 2012 | 7509 | A | 2163 | 807 | 1389 | EPMAENKTKPSELDQGKYDADDNV KIICLGDSAVGQSKLMERFLMDGFQ PQQLSTYALTLYKHTATVDGKTILV DFWDTAGQERFQSMHASYYHKAH ACIM/LDINVTQKSFNFAKKFSLPLY FVSA\ADGTNNVVKLFNDAILAVSY KQNSQDFMDEIFQELENFSLEQEEE DVPDQEQSSSIETPSEEVASPHS |
| 2013 | 7510 | A | 2164 | 3 | 923 | RAARTRAEPEVECAAAARAGPAGVV RERAESRHGGRARGADPQRPWSLQ PSLGTARDNTLPSLGPGLSTARS QWAKNKTTPSELDQGKYDADDNV KIICLGDSAVGKFKLMERFLMDG\ FQPQQLSTYALTLYKHTATVDGRTI LVDF\FTAGQERFQSMHASYYHK AHA\CIMVFDVQRKVTYRNLSTWY TELSGSFRPEIACIVVANKIDADINV TQKSFNFAKKFSLPLYFVSAA\DTN NVVKLFNDAILAVSYKQNSQDFM DEIFQELENFSLEQEEEDVPDQEQSS SIETPSEEAASPHS |
| 2014 | 7511 | A | 2165 | 1 | 2715 | |
| 2015 | 7512 | A | 2166 | 1 | 2256 | |
| 2016 | 7513 | A | 2167 | 339 | 1086 | IQMNRFL\LM\SLYLLGS\ARGTSSQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PNELSGSIDHQTSVQQLPGEFFSLEN PSDAEALYETSSGLNTLSEHGSSEH GSSKHTVAEHTSGEHAESEHASGEP ATEHAEGEHTVGEQPSGEQPSGE HLSGEQPLSELESGEQPSDEQPSGEH GSGEQPSGEQASGEQPSGTILNCYT CAYMNDQGKCLRGEGTCITQNSQQ CMLKKIFEGGKLQFMVQGCENMCP SMNLF SHGTRMQIICCRNQSF CNKI |
| 2017 | 7514 | A | 2168 | 2 | 425 | |
| 2018 | 7515 | A | 2169 | 2 | 169 | GRVGD TLKAGINAVERRSNRCNGN SGFEGQSRYPSSGMSAKELCEND DLSTSLVLDPYLGFQTHKMNTR*FG S |
| 2019 | 7516 | A | 2170 | 2 | 227 | |
| 2020 | 7517 | A | 2171 | 177 | 1400 | LNAPGSQLSVGMKGLGESKNMVV NGRRNGGPLSNDHQNQSKLQHTG \KDTLKAGKNAVERRSNRCNGNSG FEGQSS/RYPVPSYGMTAKELCENDD LATSLVLDPYLGFQTHKMNTSAFPS RSSRHFA SQSDSLSHNNPVRFRPIKG RQEELKEVIERFKKDEHLEKAFKCL TSGEWARHYFLNKNKMQEKLFE HVFIYLRMFATDSGFEILPCNRY SSE QNGAKIVATKEWKRNDKIELLVGCI AELSEIEENMLLRHGENDFSVMYST RKNCAQLWLGPAAFINHDCRPNCK FVSTGRDTACVKALARDIEPGEEISC YYGDGFFGENNEFCECYTCERRGT GAFKSRVGLPAPAPVINSKYGLRET DKRLNRLKKLGDSSKNSDSQSV/SA LNTDADTTQEKNIASK |
| 2021 | 7518 | A | 2172 | 3 | 114 | |
| 2022 | 7519 | A | 2173 | 328 | 471 | |
| 2023 | 7520 | A | 2174 | 1 | 190 | |
| 2024 | 7521 | A | 2175 | 2 | 132 | SGLGRLPGPWQEAGSSRGPSGDM AGVKALVALSFSGAIGLTF/LHMLG CALEDYGVYWPLFVLIFHAISPIPHF IAKRVTYDS DATSSACRELAYFFT GIVVSCLWISPVILARVALIK\WGAC GLCV/VAGNAVIFLTIQGFFPIFGRG DDFSWE\QWGYWTD FS |
| 2025 | 7522 | A | 2176 | 191 | 479 | NTSLPNPSEVSHSSLRLDSGGAEAF VGGGTGVLKKPEGAGPAAPS/LGW RPRG*APHRTGSAQPPTAVPCR/PGA LGEDSSPGPPGALGGLGVIPQPSM |
| 2026 | 7523 | A | 2177 | 1920 | 2524 | TQYPPAEQRSQTLMQDV FALPLNSL CAQSSKTLNCKTQCHPCSILCKNLL KNKCLILHSRFTIQTAFEGGQLRI PLFPKPKVRSSQFQASVLELRRSQK PFVGGGTGVLKKPEGAGPAAPTSG WRPRGEAPHRTGT AQPTAVP\SGG RIWGKIPLPGPPGALEGVGFPSASPR FQLQPRCLKLDAGRRLRSGSKPHVK HL |
| 2027 | 7524 | A | 2178 | 239 | 380 | |
| 2028 | 7525 | A | 2179 | 34 | 202 | EPTTRQTLYMLITFTPHNHLVRETSS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VPFEQMKN*GSEFNTLSKALQTIS AKTRI |
| 2029 | 7526 | A | 2180 | 1 | 1566 | |
| 2030 | 7527 | A | 2181 | 574 | 1949 | KSKCRFPEGLSEGFGPMRKEALSSG SVQEA EAMLDEPQEQAEGSLTVYVI SEHSSLLPQDMMSYIGPKRTAVVRG IMHREAFNIIGRRIVQVAQAMSLTE DVLAAALADHLPEDKWSAEKRRPL KSSLGYEITFSLNPDPKSHDVYWD IEGAVRRYVQPFLNALGAAGNFSV DSQILYYAMLGVNPRVYSASSSYIF GHAQLPHVINPVESRLGSSAASLYP VLNFLLYVPELAHSPLYIQDKDGAP VATNAFHSPRWGGIMVYNVDSKTY NASVLPVRVEVDMVRVMEVFLAQ LRLFGIAQPHLPPKCLLSGPTSEGL MTWELDRLLWARSVENLG\QATTT LTSLGAASWARSATLFIKGRRGHLE VLQRL LAPVQKSAEELASGHL\DL P LSPAREAVTSSELAFFDPSSLHLLYF PDDQKFAIYIPLFLPMAVPILLSLVKI FLETRKSWEKA |
| 2031 | 7528 | A | 2182 | 76 | 419 | |
| 2032 | 7529 | A | 2183 | 71 | 350 | AFIPAMAELIQKKLQGEVEKYQQLQ KDLSKSMGRQKLEAQLTENNIVK EKRYESQLRDLERQSEQQRETLAQ LQQEFQRAQAAKAGAPGKA |
| 2033 | 7530 | A | 2184 | 175 | 1032 | GLLPHLGPRVQRLPRLSLSTLPCSLT RCPHPFLLPQIHHLTRIVGIGGTFDV SKLPFLSSPDLSKSMGRQKLEAQL TEYNIAKEVRDWDLWGEEGPVLA MVLITYVPSLHQELALLDGSNVVFK LLGPVLVKQELGEARATVGKRLDY ITAEM*VFIPPCAAPCDASEPLE*R C*TIAEQLSIVAPSPVPPTLSFPF*PP FFSLPWISRFSTYLFLAFSTLHSESY* FLPFCLSPSLLSKRYESQLRDLERQ SEQQRETLAQ LQQEFQRAQAAKAG APGKA |
| 2034 | 7531 | A | 2185 | 112 | 520 | AFIPAMAELIQ\KKLQGEVEKYQQL QKDLSKSMGRQKLEAQLTENNIV KEELALLDGSNVVFKL\LG PVLVK QELGEARATVGKRLDYITAEIKRYE SQLRDLERQSEQQRETLAQ LQQEFQ RAQAAKAGAPGKA |
| 2035 | 7532 | A | 2186 | 635 | 1015 | GGQKHPTGLLKPPANTAATMPKRK AKGDAKGDKAKVKDEPQRRSARLS AKPAPPKPEPGLKKAS\AKKGEKL\ P KGRKGGKADA\GKGLGNNPAKNPR LPLHFQFQKAE\GTGGLPSEMFIFES SGTYW |
| 2036 | 7533 | A | 2187 | 302 | 471 | TLSHRVLVEAQSREQLAALKKHHE EE\VHHK\KEIERLQKRNL SRHK\QK DSKLLKH |
| 2037 | 7534 | A | 2188 | 3 | 399 | LARNERLLAGGRDARGAAPASQWP VTA VGRRGTWLGRV/WGVRTMQA \RGFGSDQSENFPTGPRAPHP/RKAG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GALGKREQAEEERYFRAQSREQLA ALKKHHEEENVHHKKENERLAEEK FERHKQK\KMLKH |
| 2038 | 7535 | A | 2193 | 2 | 406 | ARAEMSRVALAVLALLSLSGLEAI QRTPKIQVYSRHPAENGKSIFLKCY VSG\FHPSDIE\VDLLKNGKE/RLKK VEPSDLS/FSAKDWSFY\LPYTEFH PQLKKDGVCPARVN\HVTLSAPARL VK\WDRRHVKQHQ |
| 2039 | 7536 | A | 2197 | 319 | 393 | WL/TPVIPTLWEAEVGGSFHRSSR |
| 2040 | 7537 | C | 2198 | 84 | 290 | MLPSKGLSFFSLQHRLDRSLLFPM SMITMLELECCRASSNHEVRWLKX HXVSQICSLICFPXMLTIRA* |
| 2041 | 7538 | A | 2199 | 2 | 743 | PRVRSEVSRYRSLADPEPTGRDTMT YADLFKYIIIGDTGVGKTCFLLQFTD KRFQPVHDLGVEFGGSLCSTLME NQFKLHIWD\TAGQESFRSITRSYY RGAAG\ALLVYDITRALKPFNHL\AS WLGGLPGQHFSFPTWVIHCFIGNKS DLESRRDVKREEGEAFAREHGRIFR GTSAKTACN\VEEAFINTAKR\YRKI HQGLFDVHNEANGIKIGPQQSISTSV GPSASQRNSRDIGSNSGCC |
| 2042 | 7539 | A | 2202 | 20 | 222 | |
| 2043 | 7540 | A | 2203 | 1 | 458 | RSSLTSLSNSAAAMAPVKKPCGEG GAKKKKQVLKFTL\DCTHPVEDGI MDAAQF*ASFCKERIKVKRKKLGT LSGGG/V*PIERSK\SKITVTSEVPFS KRV/YLKYLTKKY\LKNNLRDLV CRVVAYQPKRELNRNYSYFQINQDE GRREDED |
| 2044 | 7541 | A | 2204 | 2 | 321 | FIFFSFSFFSFFFSETGSCSVAQAG VQCHDHGSPQS/PNLPGSSDLPTSAS \KVLGITGVRHHSPLPLGFQMGIFLL FSMLKFCFWVCSALLCTVLEFLRTN YFLS |
| 2045 | 7542 | C | 2205 | 46 | 234 | MTLRXWITWPFLFLSPSSKCLHLI ASILLDLQLGSTHSSLSTIFFVVLAF RKIGLVCPP* |
| 2046 | 7543 | A | 2206 | 1 | 243 | |
| 2047 | 7544 | A | 2207 | 144 | 479 | RPLKPRRTF\CKK\CGKAPNPHKSDH STKKGKDSLYAPGKAAMTRKQS GYGGQ\TKPIFRKKAKTTKKIVLKA LSALSPTCRSKRMLAFKRWQAFLN LGGDKKRKGPSASS |
| 2048 | 7545 | A | 2208 | 75 | 540 | GGSGSVRVLRSESPREEAVEEEVAA VAVVVAAEEAGTNQLRAETMANI AVQR\KREFKEVLKSEETSKNQIKV DLVDENFTELRGEIAGPPDTPFERG RFPLELKIP\ETYPFNPPK/VFRFYAL KLWHPNISSV\TGAICLADILKDQWG SWQWT |
| 2049 | 7546 | A | 2211 | 1 | 2640 | MYSGNRSGGHGYWDGGGAAGAE GPAPAGTLSPAPLFSPGTYERLALLL GSIGLLGVGNLLVLVLYYKFQRLR TPTHLLL\VNISLSDLLVSLFGVTFTF VSCLRNGWVWDTVGCVWDGFSGS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LFARPAPLPARPRAPRPTPPRSPLAS STLPDPSRMAGAFLLRPLPPHAVQ DSIPVVSHLPPTCHQTL LLPKMADN LPTEFDVVIIGTGLPESILAAACSRSG QRVLHIDSRSYYGGNWASFSGLL SWLKEYQQNDIGEESTVWWQDLI HETEEAITLRKKDETIQHTEAFCYAS QDMEDNVEEIGALQKNPSLGVSN FTEVLDSALPEESQLSYFNSDEMPA KHTQKSDTEISLEVT DVEESVEKEK YCGDKTCMHTVSDKDGDKDESKST VEDKADEPIRNRITYSQIVKEGRRFN IDL VSKLLYSQGLLIDLLIKSDVSR VEFKNVTRILAFREGKVEQVPCSRA DVFNSKELTMVEKRMLMKFLTFCL EYEQHPDEYQAFRQCSFSEYLKTKK LTPNLQHFVLHSIAMTSESSCTTIDG LNATKNFLQCLGRFGNTPFLFPLYG QGEIPQGFCRMCAVFGGIYCLRHKV QCFVVDKESGRCKAIDHFGQRINA KYFIVEDSYLSEETCSNVQYKQISR AVLITDQSILKTDLDQQTSLIVPPAE PGACAVRVTELCSSTMTCKMDTYL VHLTCSSSKTAREDLESVVKLFTP YTETEINEEELTKPRLWALYFNMR DSSGISRSSYNGLP SNVYVCSGPDC GLGNEHAVKQAETLFQEIPTEEFC PPPPNPEDIIFDGGDKQPER/PLGTNN VVMAKLESSEVESKNLÆSPEKHPSK LEKSNLEMLFWTSFMASEFSLKD RFPI |
| 2050 | 7547 | A | 2212 | 328 | 583 | |
| 2051 | 7548 | A | 2213 | 1 | 416 | PSSGDMAGVKALVALSFSGAIGLTF LMLGCALEDYGVYWPLFVLIFHAI SPIPHFIKRVTYDS DATSSACRELA YFFT TGIVVSCLWISPVILARVALIK WGACGLVLGNAVIFLTIQGFFLIF GARGDDFSWEQW |
| 2052 | 7549 | A | 2214 | 1 | 180 | AAATGAVGAATYPCAAPNWK*RND EKTAADYKILGGSVLHLVLALRGG GGLRQ |
| 2053 | 7550 | A | 2215 | 162 | 557 | VASEHSPKIGASQGLDYEPLL VVAK VWYLTRPTGTKAGSVFSQYLPFLEP GILGPASLPWLRQTLTGKEIEIDIEP TDKVERNQRSVWEEKEGNPPPQQQ RLHLQVAKQMNDEKDSSLIYKILR WVQSFQT |
| 2054 | 7551 | A | 2216 | 684 | 1496 | LETSGLSENPLGQAVGFGQDEFFLE QTKKKGVKRPARLHTKPSQAPAVE EAPSGAISYNPSFEDHQTL LSA AHE VELQRQKEAEKLERQLRPCPATEQ ARHPRSSTFQELCEGLLEESDGE PGQGEPEAGDAEVCSTPARLATT EK\KTEQQRREKAVHRLRV TARA ALRAA\RLRATQELVFRVRGIQR PQ VALRLA\ELARRRRRRQ\ARREAEA \DKPRRLGT/RFKYQAPDIDVQLASSE LTDSLRTLKPEGQHPSRPVQELPRG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GI |
| 2055 | 7552 | A | 2217 | 116 | 285 | KLRNQRIQERHTDGGEPLKSL*CSP KTRVESRSASRRGPLFLNKGHARAR SSLTLA |
| 2056 | 7553 | A | 2218 | 3421 | 3698 | AGRGPLRLQSHRFGGPSQVDCLSPA APDQPGQHKGTPSPQKUQKLAGHG GAHLQSQPLGRLRREDPLSPGGGGC SEPRSHHCTPAWAREYGD |
| 2057 | 7554 | A | 2219 | 381 | 1772 | KMAESEN\RQELSES\SQEEAGNQIM VEGLGEHLERGEDAAAGLGDDGKC GEEAAAGLGEEGENGEDTAAGSGE DGKKGGDTDEDSEADRPKGLIGYV LDTDFVESLPVKVKYRVLALKKLQ TRAANLESKFLREFHDIERKFAEMY QPLLEKRRQIINAIYEPTEECEYKS DSEDC\DDEEMCHEEMYGNEEGMV HEYVDEDDGYEDYYYDYAVEEEEE EEEEDDIEATGEENKEEEDPRGIPD FWLTVLKNVDLTLPLIKKYDEPILK LLTDIKVKLSDPGEPLSFTLEFHKP NEYFKNELLTkTYVLKSKLAYYDP HPYRGTAIEYSTGCEIDWNEGKNVT LKTIKKKQKHRDL/WGTIRTVTEDF PKDSFFNFFSPHGITSNGRDGNDDFL LGHNLRTYIIPRSVLFFSGDALESQQ EGVVREVNDAIYDKIYDNWMAAI EEVKACCKNLEALVEDIDR |
| 2058 | 7555 | A | 2220 | 17 | 250 | |
| 2059 | 7556 | A | 2221 | 2 | 899 | GFSKKCVSSRSPELRVTRLRYLRIQ AFRGSCLATADLLLLVSPLRHPEPA KVLVLFLLSFASCWAGPGRAGPPG RSLTMA SLFKKKTVD DVIKEQNR ELRGTORANRDRAALEKQEKQLEL EIKK\MAKIGNKEA\CKVLAKQLVH LR\KQKT\RTFAVSSKVTSMTQTKV MDS\QMKMAGAMSTTAKTMQAVN KKMDPQKTLQTMQEFPGRENMAK MEMTEEMINDTLDDIFDGSDD\EEE SQDIVNQVLDEIGIEISGKMAKAPS A\ARSLPSA\ST\SKATISDEEIERQLK ALGVD |
| 2060 | 7557 | A | 2222 | 3 | 586 | ARAMGISRDNLHKRRKTGGKRKPY HKKRKYELGRPAANT\KIGPRRIHT VRVRGGNKKYRALRLDVGNFSWG SECCTRKTRIIDIVYNASNNELVRTK TLVKNCIVLIDSTPYRQ/WTPEEEEL NKKRSKKIQKKYDERKKNAKISSLL EEQFQOGKLLACIASRPGQCGRAD GYVLEGKELEF\YLRKIKARKGK |
| 2061 | 7558 | A | 2223 | 2 | 727 | LFPASAEQMGISRDNW\HKPRKTG GPRESPTYQAEKSM SLGRPAANTK ILAPRRIQHSPVCRGG*QVNTVPLRF DIVGNFSWG/SKECCTRKTRIIDVV YNAI**PSWVRYPRPLVERIC\VLID EQHPY\RWVRSPTYAL\PLGPQRK GAKLDSL RKEEIFKPKTDLK*IQKK YD*/ERKKNCQNSASLPGRSSFQOG KASLR CIAFK/RPGQC\GRA\DG YMT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ERLQQKTGIPFS\QMIL\FDDERRNIV DVSKLGTE |
| 2071 | 7568 | A | 2233 | 79 | 564 | SPTSAARSLRLRVMARLPKLAVFDL DYTLWPFWVDTHVDPFFHKSSDGT VRDRRGQDVRLYPEVPEVLK\DLQS LGVARCGCFQGQVRLGRGQPATGA LLTFFRYFVHR\EIYPGSKITHFERVA AETGISF\SQMIFFDDERREYCRRSA NWCVTCTSHPEW |
| 2072 | 7569 | B | 2234 | 48 | 209 | XKNQCETRTMQENGYSSHAVDGT GPAGGAGRPAGSTGAQVSVQPNFQ QDKFLGRX* |
| 2073 | 7570 | A | 2235 | 2 | 353 | |
| 2074 | 7571 | A | 2236 | 3 | 676 | SAVEFPFSLSHTTGTRPRTPIILLQGE NGYFIHTLWMGLALLGVLGDLGSGQ HRRPRSPCQPNFQQDKFLGRWFKR G\LASNSSWLREKKAALSMCKSVV APAT\DGGFNL\TSTFLQEKTSVETR TML\LOPRGVPSASLQLTGVPHWGO A/HYSVSVVETDYDQYALLY\TRAS KGPGEDEFMATLYSRTQT\PARAELK EKFTAFC\KAQGFTEDTIVFLPQTDK CMTEQ |
| 2075 | 7572 | A | 2237 | 1 | 1165 | MGVTEVFLKDVITILLNLEELVQCRQ TWGEARTRGKRVLGSLADEIVVRT QPPSLEHKAWNATCKHWLAEEA ALEKYYSIFYGIEFVVGVLGNTIVV YGYIFSLKNWNSSNIYLFNLSVSDL AFLCTLPLIRSYANGNWIYGDVLC ISNRYVLHANLYTSILFLTFISIDRYL IIKYPFREHLLQKKEFAILISLAIWVL VTLELLPILPLINPVITDNGTTCNDF ASSGDPNYNLIYSMCLTLLGFS\PLF VMCLFYKIALFLKQRNRQVATAL PLEKPLNLVIMAVVIFS\VLFTPYHV MRNVRIASRLGSWKQYQCTQVVIN SFYIVTRPLAFLNSVINPVFYFLLGD HFRDMLMNQLRHNFKSLTSFSRWA HELLSFREK |
| 2076 | 7573 | A | 2238 | 1 | 567 | |
| 2077 | 7574 | A | 2239 | 58 | 544 | GKKMGSKAKKRVLLPTRPAPPTVE QILEDVRGAPAE\DPVFTILAPEDPP\ VPFRRMME\DAEAPGEQLYQQSRAYV AANQRLQQAGNVLRQRCELLQRA GEDLEREVAQMKQAALPGGEGWL LGLTLWGLGALGRAQGWSATQAL PGGPSAPDWH\SRGPSRGC |
| 2078 | 7575 | B | 2240 | 1 | 1551 | MCELDILHDSLYQFCPELHLKRLNS LTLACHALLDCKTLTLTELGRNLPT KARTKHNIKRIDRLLGNRHLHKERL AVYRW\HASFICSGNTMPIVLVDWS DIREQKRLMVLRASVALHGRSVTL YEKA\PLSEQCSKKAHDQFLADLAS ILPSNTTPLIVSDAGFKVPWYKSVE KLGWYWLSRVRGKVQYADLGAEN WKPISNLHDMSSSHSKTLGYKRLTK SNPISCQILLYKSR\SKGRKNQRSTRT HCHHPSPKIYSASAKEPWV\LATNLP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VEIRTPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDIMLLI ALMLQLTCWLAGVHAQKQAFDC DSSAVHRLRYCKGRDYNRVRSSCV QRHAPVLNRKIGTGSDQHANEFGLS WILLGARTPTCKADLSRPYSCPHP QPQQRFLGDSGITTTSVPRYRGQEH CLHPKLQSTKRFIKCTTAWNENRRK YQVMPIEAQRPKCQLLPNRSPTWQ ISIDKGPRQDTFMLFPPIKI* |
| 2079 | 7576 | A | 2241 | 2 | 456 | GTRSTRARRRWLSSPPRACPGTEV RSTACTPSCAPPVSMRLAALLLL LLALYTARVDGSKCKCSRKEPKIR YSDVKKLEMKPKYYPHCEEKMMVIT TKSVSRYRGQEHCPHPKLQSTKRFI KWYNAIWNEKAQRRVYEEAQGLR RRIG |
| 2080 | 7577 | A | 2242 | 308 | 615 | ETRVASGTGAAEV*GMVRLDISE GRAAVAAVVGGVAVGTVLVALS AMGFTSVGIAASSIAAKMMSTAAIA NGGGVAAGSLVAILQSVGAAGLSV TSKVIG |
| 2081 | 7578 | A | 2243 | 332 | 484 | |
| 2082 | 7579 | A | 2244 | 240 | 610 | LWVEVQSEWRLTEAKGPTMGKES GWDSGRAAVAAVVGGVAVGTV PWRSSAMGFTSVGIAASSIAAKMM STAAIANGGGVAAGSLVAILQSVGA AGLSVTSKVIGGFAGTALGAWLGS PPSS |
| 2083 | 7580 | B | 2245 | 158 | 2382 | MARGKAKEEGSWKKFIWNSEKKEF LGRTGGSWFKILLFYVIFYGCLAGIF IGTIQVMLLTISEFKPTYQDRVAPPG LTQIPQIQKTEISFSSMAIRDAGFEIS AMQMFMNMDRVNVEQFYEVYKGV VTEYHDMVTEMYSGPCVAMEIQQ NNATKTFREFCGPADPEIARHLRPG TLRAIFGKTKIQNAVHCTDLPENGL LEVQYFFKILNN* |
| 2084 | 7581 | A | 2246 | 753 | 1007 | LAQGCSPGPSQDTALPGPPPCTEP/ CPVPYVLRSTPEPPQHGTCHSPCLLP IPLCSSPSLGGGGNSEGEKALTFHV CGDHPVKN |
| 2085 | 7582 | A | 2254 | 188 | 833 | ALIMSFIFEWYNGFSSVLQFLGLYK KSGKLVL\GLDNAGKTTLLHWLK DDQIGPTLFPPLPPTSEELTIAG\MT FTTFDLGGHGAHVAVWKN\YLPS QLMGFVFLVDCA\DHFSWNPKE LNALMT\DETILPMCPL\ILGNK\IDR TDAISEEKLREIFGLYGQTTGKGNV TLKELNA\RPMEVFHVAVLLKEGK VYGRGFSAGLLPVLFD |
| 2086 | 7583 | A | 2256 | 333 | 621 | CRKNSCYQAQNFNLRIPFSTTKLINL FHF*ND SQKST*/SDSHLARSSQFCS LN*NY*I*TAKSHDVVCTRQHFP SLS ESYIWHVKEKKYNPTAAAI |
| 2087 | 7584 | A | 2257 | 29 | 659 | LSVASFSFLSNASAEDTMSRLSRSL WAATCLGVLCVLSADKNNTTQHPNV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TTLPPIVRETSAPVTPLPLVTTTPAPET CEGRNSCVSCFNVSVVNTT\CFWIE CK\DESYCSHNST\VSD\CQVGNTTD FCSVST\ATPVPTANS\TAKTHSSSP LLQLPRQLLHQGTNNNTVNS\TSQP VRKSTFDAASFIGGIVLVLEIRCHTR NYIPDLKK |
| 2088 | 7585 | C | 2258 | 101 | 411 | MEMKMQSERLSKEYDQLLKEHSEL QKQREILPHRRGESTVTTXXXXXX XEPQQRNADXXXXXXXXXXXXXXXX XXSSSRSMALQIPIKXXXXXXXXXX XXXXXL* |
| 2089 | 7586 | A | 2259 | 2 | 575 | |
| 2090 | 7587 | A | 2260 | 1 | 265 | SDALSKAQNDVMEMKMQSERLSK EYDQLLKEHSELQHSSFGFLSKRS HKNGSIGKQTGSRKGSFRKRQKEK TVNFIKDTLQYTVSK |
| 2091 | 7588 | A | 2261 | 47 | 906 | RKKLPLQWPAVPPFLYAEIGLILIFC LPFIPPQRWQKIFSFNVWGKIATFW NKAFLTIIILLIVLFLDAVREVRKYSS VHTIEKSSTSRPDAYEHT\QMKLFRS QKNLYIPGISLFFWLVLRLVTLITQ LAKEPVTQRCALYLQAENTNKA KAFMEENEKLRILKSHGKDEECVL EAENKKLVEDQEKLTTELKTSDA LASKAQNDVMEMKMQSERLSKEYD QLLKEHSELQVPLGSFYILAFAPGL HNPHSPSSPRSGGGFSAIDNPRGALPP CLVCVLFHHL |
| 2092 | 7589 | A | 2262 | 669 | 995 | KVFFCFYRIYVCICVCVCVCVC/TLQ TL/CYSIANMLTSSQCLQSCGSQSW CQMHKSSKAJMTIPCKFISRKPWEG DCSSLEPHGVSAFDIWVPQLCIKKV LNHFSPRKN |
| 2093 | 7590 | A | 2263 | 3 | 379 | WPFLKLRLGTCTCCSHEGRAAA WSAESSLQHSAAVVTMSLPLNPKPFL NGLTGKPMVKLKWGMEYKGYLA VSVD\GYMNMQLANTEEYIDGALS GHLGEVLIRCNNVLY\RGVEEEEED GEMRE |
| 2094 | 7591 | A | 2264 | 68 | 268 | QYLSLLLTQYSLVFICWLFICL\LYV YLFLCMLLCKYGLQLFLCGILSFRIS CKLLESRIHVPLFL |
| 2095 | 7592 | A | 2266 | 190 | 554 | HGVRSDLGRWPDHLCAVCRHYHH LLHLLLLLPLQDVPPTTSWLSPPPHP PLWCM/PPYPQPPSVPPSYPGPSLPG LPHHAASARECQQHPYPIAVPHTLT HAHAHGPTTRPTTRPLAGRSSRD |
| 2096 | 7593 | A | 2267 | 2 | 445 | |
| 2097 | 7594 | A | 2268 | 200 | 894 | TSPRARPHCSLCLPNLPPVTYMHY ETDGFSLGVFLLKSGTSIPLHDHPG MHGMLKVLYGTVRISCMDKLDAG GGQRPRALPPEQQFEPPLQPREREA VRPGVLRSAEYTEASGPCILTPHR DNLHQIDAVEGPAFLDILAPPYDP DDGRDCHYYRVLEPVRPKEASSA CDLPREVWLL\ETPQADDFWCEGEP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YPGPKGLPLKPLAHQERWAEDVPY PTTRAVSLPP |
| 2098 | 7595 | A | 2269 | 257 | 781 | QELLSGLVNYFSLSWFLYVAQESIP SLPQSPMRETPSKAFHQYSNNISTLD VHCLPQLPEKASPPASPPIAFPFAFE AAQVEAKPDELKVTVKLKPRLRAV HGGFEDWRPLNKKWTGMKWKKG KIYIGTPNGTLKTPLAEDEID/EFSKE MGHFLKPDGPKIIGKVWHEKGM NDK |
| 2099 | 7596 | A | 2270 | 271 | 404 | |
| 2100 | 7597 | A | 2271 | 2 | 5684 | PTSPCGEGYGISLNLTFIISNMRVLR AHFIELQFPFMGQVVTGTQNSEGQN LGPQAIPQDGSITHQISRPNPPNFGP GFVNDSSQRKQYEWQETQQLLQ MQQKYLEEQIGAHRKSKKALSAKQ RTAKKAGREFPEEDAEQLKHVTEQ QSMVQKQLEQIRKQKKEHAELIED YRIKQQQQCAMAPPTMMPSVQPQP PLIPGATPPTMSQPTFPMVPQQLQH QQHTTVISGHTSPVRMPSLPGWQPN SAPAHPLNPPRIQPPIAQLPIKTCTP APGTVSNANPQSGPPPRVEFDDNNP FSESFQERERKERLREQQERQRIQL MQEVDQRALQQRMEMEQHGM VGSEISSRTSVSQIPFYSSRLYLCDF VMQPLGPLQQSPQHQQQMGQVLQ QQNIQQGSINSPSTQTFMOTNERRQ VGPPSFVPDPSIPVGSPNFSSVKQG HGNLSGTSFQQSPVRPSFTPALPAAP PVANSSLPCGQDSTITHGHSYPGST QSLIQLYSDIPEEKGKKKRTRKKKR DDDAESTKAPSTPHSDITAPPTPGIS ETTSTPAVSTPSELPPQADQESVEPV GPSTPNMAAGQLCTELENKLPNSDF SQATPNQQTYANSEVDKLSMETPA KTEEIKLEKAETESCPGQEEPKEEQ NGSKVEGNAVACPVSSAQSPPHSA GAPAAKGDGSGNELLKHLKKNKKSS SLLNQKPEGSCSEDDCTKDNKLVE KQNPAGLQTLGAQMGGFGCGN QLPKTDGGSETKKQRSKRTQRTGE KAAPRSKKRKKDEEEKQAMYSSTD TFTHLKQVRQLSLLPLMEPIIGVNFA HFLPYGSGQFNSGNRLGTFGSATL EGVSDYYSQLIYKQNNLSNPPTPPA SLPPTPPPMACQKMANGFATTEELA GKAGVLVSHEVTKTLGPKPFQLPFR PQDDLLARALAQGPKTVDPASLP TPPHNNQEELRIQDHCGDRDTPDSF VPSSSPESVVGVEVSRYPDLVLKE EPPEPVPSPIIPILPSTAGKSSESRRND IKTEPGTLYFASFGPSPNGPRSGLIS VAITLHPTAAENISSVVAAFSDLLH VRIPNSYEVSSAPDVPSMGLVSSHRI NPGLEYRQHLLLRGPPPGSANPPRL VSSYRLKQPNVPFPPTSNGLSGYKD SSHGIAESAALRPQWCCHCKVVILG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SGVRKSFKDLTLLNKDSRESTKRVE KDIVFCSNNCFILYSSTAQAKNSEN KESIPSLPQSPMRETPSKAFHQYSNN ISTLDVHCLPQLPEKASPPASPIAFP PAFEAAQVEAKPDELKVTVKLKPR LRAVHGGFEDCRPLNKKWRGMKW KKWSIHIVIPKGTFFKPPCEDEIDFL KKLGTSLKPDVPKDYRKCCFCHEE GDGLTDGPARLLNLDLDLWVHLNC ALWSTEVYETQAGALINVELALRR GLQMKCVFCHKTGATSGCHRFRCT NIYHFTCAIKAQCMFFKDKTMLCP MHKPKGIHEQELSYFAVFRRVYVQ RDEVRIASIVQRGERDHTFRVGS LI FHTIGQLLPQQ\MQAFHSPK\ALFPV GYEA\SRLLLGGTRYANRRCR\YLC SIEGGRDG\RPVFVIR\IVGNKGHGR TGV LKVD\SPKGVWDKILEPVACV RKKSEMLQLFPAYLKGEDLFGTLVS AVARIAESLPGVEACENYTFRYGRN PLMEPPLAVNPTGCARSEPKMSAH VKRFVLRPHTLNSTSTSKSFQSTVT GELNAPYSKQFVHSKSSQYRKMT\ EWKSNVYLAARSRVSGGWGLLWL VVRTLEETHHGSFEYIGTNHFETKL GQQGKEKLYESQNRGVYMFMRMDN DHVIDATLTGGPARYINHSCAPNCV AEVVTFERGHKIISSSRRIQKGEELC YDYKDFEDDQHKIPCHCGAVNCR KWMN |
| 2101 | 7598 | A | 2272 | 1 | 2806 | |
| 2102 | 7599 | A | 2273 | 288 | 843 | AGSGVLQGLFICPKAPGPRPTGAEG KR\KLQIGVKKR\VD\HCPIKSRK\GD VLHMHYTG\KLEDGT\EFDSKPAPR TSPFVFSL\GTGQVIK\WDQG/LCL GMCEGE\KRK\LVIPS\ELGYGE/RGE LPPKIPRPVQPLVFEVELLKIRADEL SCNQTGEGQGEKAPHQGPDCSKKK NKKQKPIKKTLSKPK |
| 2103 | 7600 | A | 2274 | 80 | 308 | VLTHLGNWILGSTEGPMGGP*FCTN LSEGLRFGISPSWREALYGWHA |
| 2104 | 7601 | A | 2275 | 2 | 456 | RSFFFFCEVGSWVGSMRVVMARL LSEGEQGIPTACAAFAQQPGGRPRR GLAGVGEGGPQCSWVNYRCTLEFL VSL LGTDLARGRGNSASGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCHVV QGWVSTSWGSSSPVPQFFPKLLEF TGK |
| 2105 | 7602 | A | 2276 | 2 | 81 | |
| 2106 | 7603 | A | 2277 | 325 | 485 | ELRVDPVNF\KL\LSHCLLVTLAAHL PAEF\TPAVHASLDKFLASVSTVLTS KYR |
| 2107 | 7604 | A | 2278 | 291 | 529 | LFLCKVGTWHQGNHQA KAPKAPG TPPTPSYPGTSPSRQLLWQWVQPRPA LPA\PLPAVGTSSSTSPGRQCPGFS AQ HHLFP |
| 2108 | 7605 | A | 2279 | 52 | 109 | TVRLPR\HPGSRKNMASYCRIPACIA AERRYGT C MYQGR I WAFSS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2109 | 7606 | A | 2280 | 3 | 452 | |
| 2110 | 7607 | A | 2281 | 26 | 526 | NSTDSE RTHPWLLSPADKTTVK/AP AWGKVG AHAGEY G\SEALERMFLS FPTTKTYFPHFDLSHGFCPLRATG KKVADALTKRRGAPLDDMPNALV RPL\SDLHAHKL\RVGPGSTFKLLKP LACL\LTGPAHLPRPSFTPGGCKAS LGQSFLGFLKHRCLNLPNYR |
| 2111 | 7608 | A | 2282 | 447 | 539 | |
| 2112 | 7609 | B | 2283 | 8 | 694 | MQYNRRFVNVVPTFGKKKGTTFTK IFVGGLPYHTT DASLRKYFEGFGDIE EAVVITDRQTGKSRGYGFVTMADR AAAERACKDPNPIIDGRKANVNLA YLGAKPWCLQTGFAIGVQQLHPTLI QRTYGLTPHYIYPPAIVQPSVVIPAA PVPSLSSPYIEYTPASPVYAQYPPAT YDQYPYAASPATADS FVGYSYPAA VHQALSAAAPAGTT FVQYQAPQLQ PDRMQ* |
| 2113 | 7610 | A | 2284 | 3 | 191 | |
| 2114 | 7611 | A | 2285 | 101 | 444 | CSLFVPRPRSLQPLRRVTGQETGRP RSKAHVASTWRAFPEDQVLLAG APLEDEATLGQCGVEALT TLEVTVG \RMLGGKSPWFPWPVLGKVMKVRL LKVAKQGERRKKKTGSG |
| 2115 | 7612 | A | 2286 | 2622 | 2881 | KKSKDNKTFFFFFETESCSALQAGV QWCNLGSLQTLPPGSND SHASASR VAGTKGMCHHARLIFVFLVETGLH HVGQACLGT PDLK |
| 2116 | 7613 | A | 2287 | 41 | 655 | TKLVMMQKLLKCSRLVLALALILV LESSVQGYPTRKPRHQWVPCNPDS NSANCLEEKGPMFELLPAESTKIPR LRTDLFPKTRIQ\DLNRIFPLSEDYS GSGFGSGSGSG\SGS\GSWFPNGKW EQDYQL\VDESDAFHDNLR\SLARI LASASRDWGQHGLAEFNVIKEDL PTLTTRQM VVKQYFNVP MVNMIN WDKEFYRNF |
| 2117 | 7614 | A | 2291 | 163 | 703 | READMGTMKTQRDGHSLGRWSLV LLLGLVMPLAIIAQVLSYKEAVLR AIDGINQRSSDANLYRLDLDP RPT MDGGPADTTKPVSF TVKETVCPRP TQQ\SPKDGDFKRDG LLNRGMGTV\ TLN\QARGSF DISCDKNKR FALLG DFFRKSKEKIGKEFKRIVQRIKDFLR NLVPRTES |
| 2118 | 7615 | A | 2292 | 100 | 546 | PPRTGQRQPLHSARRHGPSVS\ELAC IYSALISARTDEVTVT EDKINAL\IK AAGVNVEPFWPWLCLQRPLA\NV NIGSL\CNVRGPVEPAPSSLVAAP\ AGRSLPPPLACCSKLKEERKLEAKK RKNPKEVLNDDIGLLVLFELKPLL |
| 2119 | 7616 | A | 2293 | 33 | 494 | |
| 2120 | 7617 | A | 2294 | 1 | 609 | PLKRSDGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPEEKSAVTALW GKVNVD EVGGEALGRLLVVYPWT QRFFESFGDLSTPD AVMGNPKVKA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HS\KKGLRGAFSDGLAHLADNLKGT FATL\SEL\HCDKAAPWIPEELQAPW ATCLVCVAWPITFGKRISTPPVAGL PNQENWLAWCWLNALGPTSNHLS LAFLAGPISN |
| 2121 | 7618 | A | 2295 | 1 | 338 | AALAWAVSRLHFSRLSFPPWAFRG AFAAVPTTAAMISLTDQKIGMGLT GFGVFFLFFGMILFFDKALLAIGNG\ FFPVVDGFIIRVPVLGSLNLPGIRS FVDKVGESNNMV |
| 2122 | 7619 | A | 2296 | 67 | 283 | LPFPGCIIFFLF*VLFVAGLAFVIGLER TFRFFFQKHKMKATGFFLGGVFVV LIGWPLIGMIFEIYGFFLLFR |
| 2123 | 7620 | A | 2297 | 3 | 209 | |
| 2124 | 7621 | A | 2298 | 3 | 544 | TRAALAVAVSRLHFSRLSFPPWAFR GAVAAVPTTAAMISLTDQKIGMG LTGFGVFFLFFGMILFFDKALLAIGN VLFVAGLAFVIGLERTFRFFF\QKH KMKATGFFLGWVYLVLIGL/WPLI GMIFEIYG\FLLFRGFFPCRCWTFI RKECPVLGIPSPNLPGIRSFVDKVGES NNMV |
| 2125 | 7622 | B | 2299 | 54 | 1731 | XKLSRECEIKYTGFRDRPHEERQAR FQNACRDGRSEIAFVATGTNLSLQF FPASWQGEQRQTPSREYVDLAREA GKVYLKAPMILNGVCVIWKGWIDL QRLDGMGCLEFDEERAQQEDALAQ QAFEEARRRTREFEDRDRSHREEME VHELEKSKRALETQMEEMKTQLEE LEDELQASEDAKLRLEVNMQALKG QFERDLQARDEQNEEKRRQLQRQL HEYETELEDERNERALAAAANKKL EGDLKDLELQADSAIKGREEAIKQL RKLQAQMKDFQRELEDARASRDEI FATAKENEKKAKSLEADLMQLQED LAAAERARKQADLEKEELAEELAS SLSGRNALQDEKRRLEARIAQLEEE LEEEQGNMEAMSDRVRKATQQA QLSNELATERSTAQKNESARQQLER QNKELRSKLHEMEGAVKSKFKSTIA ALEAKIAQLEEQVEQEAREKQAAT KSLKQKDKKLKEILLQVEDERKMA EQYKEQAEKGNARVKQLKRQLEEA EESQRINANRRKLQRELDEATESN EAMGREVNALKSKLRGPPPPQETSQ* |
| 2126 | 7623 | A | 2300 | 1 | 2448 | |
| 2127 | 7624 | A | 2301 | 1 | 2655 | |
| 2128 | 7625 | A | 2302 | 5 | 605 | VDPDSGQIQVPCTPRGLKWSPNMN PARKTDACGEDTHPSLLGVPPFSRPP LGILRFALQNPRSPGKESEMLPPPA WVYLKAPMILNGV/CVIWKGWIDL QRLDG/MGCLEFDEERAQSWPW*A HPQC*EGRRPSCRELGNVALGADG DSPGSIYTRRWKLRSQRVPAPPPQE PKMPSLCCRNTSTTFSGRPSQSPRTK KQRPR |
| 2129 | 7626 | A | 2303 | 1 | 588 | MGFCHVDQTGLELLTQPLLALIGAA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LEGGRAGGAADLAPDFGRLALQIK YTGFRDRPH/EERQARFQNA CRDGR SE/IFFPASWQGEQRQ/TPSREYVDL EREAGKLNIPKGPAGDETPSSLSSM MIVLSSDSGPAVLAIPNLVTPPRYTP MVPCGGHHQAQRKRPLCTPPPSIQ QGSMSVKSMPTPVAAHKSFTSALC |
| 2130 | 7627 | A | 2304 | 1 | 615 | GLKGGKMPRVVPDQRSKFENEFF RKLSRECEIKYTGFRDRPHEERQAR FQNA CRDGRSEIAFVATGTNLSLQF FPASWQGDQRQTPIREYVDL EREA GTVYLKAPMILNGVCAIWKGWIDL QRLHGMGCLEFDEERAQQEDALTQ QAFEEARRMTREFEDRDRSHRQEM EARVSQLLAVTGKKIQLDPRPGSNL GGGDDLKLR |
| 2131 | 7628 | A | 2305 | 73 | 168 | |
| 2132 | 7629 | A | 2306 | 322 | 671 | RLWASPAAPGKKKEMGNSMKSTP APAERPLPNPEGLDSDFLAVLSDYP SPDINPPIFRRGEKLRVISDERGWW KAUSLSTGRESYIPAICVARSYHGW LLRGP GK NMAEELLQLPD |
| 2133 | 7630 | A | 2307 | 624 | 1581 | KAATSENKICCEWRTSQAALMLHR LWASPAAPGKKKEMGNSMKSTPAP AERPLPNPEGLDSDFLAVLSDYPS DISPPIFRRGEKLRVISDEGGWWKAI SLSTGRESYIPGVCVARVYHGL/W LFEG LGRDKAEELLQLPDTKVGSF MIRESETKKGFYSLSVRHRQVKTY RIFRLPNNWYYISPRLTFQCLAE DLV NHYSEVADGLCCVLTPCLTQSTA APAVRACSSPVTLRQKTVDWRRVS RLQEDPEGTENPLGVVESLFSYGLR ESIASYLSLTSEDISSFDRKKKSISLM YGGSKRKSSFFSSPPYFED |
| 2134 | 7631 | A | 2308 | 52 | 454 | SQTQREPTMVLSPADKTNVKAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR |
| 2135 | 7632 | A | 2309 | 3 | 452 | |
| 2136 | 7633 | A | 2310 | 26 | 502 | NSTDSE RTHHGARLLPDKTKAQRPP RLKLGANA\GEYGFGGPWKGMFLS FPNPPKTYFRQFRP*ANGFAQG*RG HGQRKVA\DAL TQSPCRNV DMPQ TALSAP EATLHG\HKL\R VDPVNFKL VLSH\CLLG*PWPAHLPRPSFTPCGCT PSLEQSSW AFC |
| 2137 | 7634 | A | 2313 | 43 | 595 | LRNMWQLERNIETUINTFHQYSVK LGHPADTLNQGEFKELVRKDLGQN FLKKENKNEK VIEH\IHEDLDTNAA Q\QLSFEEFIMLMARAKPGALPTRR MHEGDKGPWPPPHKPGLGEGTPPR PQWPRSPVATAHGHKSWWPRPQA TNHGGQATLPLPKPGPRGLLCQTVL AVGLGGWGQIKSLP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2138 | 7635 | A | 2314 | 3 | 419 | SLYHNSSQKRHWTFSSSEQLARLRADANRKFRCKAVANGKVLPNDPVFL EPHEMTLCKYYEKRLLLEFCSVFKP AMPRSVVLTCAFLACKVDEFNVS NQFVGNLRESPLGQEKALEQILEYE LLLIQQLNFHLIVHN |
| 2139 | 7636 | B | 2315 | 324 | 487 | MQRVRAGRVIVTTARQRRLPDALG FREIFSSEQLARLRADANPNDSAK PWPTGS* |
| 2140 | 7637 | A | 2316 | 1 | 1050 | |
| 2141 | 7638 | A | 2317 | 191 | 229 | |
| 2142 | 7639 | A | 2318 | 186 | 1232 | CVWVLVCRPSGPGHDSIMYHNSSQ KRHWTFSSSEQLARLRADANRKFR CKTRAH\GKVFPNDPVFLEPHEMT LCKYYEKRVIIEFCSVFKPAMPRSV VG/SRACMYFKRFYLNNSVMEYHP RL\IML\TCAFLACKVDEFNVSSPQF VG\NL\RESPLG\QEKALEQILEYELL PYTSNFNHFL\VHNPNY\RPFEGFLND LRTR\YPILENPEILRK\TADDFLNRI ALTDAYFLYTPSQ\IALTAILSSASRA GITMESYLSESLMLKENRTCLSQLL DIMKSVRN\LVKKYEP\PRSEEVAVL KQKLERCHSAELALNVITKKRKG YEDDDYVSKKSKHEEEEWTD\DLV ESL |
| 2143 | 7640 | A | 2319 | 152 | 371 | DVLLATSSSEPSLFCPLCLTASTPKP LPPPG\PLPCPVWAMWGTGGFPLPG PPGQPRVRGPTAARGTPCCRPS |
| 2144 | 7641 | A | 2320 | 4 | 474 | PQYPAWHEGERAEWLCGRVSETGS ACSMADQL\TLKEQIAEFKEAFSL\F DKDGDGTITTK\ENLGTVNEILLGSN PTEAELQDMINEVDADGNGTIDFP EFLTMMARKMK\DTDSEGRKL\EEA FRVFGLRVGNGLYL\ACRNFRHV DGQTLGGGSLPD |
| 2145 | 7642 | A | 2321 | 291 | 648 | LTQLKTHCPLIKSKTMNKKRAIREP AQEPGPQKEENPKKHRSPSFTSTSP GLEVPASYSPTKAEQPGQVRKAV QPAVRLEPRAS\HPAGPPVPPSGVLV SRRRPEPGQGKPPESDFDH |
| 2146 | 7643 | C | 2322 | 155 | 316 | MTGPVSGSFIHWVLFSGFSSMSSNA SNVFGLVRPSCCTGLSRMAADSAG CCSL* |
| 2147 | 7644 | A | 2323 | 28 | 1323 | PSGARVAGAGPCGGGGMFVQEEKI FAGKVLRLHICASDGAEWLEEATE DTSVEKLKERCLKHCAHGSLKDPK SITHHKLIHAASERVLSDARTILENI QDQDVLLLIK\RAP\SPLPKMADVS AEEKK\QDQKAPDKEGILGATAN LPSNKLDRAAVQTNMRDFQTELK ILVSLIEVA\QKLLAL\NPDA\VELFK EGECNCWDEDGGMSVWDEACPA AQREMGLFRENRA TKALQLNHMS VPQAIGSWL\NEHA\EDPTIDTPLPG QAPPEAQG\ATAAASEAAAGASAT DEEARDELTEIFKKIRRKREFRADA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RAVISLMEMGFDEKEVIDALRVNN NQONAACEWLLGDRKP\SPEELDK GIDPD\SPL\FQAIWDTRWVQLGLTN PKTLLAFEDMLENPLNSTQWMNDP ETGAPVMLQISRIFQTLNRT |
| 2148 | 7645 | A | 2326 | 307 | 412 | SVQTIVFQPQLASRTPTGQS*SSCPY PLFATINAE |
| 2149 | 7646 | A | 2327 | 50 | 247 | |
| 2150 | 7647 | B | 2328 | 276 | 779 | MRTLAILAAILLVALQAQAEPLQAR ADEVAAAPEQIAADIPEVVDSFAW DERAPLQVSGKSSPVCARLLLLQET RDRGLLFALPLHSAYLEDLLRQSHF RQELMKLQPRSSLEQMIRKWLMPL HGMKVPLFRFQPDKIIVLSTLIPTGD YSPHNLKNLFMRMVTSP* |
| 2151 | 7648 | A | 2329 | 3 | 333 | |
| 2152 | 7649 | A | 2330 | 35 | 717 | RRSSPSLLPLAERGGARARGRPERA PHPSTPATRTAPPPWARRMMKLKS NQTRTYDGDGYKKRAACLCFRSES EE\EVLLVS\SSR\HPDRWIVPWKEG MEARRKEAKCGKQVREVCEGRLG VKGT\LGRLVGIF\ENQERKHRTYV YVLIVTE\VLEDWEDSVNIGRKREW FKIEDAIKVLQYHKPVQASYFETLR QGYSANNGTPVV\ATTYSVSGFRA SMFRAFRWT |
| 2153 | 7650 | A | 2331 | 104 | 381 | IQGGSMTSSSFSTSICQKILNKEKQS CCSN*SKWSRNVSSNGKPNWTGTS LPALTEMARTTIWKKHIFTKKFSSV SIFQVFKSF*I*GSVLS |
| 2154 | 7651 | B | 2332 | 228 | 445 | METSSRELQAAEYLEKHQIKEVVSY LTSALLFLRPALKTLGLCTEDEDLQ DDGHKITLDKFKEEVNKRMEIX* |
| 2155 | 7652 | A | 2333 | 3 | 1459 | GSKQVSEGTDNGDLPSYVSFAFIEKE VGNDLKSLLKKLDKLIEQRTVSKMQ LEEQVLTISSEIPKRIRSAKNAEESK QFLNQFLEQETHLFSAINSHLLTAQP WMDDLGTMISSQIEEIERHLAYLKWI SQIEELSDNIQQYLMTNNVPEAAST LVSMALDIKLQESSCTHLLGFMRA TVKFWHKILKDKLTSDFEEILAQLH WPFIAPPQSQTIVGLSRPASAPEIYSY LETFLCQLLKLQTSHELLTEPKQLPE KYSLPASPSVILPIQVMLTPLQKRFR YHFRGNRQTNVLSKPEWYLAQVL MWIGNHTEFLDEKIQPILDKVGSV NARLEFSRGLMMLVLEKLATDIPW LLYDDNLFCHLVDEVLLFERELHSV HGYPGTFASCMHILSEETCFQRWLT VERKFALQK\MDSMSLSSEAAWVSQ YKDITDVDEMKVDPDCAETFMTHLL VITDRYKNLPTASRKLQFLELQKDL VDDFRILINTK |
| 2156 | 7653 | A | 2335 | 46 | 1146 | |
| 2157 | 7654 | C | 2336 | 17 | 196 | MTTLVTTTTMDMVIIATSRVVMGR YPGEVVIIKATNHTKLFHLQLIPNSG NFIAGPVS* |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2158 | 7655 | A | 2337 | 208 | 1504 | FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSAESEGA KIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLDPITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEVESIELPMDNKTNRG FCFITFKEEPPVKKIMEKKYHNVGL SKCEIKVAMSKEQYQQQQWGS GGFAGRARGRGGGPSQNWQGY NYWNQGYGNYGYSSPRLRWLWRI *LHWLPTTTYGYGDYSN\SQSGYGK VS\RRGGHQN\SYKPHLNY\ICNL\AS PTGGEAVFS\NLKIQFESGS/CH*LLI AVQTKFLYQVPEWKYD\VGSL |
| 2159 | 7656 | A | 2338 | 208 | 1466 | FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSAESEGA KIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLDPITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEWDPIELPHGQTRPNKRR GFCFITF*G\EEPVKKIMEKKYHNVG LSKCELK\VA\MSKEQYQQ\Q\QQW DSRGGCAGRA\RGGRGDQ\QSGYG K\VSRRGG\HQN\SYKPYLNYSICNL SPTAGTSLQALCRADFRFSQARSMR TG*RDAPRSRMLPFGGEAVFS\NLKI HL/NGGSCHLLIAVQTKFLYQVPE WKYDVGSL |
| 2160 | 7657 | A | 2339 | 1070 | 1238 | PQRDFQFFLLWPPGGEA\VFSNLK\IP FERGSCHLLIAVQTKFLYQVPEWK YDVGSL |
| 2161 | 7658 | A | 2342 | 1 | 456 | RPRRPQREPTMVLSPADKTNVKAA WGKVG AHAGEYGAEALE/RMFL/SF PTTKTYFPFHDLSHGSSQVKGHGKK VADALTNAVGHVDDMPNALSALS DLHAHKL RVPVNFKLLSHCLLV LAAHLPAEFTPAVHAFLDKFLASVS TVLTSKYR |
| 2162 | 7659 | A | 2343 | 2 | 512 | GLEFGTSHRLRENPPWCLSPA\DKT NVKA\A WGKVG AHAGEYGAEALE RMFLSFPT\TKTYFPFHDLSHGFAQ VKGATAKKVA\DALTKAVAHRGRT CPN\ALSALSGPATAHKL RVGPGST FKLLKPLACLVDPGPAHLPRPSFNP WRLQGFLGTKFLGFLVEAPLLEPSK |
| 2163 | 7660 | A | 2344 | 265 | 426 | SFSISVFAACLALPMAQPQ*PCSQK V*QHCRVYMHAWPLCLQDVLV ECCSQS |
| 2164 | 7661 | A | 2345 | 56 | 341 | IVTLDWSRNLKYNRCWSKCYILSSS DSSSSFRDSFTNPAEF*FKSFILNFV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MYVNYFCNFFNDITAGHFFHLKL LYFRLCSLPGFADGTAPITV |
| 2165 | 7662 | A | 2346 | 333 | 534 | LMEDMKLFQKI*EKKQRNMLRNL* RKKMNQMM/YNM*HLLQHLLYFK FLLAHPM*LFSPGLYILSNFH |
| 2166 | 7663 | C | 2347 | 117 | 386 | MDILICTDFGSVNYFNVWRLPKSYL SLFYSRIVHDEVKDKAFELELSW VGELTNGRHEIVPKDIREEAKEYAK ESLKEEDESDDDNM* |
| 2167 | 7664 | A | 2348 | 2 | 359 | FEDGVLLCHPRLEGSGTNSAHCNLS LPGFKRSSCLRLPASSWDYRNMPY PGYFCIFGFTNNTETGFHQASFKLL NSRDLPTLAPVKCWDYRHEHCTRP LKYIFYQRYSHCMLEQHLLN |
| 2168 | 7665 | A | 2349 | 648 | 887 | SWKLLLLLCLLKNEHLPTKPATGHS NIADQTLKKSFCLEPFFHKV*KGLIF LTPRTTSLHLPIAVLLFSTAFIAYS T |
| 2169 | 7666 | A | 2350 | 306 | 449 | EIKKKYLLPGVVAHACKPSTLGGGR GGQIISGQEFETSLTNMAKPCFF |
| 2170 | 7667 | A | 2351 | 1 | 625 | NFALEAKNSARAISYVQTPMGHFT RGGPRLTITSLWGK\VNVEDAGGE TPGKGSLLVYPWT\QRFDFSFGNLS SAFCPSWPTPKVKAHGK\KVL\SLG DAHKSTWDDLKGHLLPKPEVNLHC \DKPAMWDPENFKAPGEMCLVTRF GQSLFRQKNFTPEGCRASLGKKDG ELQLASCPGPSQITTEASWPMNSEA FKDKAFILASNYK |
| 2171 | 7668 | A | 2352 | 1324 | 1671 | IVQTLSTSKSSCRSTEPCTSCLPDLP QVGTTCRPHGTCC/NRCHVGGLMN PLKPNC/GCRKCNCGYLYIYKQQR LHPRGKFQPGNNHRFSTQSVHMDI THGSGMFSLCFPGSTMF |
| 2172 | 7669 | A | 2356 | 8 | 564 | SAQMAVTTADPRVRPRVRTQLCSL ASLIQTLLVHLTPEEKSAVTALWGK VNVDE\VGKALGRLLVYPWTQR FLAESFGDLSTPNAVMANPKVKAHS \KK\LGALLVGLAHL\DNLKGTF HTEVSLHCDKLH\DPENFQAPGAT CLVLCAWANHFQKNFTPPVQAC LFRKLVAG\VANALAHK |
| 2173 | 7670 | A | 2357 | 23 | 679 | GLLTSGGAHLSPSRVTQGIYMSAL SEMPKPPDYSELSDSLTAVGTGRF SGPLHRAWMMNFRQRMGWIGV GLYLLASAAFYVFEISETYNRLA L\EHIQQHPEEPLGTTW\THSLKAQ LLSLPFW\WDSYFFWVPYLMQMF VSLYSCYKELDPQNSGGYCYPSPIW LWAVYFGNRHHAF/VVKASNSDSA DLQLIDTVKSVTRFFPLRITKTGQS |
| 2174 | 7671 | A | 2358 | 17 | 392 | SFKMADQDPAGMSPLQQMVASGT GAVVTSLFMTPLDVVKVRLQSQR SMASDAFVKIVRHEGTRTLWSGLP ATLVMTVPATAYFTAYDQLKAFL CGRALTSPLYAPMVAGALARREHR LGPLTS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2175 | 7672 | A | 2359 | 1 | 725 | RFTGTMDAFVKIVRHEGRTLWSG LPATLVMTVPATAIYFTAYDQLKAF LCGRALTSPLYAPMVAGALARLSI VLGL*PPSVPTSAQTQSVAPSPNLC QPRDRGVF*VPRPGTAGR*CHVRPV ISLLPIVTPNPHTVGTVTVISPLELMR TKLQAQHVSYRELGACVRTAVAQG GWRSLWLGWGPTALRDVPFSALD WFNYELVKS/WLNGLRPKDHTSVG M/SFVAGGISRTVAAELTLPY |
| 2176 | 7673 | A | 2360 | 102 | 1573 | SFKMADQDPAGISPLQQMVASGTG AVVTSLFMTPLDVGKVRQLQSQRPS MASELMPPSSRLWSLSYTKLPSSLQS TGKCLLYCNGVLAEPYLCPNGAR CATWF\QDPTRFTGTMD\AFVKIGE ARGAPRTLWSGLPATLVMTVPATA IYFTAYDQLKAFLCGRALTSPLYAP MVAGALARLGPVELWISPLGALCS NKACRVQHVVNRNRELGACVRTAV AQGGWRSLWLGWGPTALRDVPFS VHPPPQAL\YWFNYEL\VRSWLNG LRPK\DQTSVG\MSFVAGGISRTVA AVLTLPF\DVVKTORQ\VALGAL\EA VKSEPPCNVDSTWLL\LRRI\AESG TKGTLLQASFPRIKGCPPSCA\IMIQ HLIEFRQKAFFPRGLNPGTGFLGGL EKGPKGKDPVSSQREWGRGQGGD PSQSAFSSALREGGLFSLPLPATKLP GQGCPSGRPSTSSRHNFLLLPVVG ITYPPPKFKTKSSELPFVFPCGLL |
| 2177 | 7674 | A | 2361 | 1 | 215 | QPVMSEESDQYLAVLTFPRCVLV MIHTHAQVLNHVCIYVCVHMSVAV Y/ISACRATDPDTHTCVYMYIQTY |
| 2178 | 7675 | A | 2362 | 3 | 543 | TRNTLGWEVSSFSPLLSSCLNMVRT KADSVPGTQEKVVAARAPRKGL\G SSTSAHLIRPSVSIEESLKNKYARRE PPFCVRP/TLPKWAKREIGEFFR\LS KDSEKENQ\PEEAAGSSGL\GKRQRR KSMFLLQPGFTQLMEKGLGTFLHFI FGLTSPLFYPGYSRKVKFTINGVWF QLGFG |
| 2179 | 7676 | C | 2363 | 69 | 290 | MCLWNCCRKTQLAADILWLTAPAS PRDLRLGCVAEVFLARWELFGEDSF REKFFGFFFRDGWQPFFLLSAGER* |
| 2180 | 7677 | A | 2364 | 663 | 793 | DGDSVMVLPTIPEEEAKKLFPGGVF \TKELPFGKKYLRYTPQP |
| 2181 | 7678 | A | 2365 | 1 | 726 | MPGGLLLGDVAPNFEANTTVGRIRF HDFLGDSWGHFSFSQP/RGGFTPWCA PRSFARAAKLAPDFAKRNVKLIAS IAVFEDHLC/AESKDIHVYHCE/ESPT EKLFPPIIDDRNRELANPVGACWIP AEKDEKG/LCPVTASVWCFVFGP** RKLKAVYPSYPSYPLAGNFE*RFLR VVHLLSQLTA/EKKRVAHPQLIWKD GD\SVMVLNPSPEEEA\KKLFPEKE SFTQKELPNLAKKYLRYTPQP |
| 2182 | 7679 | A | 2366 | 3 | 452 | |
| 2183 | 7680 | A | 2367 | 1 | 627 | TLLVPQDSERTHPWLLSPADK\TNV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KAAWVGKVGAAVRSMAEALER MFLSFPTTKTYFPHFDLSHGSAQV KGATGKKVADALTKRRGAPLDDM PNAL/SSALEATLHAHKL\RVGPGST SKLLKPLACLVDPGPAHLPRPSSTP GGCNVFPGTKFPGLFVEAPLLEPSK LPLKLGSLRLAIVFLPLWGFPPAPPP LSCTRTPVVFEIKS |
| 2184 | 7681 | A | 2369 | 1 | 467 | GTSACGVASLSVDCVPAPFSQQQP LPEGERTLGGRHRLRTRARALHPAP ACFCHASLCVCM/CA/CVLVCGLLC EHQSDSIHCLCHLCLCKCNYLCIRA ASSQHLKCHWVGGNKTCFGPDDL GGRSEPTFETLSGEPATPADGKTGS CTGPERYQM |
| 2185 | 7682 | A | 2370 | 131 | 406 | EAMGILKLQVFLIVLSVALNHLKAT PIESHQVEKRKCNTATCATORLANF L\VHSSNNLGGILSSTNVGSNTY GK RNAVEVLKREPLNYLPL |
| 2186 | 7683 | C | 2371 | 257 | 422 | MQVCFRQGFTLPKGHHGLIATLGA PQLYMFLVLRASLFLWLSXFXRSX KLXXXRN* |
| 2187 | 7684 | A | 2372 | 621 | 1202 | GVPEPRARPSTSGMNGDRIRLPCWR NDRQK\THML\DVMDHFSRASSIH RRALSRDRFFTREPQ\DTYHYLAPFQ PCPHRRPAHFFPKSRNRPAACPFSS \TKPLNFHAMFQPFLEMIHEGSAGP WDIHFHSPAFOHPPTFEIREGD\DDR DCCAGEIRHNSTGLPCGLKDQVVT K\CREDLVLWDCFHQQLPG |
| 2188 | 7685 | A | 2375 | 154 | 1702 | IGHRDPARGRSCRCSGYYSRMVCE KLAPQSEMASAG\VSLRATILCLLA WAGLAAGDRVYIHPFHLVIHNESTC EQLAEANAGKPKDPTFIPAPIQAKTS PVDEKALQDQLVLVAAKLDTEDKL RAAMV\GMLANFLGFPYMGMS ELWGV\VHG\ATVLSPTAVFGTLAS LYLGALDHTADRLQAILGVPWKDK NCTSRDLAHKVL\SA\QAVTGLLVA PGRADKQA\QL\LSTVVGVTAPG LHLKQPFVQGLALYTPVVLPRSLDF TELDVAAETIDRLMQAVTGWKTG CSLTGAKADSTLAFNTYVHFQGKM KGFSLLAEPQ\EFWVDNSTSVSVP LSG\MGTFQHWSDIQ\DNFSVTQVPF TD\SAFLLLIQPHYASDLADKVEGLT FQQNSFNWMRKLF\PRTHLTMPQL VLQGSY\DLQDLLRPGSSCPPFLHTE LNLGRISGNDRIRVGEVLNSIFFEL EADEREPTTESTQQLNKPEVLEAVPL TRPFLFAVY\DQGATALALSWGRV GKPA |
| 2189 | 7686 | A | 2376 | 181 | 353 | VGDRCEGNGNEARGHWKREVCCP GARSGASV*GSSGRLGLCL*VGTRE AG*PGYPASLVPT |
| 2190 | 7687 | A | 2377 | 1550 | 1823 | GRLLEDPAAHKFLRGEMGGQSPG VRGTELLGAFSLPGES/GSPGRASPL PFPNLEKTVTFQSLGPKIPKEPG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LKEIKLTNVKKSCTLP |
| 2191 | 7688 | A | 2378 | 134 | 321 | GCF*KGRDLFADKMQEHSLO*FTAL FQPTNQKISSWVCGPKVNFKAIKTG SRSGKAIQNVES |
| 2192 | 7689 | A | 2379 | 1 | 602 | RTRASTRPSRDYGNVWLWTRTSHP RPLTEPEPRATMSHGKGTDMLEIA APVGFLLSLLRTRGCVSEQLKVFS GALQEA\LTEHYNHHWFPEKPSRG SG\YRCIR\NHK\MTPIISRVASQ\VG LSQAQLHQLL\SELTLWVDPYEV S\YRIGEDGSICVLYEEAPLAASCGA SFT/CARNQVACWGRSSPSK\NYVM AVSS |
| 2193 | 7690 | A | 2380 | 28 | 423 | SKPLKMADDLDFETGDAGASATFP MQCSALRKNGFVVLKGRPCKIV*M STSKTGKHGHAKVHLVGIDIFTGKK YEDICPSTHNMDVPNIKRNDLQIGI QDGYLSLPQESGGGIRDPLNLQRPP PRAWPGSG |
| 2194 | 7691 | A | 2381 | 1 | 930 | |
| 2195 | 7692 | A | 2382 | 171 | 695 | NRQDDLDFETGDA\GASATFPM\QC SALRKNGFVVLKGRPCKIVEMSTSK TG\KHGHAK\VHLVGIDIFTGKKYE\ DICPSTHD\MDVP\NIKRNDLQIGI QGWTLSLQ\DSGEVREDL/RVSP EGDL\GKEIEQKYDCGEEILIP\VLSA\ MTEEAA\VAIKAHGKITGSPGVAVV ASK |
| 2196 | 7693 | A | 2383 | 789 | 1380 | IPYFLMVYGLQTLMCKHITRRIRDH LHEAMNYFLIPSSPFLEANPPPTPG TICPAC/YPPPPRAGQQLACFLSIPPL FPNLPPIPPQKKDYWVLLSLGAPKFK GYLVLCCLMLQEPCRKQPGKSTGWI RNYPSPWMHLATSTPQLRRGSKEVH NYKTMGSRPQKRYETGPGTQGGAE RILLSKPGRWGSPGQEQVLGLQ |
| 2197 | 7694 | C | 2384 | 248 | 433 | MSGILVLNLFLLTGSVGPSSSVTLV LSVHQLPACAKLEKGNLHPCPNSS FPPRDFCVHPP* |
| 2198 | 7695 | A | 2385 | 1 | 1108 | |
| 2199 | 7696 | A | 2386 | 1 | 1528 | MGTRAARPAGLPCGAENPARRRLA LGARQQIHWSRPSTRLTAPAGP ARGVARPAMAPDPVAAETAAQGPT PRYFTWDEVAQRSGCEERWLVIDR KVYNINEFTRRHPPGSRVISHYAG QDATDPFVAFHINKGLVKKYMNSL LIGELSPEQPSFEPTKNKELTDEFRE LRATVERMGLMKANHVFLLYLLH ILLLDGAAWLTWVFGTSFLPFLC AVLLSAVQAQAGWLQHDFG\HLS VFSTSK\WNHLL\HHFVIGHLKGAPA SWRNHMHFQHHAKPNCFRKDPDIN MHPFFFALGKILSVELGK\RKKKFM PYNHGHKYFFLIGPPALLPLYFQWY IFYFVIQRKKWVDLAWMITFYVRFF LTYVPLLGLKAFLGLFFIVRFLAESN WFVWVTQMNHHPMHIDHNRNMD |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WVSTQLQ\ATCNVHKSC/AFNDWV SVG\HFNFQIEHHLFPTMPRHNYHK VAPLVQSLCAKHGIEYQSKPLLSAF A\DIHSLKESG\QLWLDAYLHQ |
| 2200 | 7697 | A | 2387 | 45 | 949 | APWWWYHPERLLGYPIAATLPSRL VLPGEVEPSTQWCSPLRLEPQFHLL PLQHLRRDSSSLSPPLPALGRTRGR SSAPAHGDESCSLPRPLSLAHGEP GRRRAEACSRLSRGRHSMTEPR STSASAAHAAAFCCFCCCRPPRPRP LAPPPP*PCR*SRRGCAGIDGAAAD VALGHPPE/HCPVPDVQMTSRRLMF IQLSQSPGVHCTSPHFSAPPTWCRR GPGSPATSPPLHTLPAVVAAPRAL RRAADRGRGRGLDRGVACAAERL QRQQLSRQSQQSRSEAQPDPAEQ PRKRW |
| 2201 | 7698 | A | 2388 | 804 | 985 | VGGDSQDLRDPVPPQTAPPPPNLS PPALSPRCASPSYPQKCLP/PPVTHR SACLSSAHRTHKKGQELVTG |
| 2202 | 7699 | C | 2389 | 258 | 461 | MSVTFIAVARGKLFFENLGHSELPL SLEWQTS DGEVEARGSRGGEALPR PGSMQPCPADVTRRPPTRP* |
| 2203 | 7700 | A | 2390 | 1 | 370 | GTRVTSGGGSRRPGMAAWSPAAA APLLRGIRGLPLHHRMFATQTEGEL RVTQ\ILKRKVSPRLQLIKVTDISGG CGAMYEIKIESEEFKEKRTVQQHQ MANQALKEEIKEMHGLRIFTSVPK R |
| 2204 | 7701 | A | 2391 | 1 | 1107 | |
| 2205 | 7702 | A | 2392 | 1 | 1230 | |
| 2206 | 7703 | A | 2393 | 1 | 908 | |
| 2207 | 7704 | A | 2394 | 177 | 934 | PGLSQEPSGSMETVVIVAIGVLATIF LASFAALVLVCRQRYCR\PRDL\AQ RYDSKPIVDLIGAMETQSEPSVELE L\DDVVITNPHIEAIL\EN\EDWIEDAS GLMSH\CIAIL\KICHTL\TE\KLVCHD NGALGAKMKTSASVSDIIVVAKRIS PRVDDVVKSMYPPLDPKLL\DART TALLSV\SHLVLVTRNACHL\TG\G LDWINDQSLS\AAEEHLEVLREAAL\ ASEPDKGLPGPEAFLQEPVLQFSAY RPAA |
| 2208 | 7705 | A | 2395 | 1 | 333 | GTRGERKAGLARGQVCGLSPFPK TNKESFPNSQLNPFWN\CGASLSLV SFSCPATRLCGNALLPSLFFSMRGF GLAVRIRDNDSRLLSRMTSMCSISR VPEHVEFPNPK |
| 2209 | 7706 | C | 2396 | 7 | 279 | MXKGS PRXNFLECEKKSGQNPWAG LLRPWWVGHP\SAKPLIPVFSSISFPL YNPHFPIXILCNK\KSHVCKKASKY TNNPISQQWTL\SF\K* |
| 2210 | 7707 | A | 2397 | 35 | 416 | SRAVEFVRSCAGYGERKAGLARGQ VCGLSPFPKTNKESFPNSQLNPFW\ NYVWGLGPCGASLSL\VSFSCPATR LCGNALLPSLFFSMRGFGLAVRIRD NDSRLLSRMTSMCSISR\PEHVEFP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NPK |
| 2211 | 7708 | A | 2398 | 3 | 344 | |
| 2212 | 7709 | A | 2399 | 1 | 1359 | |
| 2213 | 7710 | A | 2400 | 1 | 463 | LAQAACGPAALQLCPAGHGAAMA ATFFGEVVKAPCR\AGTEDEEEEE GRRETPEDREVRLQLARKREVLLR RQTKTSLEVSLLEKYPCSKFIIAIGN NAVAFLSSFVMNSGVWEEVGC AKL WNEWCRTTDTTHLSSTEAF CVFYH LKS NPSVFLCQCSCYVAEDQQYQW LEKVFGSCPRKNMQITILTCRHCT\ DIKTSESTGSLPSPFLRALKTQNFK DSACCP LLEQPNIVHDLPAAVLSYC QVWKIPAILYLCYTDVIGLDFITVE AFKPILSYR\SLKGLV\KNIPQSTEIL\ KKLMTTNEIQSNIYT |
| 2214 | 7711 | A | 2407 | 160 | 441 | |
| 2215 | 7712 | A | 2408 | 107 | 691 | RTAILSRMKIFLPVLLAALLGVERAS SL\MCFSCLNQKSNLY\CLKPTICSD Q\DNV\CVTVSAS\AGIG\NLVTFG\H SL\SKTCFPCLAPFPEGRSMLGVAS MGHSAFCQSFLVAIFSCGPMAGLRG KRSPLLGARACCLSLAGRALL\RFG PLDRPEPCSPDPPAQEGKPSPFWIPQ CMGAPDSSRALICALGPRSG |
| 2216 | 7713 | A | 2409 | 2 | 432 | GRPPPDVEVMTSLKVDNLT YHTSP DVYIPRDRYTKE SRCFAFVRFHDKR DAEDAMDAMDGA VLD/GSELRLQ MARYGRTPDSHHSRRGPPRSYGC VGYGRRSRSPRLRRMP/RSRSRSRSR SRSRSRYSRSKSRSRTRSRSRSTS |
| 2217 | 7714 | B | 2410 | 1522 | 2003 | MAIIYGVFSASNLITPSVVAIVGPQL SMFASGLFYSMYIAVFIQFPWFSFY TASVFIGIAAAVLWTAQGNCLTINS DEHSIGRNSGIFWALLQSSLFFGNLY IYFAWQGKTQISESDRRTVFIALTVI SLVGTVLFFLIRKPDSENVLGEDESS DDQDMEVNESAQNNTKA VDAFK KSFKLCVTKEMLLLSITTA YTGLEL TFFSGVYGT CIGATNKFGAEKSLIG LSGIFIGIGEILGGS LFGLLSKNNRFG RNPVLLGILVHFIAFYLI FLNMPGD APIAPVKGT DSSAYIKSSKEVAILCS FLLGLGDSCFNTQLLSILGFLYSEDS APAF AIFKFVQSICAAVAFFYSNYLL LHWQLLMVIFGFFGTIFFFTVEWE AAAFVARGSDYRSIMLKSFLDSGDI LAQLCRROQPRAPLTIRTSPDTLRR VFEKYGRVGDVYIPRDRYTKE SRGF AFVRFHDKRDAEDAMDAMDGA VL DGRELRVQMARYGRPPDSHHSRRG PPPRS* |
| 2218 | 7715 | A | 2411 | 2 | 229 | |
| 2219 | 7716 | A | 2412 | 3 | 353 | FPLPFFTLVIWPGIRKFKLVHADGSL CEIFLIGPFKNMAGWNISVPY WFDQ SLSKYVPETETMCTLMEGKLNFFLF KPRCIGKQCKRRTWGKRTT*SIRRR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SPWNKQLGYLKRLFW |
| 2220 | 7717 | A | 2413 | 18 | 282 | DPLKSGPRNRS*TRWTPSPRSVARRS KSKSLSVSRSRSRSRSR\SRRESLPP VSKRESKIQVAMGEKREGSPSPSPAE EEGAGVLLRK |
| 2221 | 7718 | A | 2414 | 2 | 830 | LRSPSVLFCGKAFFVSPRGRQLPER RGVAPPRAEEAGASSRGSGPPLRA MSYGRPPPDVEGMTSLKVDNLT\Y RTSPDTLEGAVFEK\YGRVGDVVHP RGIRYTKGSSRGFAFVRFHDKRDAE DAMDAMDGAVLDGGELRVQMAR YGRPPDSHHSRRGPPPRRYGG\GY GRRSRSPRRRRRSR\SRSRSRSRSR SRYSRSKSRSRTRSRSRSTSKSR SAR RSKSKYSSVSRSRSR\SRCRCGYRSP PPVSKRESKSRSRKSSPKSS\EEEGA VSS |
| 2222 | 7719 | A | 2415 | 1 | 320 | RGRASKECSGLSAHLVIHCGEKPYK CNECTRTSGTN/SSLTQQRSHAEKP YTRNECGKVFG/HIARHQIHHSTEKP YKCN/NTLKAFSKHSGMLMAHLLIDR PEKLCHYS |
| 2223 | 7720 | A | 2416 | 733 | 1005 | NPQTPMKNCWPWLEKKAEP RPFLGS SMPLGFCPHGPPCSCDFLETHFLDE \EVKLIKMGDHLTN\HRLGDPEA GLGEYLFERLTLKHD |
| 2224 | 7721 | A | 2417 | 148 | 1057 | |
| 2225 | 7722 | A | 2418 | 87 | 241 | EGGLGNDPMTTDCSMAA*LFK**SP SS*ALGSFCEAQIIQSSKGLFSRGSC |
| 2226 | 7723 | A | 2419 | 1 | 924 | |
| 2227 | 7724 | A | 2420 | 1 | 1004 | MPVGAGRRRAKGD PATLGALAVFTV GAKRSKGHSPKPHPAGRLPPLPPLR QRSTPMIDTLRPVPFASEMAISKTV AWLNEQLELGNERLLLMDCRPQEL YESSHIESAINVAIPGIMLRRLQKGN LPVRALFTRGEDRDRFTRRCGTDTV VLYDESSSDWNENTGGESVLGLLL KKLKDEGCRAFYLEGGFSKFQAEFS LHCETNLDGSCSSSSPPLPVLGLGGL RISSDSSSDIESDLDRDPNSATDSG SPLSNSQPSFPVEILPFLYLGC AKDS TNLDVLEEFRGSSPYMILFHYGENG TSYVPITSHFRQKLAQGFVSTGTP GFIYSAK |
| 2228 | 7725 | A | 2421 | 686 | 1812 | TCPVARASLTRGEDRDRFTRRCGTD TVVLYDESSSDWNENTGGESLLGL LLKKLKDEGCRAFYLEGGFSKFQA EFSLHCETNLDGSCSSSSPPLPVLGL GGLRISSDSSSDIESDLDRDPNSATD SDGSPLSNSQPSFPVEALALPSYLG A\KDSTNLDVLEEFGIKYILNVTPNL PNLFENAGEFKYKQIPISDHWSQNL SQFFPEAISFIDEARGKNCGLVHCL AGISRSVTVTVA YLMQKLNLSMND AYDIVKKKKSNISP\NFMFG\QLL GLSRRDAGDSAGPCGQQGSRHSRL YFYHPFPTRNVLPGWDFLQSTWKD |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PTPFLAGMCLALQQFLAASAGAA FFVCGPRCQNDTKLSVLRQGYQVR ELG |
| 2229 | 7726 | A | 2422 | 66 | 187 | WGGGGSAAAAMEANWTAFLFQAH EASHHQQQAQNSLLPLLSSAVEPP DQKPLLPIPTQKPQGAPETLKDAIGI KKEKPKTSFVCTYCSKAFRDSYHLR RHESCHTGIKLVSRPKKTPTTVVPLI STIAGDSSRTSLVSTIAGILSTVTTSS SGTNPSSSASTTAMPVTQSVKKPSK ACKKNHACEMCGKAFRDVYHLNR HKLSHSDEKPFECPICNQRFKRKDR MTYHVRSHEGGITKPYTCSVCGKG FSRPDHLSCVHKVHSTERPFKCQT CTAAFATKDRLRTHMVRHEGKVSC NICGKLLSAA YITSHLKTHGQSQSIN CNTCKQGISKTCMSEETSNQKQQQ QQQQQQQQQTHVT\SWPG\KQVET LRLWEEAVKARKKEAANLCQTST AATTPVTLTTPFSITSSVSSGTMSNP VTVAAAMSMRSPVNVSSAVNITSP MNIGHPVTTTSPLSMTSPLTLTTPVN LPTPVTAPVNIAHPVTTTSPMNLPTP MTLAAPLNIAMRPVESMPFLPQALP TSPAPWRPTGPRSCSRPMKLPITNSR QHRTACCPS |
| 2230 | 7727 | A | 2423 | 3 | 777 | RTSLVYDYPLRRRWLRRQRGGGGF CFGCGGRSPGPGFGLSPTVVTLAEL LVLLAALLATVSGYFVSIDAHAEEC FFERVTSGTKMGLIFEVAEGGFLDI DVEITGPDNIGILPTRLYNLSGKYTF AAHMDGTYKFCFSNRMSTMTPKI VMFTIDIGEAPK\GQD\METEAHQN KLEEMINELAVAMTAVKH\QEY MEVRERIHRAIQRTTQNSRVVLWSF FEALVACCHDIWGQIYYLEGDFFEV RRSCFKKPLPG |
| 2231 | 7728 | A | 2426 | 89 | 136 | |
| 2232 | 7729 | A | 2427 | 1 | 916 | MFYHLVPDGKKPGATLKATSAPKG KANGGRQAHAPPRWASAGDVTHS AISELRESATAAASASSESAGSGPR MKSVIYHALSQKEANDSDVQPSGA QRAEAFVRAFLKRSTPRMSPQARE DQLQRKAVVL\EYFTRHKRKEKKK KAKGLSARQRRELRLFDIKPEQORY SLFLPLHELWKQYIRDLCG\LKPD\ TQPQMIQAKLLK\ADL\HGGLFISVT K\SKWPLLMLGITGNPFYQETKHIF QNLSPKGRPALKVIPPSLNCRVPLW KPDGFIPPTFTGSKFSLGQVNR\SA KKFQSEGNRLTL |
| 2233 | 7730 | A | 2428 | 2 | 484 | PDSSGPHRLRENPPWCLSPADKTNV KAAWG\KVGAAVVRSMCAEALER MFLSFPTTKTYFPHFDLSHGFCPGL RATGKKVD\EALTKRRGAPLDDMP NAL/SSALEATLHAHKL\RVGPGSTS KLLKPLACLVDPGPGPPSPAEFHPL RCNVFPGDKVSWVSC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2234 | 7731 | A | 2432 | 197 | 332 | |
| 2235 | 7732 | A | 2433 | 1 | 1788 | |
| 2236 | 7733 | A | 2434 | 3 | 111 | |
| 2237 | 7734 | A | 2435 | 220 | 423 | HEELKSGPYLLTFRDCFLHFWALV SKR/LALNFM*TSAPT*KALSKRNIC LVNKNRNIKIPYPKKKKK |
| 2238 | 7735 | A | 2436 | 273 | 499 | RSGVRDQPGQHKGKITSLLKIQKLAR RGGACL*SQLLRRLRQENRLNPGG GGCSEPRSCHCTPAWETEQDSISKIK |
| 2239 | 7736 | A | 2437 | 1 | 1176 | |
| 2240 | 7737 | A | 2438 | 245 | 394 | |
| 2241 | 7738 | A | 2439 | 458 | 701 | GPAPTRRGPAHGAHTR**PAGTAR AACGSA*SAGTASPAHKGKGHHPG SRASGTGPGPCQRRRRSDHSSAGK WPLREASL |
| 2242 | 7739 | A | 2440 | 365 | 814 | AALRSSSENSRHRSLVKMSDKKAK DPVN\KSGGQGPKRKNWSKGKSSG TSFNNLVLFDKATYDKLCKEVPNY \NLITPAVGSERL\KIRGSLGQGKPFQ ELLS\KGFIPNWFSKHRASSYFTPGIT KGGADAPSLLGEDCMNRSNPPVHLE K |
| 2243 | 7740 | A | 2441 | 41 | 565 | APSPRRPWGHFTEEDKATIKNLWG KGEMWKDAGGKNPWERPWLSTYP MGPQRFFDQLLANLSLCPLPIMGNP PKVKGTWPRKVLTSLGSAHKSTW DDLKGHLLPKPEVNLHCADKPAMW DPENFKAPGEMLLVTRFGQSHFRQ KNFTPGGCRASWGRKMGDLELASA LVPSRYH |
| 2244 | 7741 | A | 2442 | 3 | 284 | |
| 2245 | 7742 | A | 2443 | 1 | 3339 | VEGMTCQSCVSSIEGKVRKLQGVV RVKVSLSNQEAVITYQPYLIQPEDL RDHVNDMGFEAAIKSKVAPLSLGPI DIERLQSTNPKRPLSSANQNFNNSET LGHQGS HVVTLQLRIDGMHCKSCV LNIEENIGQLLGVSISQVLENKTAQ VKYDPSTSPVALQRAIEALPPGNF KVSLPDGAEGSGTDHRSSSSHSPGS PPRNQVQGTCTTLIALAGMTCASC VHSIEGMISQLEGVQQISVSLAEGTA TVLYNPSVISPEELRAAIEDMGFEAS VSESCSTNPLGNHSAGNSMVQTT DGTPTS VQEVAPHTGRLPANHAPD ILAKSPQSTRGSGHRRKCFFTDSKG MTCVASCVSNIERNLQKEAGVLSVL VALMAGKAEIKYDPEVIQPLEIAQFI QDLGFEAAVMEDYAGSDGNIELTIT GMTCASC VHNIESKLTRTNGITYAS VALATSKALVKFDPEIIGPRDIKIES KTSEALAKLMSLQATEATVVTLGE DNLIREEQVPMELVQRGDIVKVVP GGKFPVDGKVLEGNTMADESLITG EAMPVTKKPGSTVIARSINAHGSVLI KATHVGNDTTLAQIVKLVEEAQMS KNPNKHISQTEVIIRFAFQTSITVLCI ACPCSLGLATPTAVMVGTGVAAQN |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GILIKGGKPLEMAHKIKTVMFDKTG TITHGVPRVMRVLLLGDVATLPLRK VLAVVGTAEEASSEHPLGVAVTKYC KEELGTETLGCTDFQAVPGCGIGC KVSNEGILAHSERPLSAPASHLNE AGSLPAEKDAVPQTFSVLIGNREWL RRNGLTISSDVSDAMTDHEMKGQT AILVAIDGVLCGMIAIADAVKQEEA LAVHTLQSMGVDVVLITGDNRKTA RAIATQVGINKVFAEVLPSHKVAKV QELQNKGGKVAMVGDGVNDSPA AQADMGVAIGTGTDAIEAADVVL IRNDLLDVVASIHLKRTVRRIRINL VLALIYNLVGPIAAGVFMPIGIVLQ PWMGSAAMAASSVSVLSSLQLKC YKKPDLERYEAQAHGHMKPLTASQ VSVHIGMDDRWRDSPRATPWDQVS YVSQVSLSSLTSDKPSRHSAADDD GDKWSLLLNGRDEEQYI |
| 2246 | 7743 | A | 2445 | 14 | 503 | NNDFIVIGTGTEFGIPGPTHAYEKT IIYDDYNCL*QCELETENQNLQ YDKRKLEAMLQGMVTETTMKWEK ECERRVAAKQLEMQNKLWVKDEK LKQLKAIVTEPKTEKPERPSRERDR DKVTQRSVSPSPVPLLFQPV*NAPPI RLRHRRSRVSGDRWV |
| 2247 | 7744 | B | 2446 | 226 | 347 | XGKIIVASCFPFSSRKRRSSTVAPA QPDGAESEWTDVETR* |
| 2248 | 7745 | A | 2447 | 8 | 2985 | WIQYSSTTLPNWDNKRKKKEKKA MLSARAKTPRKPTVKKGPKRTLKT QLG/YCYCRVRPLGFPDQECCIEVINN TTVQLHTPEGYRLNRNGDYKETQY SFKQVFGTHTTQKELFDVVANPLV NDLIHGKNGLLFTYGVGTSGKTHT MTGSPGEGGLPRCLDMIFNSIGSF QAKRYVFKSNDNRNSMDIQCEVDAL LERQKREAMPNPKTSSSKRQVDPEF ADMITVQEFCKAEVDEDSVYGVF VSYIEIYNNYIYDLLEVPFDPINPNL HNLNCFVKIKNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRRIANTHL NRESSRSHSVFNIKLVQAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTAEGNRLREAGNINQSLMTLRTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAICGLTPRRRYRNQPRGPIGN EPLVTDVVLQSFPLPSCEILDINDE QTLPRLEALEKRHNLRQMMIDEFN KQSNFAKALLQEFDNAVLSKENHM QGKLNEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNLQQ ELETQNQKLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFQPDQNAPPRIRLRHRRSRAG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAES\EWDRCR\NKVFCGL WEMRIAGSQLGTWISASRHNPSAKS HETDSPSTERTFSFVWMISRKPCQK QSSRSSCRTPALVENHEPQLHHTLT PEQSFPYGSQKTTSIQ\QNVYSVCFA \SNINSRGRRLRVSSL\YEF\FIMFFLK YISCILIN |
| 2249 | 7746 | A | 2448 | 20 | 349 | SFCLEFPCRPGELLALQDSAQNSTF DKTALPLCLAPCPPPLGPQS\THIQP CFPHTGPCAPFFTTDLLQGQRLSLSL HTPLHPVPAHWALPARRALARLTD RPNARLTP |
| 2250 | 7747 | A | 2449 | 3 | 384 | PFLSVVSSQVAGHGRIQCTYLMND CQTKQPCWSGATWPHPWMQVKGT PALRAHPQTLSESRLPEGTRGSRPE DCPKPQPADPPSLGT\QCPPPWQLSP TQQKMSPTFAAAKGASQGLMWAH AVLSRA |
| 2251 | 7748 | A | 2450 | 1 | 1503 | |
| 2252 | 7749 | A | 2451 | 1 | 855 | NPRRRLRGRCRASASSPRRVRRRGQ RPRHPAPRRPQAARPSAAPRARRFL SQRPAAAAAAQAALMQAIKCAG GWKAEAVGKTCLLISYT\TNA\FPGE YIPTVFDN\YSA\NVMVDGK\PV\NL GLWDT\SGQKDYDRVTPPYPPYA/Q ADVFL\CFPFVSPAS\FENVRAKWY PE\VR\HHCNP\TP\ILVGTKLDLDRD DKD/TRIEKLKEKKLT\PI\TPQGLA\ MAKEIGAVKYL\EC\ALTQ\RG\KTV FDEAIRA\VL\CPPV\KERGRE\NCLPV VNV\SAPSFLGPVPLEPL |
| 2253 | 7750 | A | 2452 | 41 | 556 | APSPRRPWGHFTEEDQGLLSTSLWG KVNVEKCWKEKTPGKGS\LVVYP WT\QRFFD\SFGN\LSSAFAHHGQTP KVKAHGK\KVL\TFLGRCQQSTLDD LKGHLLPKPEVNCTVDKPAMWDPE NFKAPGEMLLVTRFGQSHFRQKNS PPEGCRASWAERWWT\GV\ASALVP SRYH |
| 2254 | 7751 | A | 2453 | 2 | 454 | RSFFFFCEVGSWVGSMRVVMARL LSEGEQCIPTACAAFAQQPGGRPRR GLAGVGEGGPQCSWVNYRCTLFL VSL\GTDLARGRGNSATGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCNVV QGWVSTSWGSSSPVPQFFPKLLEF TGK |
| 2255 | 7752 | A | 2454 | 94 | 218 | |
| 2256 | 7753 | A | 2455 | 266 | 547 | |
| 2257 | 7754 | A | 2456 | 2 | 494 | RGPVMAESWSGQ/SFLQALPATVLG ALGSEFLREWEAQDMRVTLFKLLL LWL\LSLLGIQLAWGFYGN\TVTGL YHRPGLGGQNGSTPDGSTHFPS\WE MAA\NEPLKNPTENKGRQQRVSKGI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HWVCWLLHWVLLLPRPQGQPAGG SGLVAGSTQLPTGLGLILPS |
| 2258 | 7755 | C | 2457 | 12 | 356 | MGDSFMDEVAPRLASVDSRFFSFSQ GAHIKXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX X* |
| 2259 | 7756 | A | 2458 | 764 | 1135 | LLQTTSRNFKNLNQCTKSPICKKK GSVFFFFFFETESCPVAQAGVQWR DLRSLQAPPPGSRHSPTSASRVART TGAHHYTRLIFVCLVETGFHHVSQ DGLDLQDQFLESFLFCLLVRLRT |
| 2260 | 7757 | A | 2459 | 1414 | 1761 | SAINFFFLFETESRSVAQAGVQWH DLRSLQAPPPGSRHSPAPASRVAGT TGTRHHARLIFFFFFFFFFLVETGF HRVSEDDLDLFTSGDLPTLTSQSAGI PGMSHCAWRIDGI |
| 2261 | 7758 | A | 2460 | 63 | 542 | TALPNQLHGGRHLCPSHAFGSQGA ARPKRPQPGPG\SASEPWVQLQSHH PLPPPTPQSPEGGEFLREQRPKPLSF KPLLHPRGPLCPAAPKLPPWPCPLR VPQFPHPPLPPSGRKRDRERGMEEGE GGWAAGERRGGKEETLGRGPFTQR ERPRNQEGGG |
| 2262 | 7759 | A | 2461 | 2341 | 2443 | GRVWWLTPVIPALWEAEVGRSLT ARSLRPAWPTL |
| 2263 | 7760 | A | 2462 | 28 | 403 | NTTTCVKGLQTQSYKTSPDGNTTK QTNKVKHTHTII*II*NAPPAVSTTAIR NKFSKNGEQRFIEPYTNRPNHISIKL *RTIQQYASSSKNLEIKDFSWKKLQ* FLENRNKHECFQLFPKVNVGAS |
| 2264 | 7761 | A | 2463 | 727 | 1156 | ETTLSEARRGRSAAASCRGSALRRG RFPESRRGREAAPVCPRHVLL*GAQ SKQAAVAGKRSRGRHASRWPKSLF TPRRRISLKRALHFWQQSADPSPS VSRAPGSTWVGPKAPTEVTSVAPSR MMWQNEKKKVGGGERQDWRK |
| 2265 | 7762 | A | 2464 | 10 | 302 | MERFEAGLSHISPWLC*CCSHCGD CCLLGSRSWGLVGGGSCGALGPWG RCVCAGGEFPDRASLPVDPALAKLE CSHKFPTPKDFHPRDRSPSRFLL |
| 2266 | 7763 | A | 2465 | 303 | 531 | VLRICKVSEENSLFPLSDITYLASIPN KTQTHCPEPAQKPSCKAQ*FWPKC KPHPPCCHWALPPGCCWACHRWD E |
| 2267 | 7764 | A | 2466 | 6 | 100 | |
| 2268 | 7765 | A | 2467 | 2998 | 3570 | QDRKQGSSAPATPSRA*AAAARAP RRPAGRWRG*DAQSPAEPAPRSPP WRRAD |
| 2269 | 7766 | C | 2468 | 125 | 404 | MMARPPPWLESHCTRVVRADGQV RXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX ADAW* |
| 2270 | 7767 | A | 2469 | 1348 | 1807 | CPTVDPLLQKNCNDGSATALARVP LHACREGRWASPSGFFCCCCCFLR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WSLALLPRLKCKGPISTHCNLRPLPG SKDSPVSAS*VAGITGARHHAQLIFF VFLVETGFHQVVGQAGLELLTSGDPP ASASQSAGITGVSHRARPSVWFSNQ SMNP |
| 2271 | 7768 | A | 2470 | 538 | 676 | VKRNPEAGAVAHTCNPSTLGGRGG WIS*AHEFDTSMGNMT*PHLYK |
| 2272 | 7769 | A | 2471 | 40 | 336 | EYLYRHFKNKLFLYANILCSSGIWR HYVLILRTVSELLD***GCRWGLSRS FDYLSNTGWV*VLLDISSFAVVTGP LIHGTGGLSAFDLHCEALSFYRD |
| 2273 | 7770 | A | 2472 | 2063 | 2406 | SQKKKIQWYLRMFRQFDIYVCFLFF SVVLLMIGGLLSHRLIPVKQYIKLHL ALLRTGAGAHACNSSTSGGQGG*II RGQEFETSLGSSNPSASASQSAGTT GVSHHAQPIFFF |
| 2274 | 7771 | A | 2473 | 22 | 273 | LTQKMDHNQVKFKSTTFYSILGKSV LSLSRPEYISGKSDTYSENIYPLSIKS EIEPIETRCLNRSNASLVQK*YGHKT GLWWLP |
| 2275 | 7772 | A | 2475 | 1269 | 1511 | INFFFF*IIDRFSLCHPGWTAVAQSR LTATLLPSRFKRLCLSLPSSWEYRP LPPYPANFCSKLLICLSTFYKDCG NSA |
| 2276 | 7773 | A | 2476 | 1411 | 1827 | LHTCCLRRRPSGRGRSQGGHCSQSG SSPPRRPRSPAPEGPGFHAP*LCIPDL GHGSRKRGCWPPCGPRTGWADLV ASAQAACGCQGPSPSGSCSL*GRG PVGGSGHGSPCWQLVELCGRCWSW PGVAGSTWQWRRHPH |
| 2277 | 7774 | A | 2477 | 1345 | 1642 | WQQFTGAVIHLIYAYVVLVCLVAFS SVSLGLNFFHKNFSFDFQRCWLF SPFKGCC*RCFFTQSLYYCQVCEFT KTLIILLIQDVPEIFWSLFCFFHGP |
| 2278 | 7775 | A | 2478 | 113 | 584 | WQDYTYKEVRVTASEKNEYKGWV LTTDPVSANIVLVNFLEDGSMSTVG IMGHAVQTVETMNEGDHRVREKL MHLFTSGDCKAYSPEDSVREKEQP* INGFRRTHIPITEQGDAPRTLCVAGV LTIDPPYGPENCSSSNEILSRVQDLI EGHLTASQ |
| 2279 | 7776 | A | 2479 | 658 | 785 | KTHGWVQWLTPVIPAL*KAETGGW LEPRSSRPAWATQRDLIS |
| 2280 | 7777 | A | 2480 | 2 | 598 | PLGKGKFTGQSAQLTTGTGRGLILA KGSHATLQKHRINHTLTHKNPFLEE FWESPSSLNLALIKGLNGFCLGTEK LFEQMTYGGGLKKVKCPIGYFALQS WEFHPPPPTLFLSLPLAILWPGGENR GPRVSTKTGIKTRWPAPFLGPLSNR LGNPQPNNPAPAAVPSLGLSPW*RG RGLPWGWAKPRCALWTPVSLPST |
| 2281 | 7778 | A | 2481 | 253 | 286 | NDDDP*LPCLGQPPRSCQPSSLP*S LLWSKMTTTPAQRSG |
| 2282 | 7779 | A | 2482 | 407 | 587 | QAGRGRARGVSEEARNKPVPPTET PQPTLSQP*MGPAQDPAPQQDYRG KKSLNAWCGRS |
| 2283 | 7780 | A | 2486 | 246 | 519 | FQFGIHNTNYQRQGAQVFFKNKGV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WGGPRSLPYSC*EGLPLGESYQFEP QSLRDA*DIP*GSVGKNPVGSHWW VSGVIGGFIITGDYSQH |
| 2284 | 7781 | A | 2487 | 470 | 977 | TPPPAGLRQRGYPPPGNRLEARNW ARAKGGKTSAGRVFTQP*FPEQQLP PGRPWWPRPGCPHGLPTRACKWSG GVLAPESPEPPSLPEGSHSWLGDG LLASRKL RAGGSVATFTSPQLCPLG PHEDREAREGEGRLAPAQPVSPPSA PAGHSLSHPSRTGKLALVPGH |
| 2285 | 7782 | A | 2488 | 393 | 618 | IREWVNIFWNIHTEEYYTVIKKN*V CQTWWLT TVIPELWEADVGGSLP RSSKLR*AMILPLYTSLDHKARLSL |
| 2286 | 7783 | A | 2489 | 308 | 626 | IRGTSNMNRKNVEKAYYAEA*LSL |
| 2287 | 7784 | A | 2490 | 1222 | 1374 | AQQVKRLEGQRGWKLRGGRGRWL TPVIPAL*EAEAGGSLEARSSRPW AKK |
| 2288 | 7785 | B | 2491 | 60 | 378 | NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIHFI SPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX* |
| 2289 | 7786 | A | 2492 | 1 | 437 | DPRATEGMVVADKTCQKSTGRLPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISK NKLDLFRP YTPVNNKKGTRLGRYRCEKGTAVL TEKITPLEIEVLEETVQTMDS |
| 2290 | 7787 | A | 2493 | 2288 | 2668 | FGRGHYCRRSVSQEEEEAKNLVSEAI AAGIFNDLGSGSNIDLCVISK NKLDF LRPYTPVNNKKGTR*VKETKFFLGPL ASWPPLVSPWHLDG VFLVLSTLSTS SVPKSTSHDLRLVTCFMTVGCCQ V |
| 2291 | 7788 | A | 2494 | 3 | 861 | FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKLPKVRKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIHFI SPNIYCCGAGTAA DTAMTVTQLISSNLKLHSLASTGRLP RV\VTAINRMLKQMLFRYQGYIGA LV LGGVDVTGPHLY\SIYPHGSTD VPYVTHGFLAPLA\AMAVFEDKFR PDMEEEEEAKNLVSEDSPPQFPPPS WRIFNGPGLPEANIDLCVISK NKLG FSPPNTQLPNKKGTRLGWRYRCEK G\TTAVLTEKIPLLWST |
| 2292 | 7789 | A | 2495 | 466 | 607 | KKKERSCLWCPS*SLKNYGLSCR KKKKGAVKKIILVQAWWLMPVITV LWEAEVGGLEARGLRPTRATW |
| 2293 | 7790 | A | 2496 | 449 | 694 | ILRILGTPISFPVNKISFLPFKCLFPDS YIENLMNIYQPIKKNEIHVPLQ*PW MHLETIILSELIQEQT KKKHKFSLIR GS |
| 2294 | 7791 | A | 2497 | 52 | 298 | YNIEEQQNKRT RQSNRHRPTPPPEPP NPEW/TPKPTPPTK/PSSPQGEG/PGW TGGPAPHAGAAPPF\PS PANPTLFPS LTTGGKV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2295 | 7792 | A | 2498 | 112 | 485 | YNIEEQQEQTYSKTE*SAQTHPSPGT AESRMEPKPTPTKRLPPTGGGGRG GTWGDGPPCWGGHPPVFPSPCPTP TLFPIFDPLGGQSLAQLGSWMVEPT LQRATTLSTFLKMGRRKETVAPPQI |
| 2296 | 7793 | A | 2499 | 32 | 392 | RPTFGIWFYYPQVFPELLELKAKYIG KHCFSIHSLPDTGPLPGCP/SPPGRA ALGIIPGNLPAPEQKPCWDP/SPSSTL VWRMLNSASTSPSPAPSYISPPFPQG SYFPAHPPTSSLSLGGIY |
| 2297 | 7794 | A | 2500 | 914 | 1417 | PQCLLPNRGGSVQVRLWGATASLS GWGFLASFHPIHPFPGKFSSLPDTW GLCLGCPFPQAERPWA*YPGTLPAP ELETLLGSLPSSTLVWRMLNSASTS PSPAPSYISPPFPQSYFPAHPPTSSL SLGGIYHQLLPL*PLPSTDPPCAPLL TSPPLTFLKSPRP |
| 2298 | 7795 | A | 2501 | 1120 | 1159 | ERAVCGC*CIFVM |
| 2299 | 7796 | A | 2502 | 1145 | 1367 | IFFSFLHIYIHNTHTHMYIYYTLCVC VCCVYGMVCVCACVYSFSSKPKQVC VWIEGNLNY*LQVVCLWYLDFFHS |
| 2300 | 7797 | A | 2503 | 155 | 454 | GGFSVWHTETPPRMRLMHQVQFNL EYLTTPESTQKGGPTPLCIYGYVFFK SDYLYSLSLFFFRFLYFSSLL*YLML VNFLFRMLFSLFMSFCYLFFIIL |
| 2301 | 7798 | A | 2504 | 901 | 969 | RWPGMVAHACNPSTLGG*VGDP |
| 2302 | 7799 | A | 2505 | 903 | 1339 | DKTVQSIRSMGGWKMDASDSKFV DLWIAEGIGTSWRNPGYQAPRPFLH HGCWGD LGKSPPLPKPVSHITDVGP WLRMMVSTGLSHLW*VPSQGQSSQ GPHPPAPGVQPPQTPPPASLKGKSL HLOGACSEGGAPFSIELFAGRS |
| 2303 | 7800 | A | 2506 | 433 | 548 | PSEYTLGFKNP KIKLTFNGGNSMSG VHF*TGFI TFL |
| 2304 | 7801 | A | 2507 | 637 | 906 | RIKKLS DGSYFLPGVSQIA*GSNYF* SKLGP DGGASRLQSHHLGRPKVGV FHHVGQDGLDLLTLVIHPPSAFPEV LGFTGREPPRPSLHL |
| 2305 | 7802 | A | 2508 | 211 | 575 | RENHDLESQCKRGAPVPAGVPSSAL PQGPVSLLPAGALCPFERSQQASP QVSPQGVDPKICSLQTTSLCSFCDR CTGMGSL/C/SSCPPCSSS/CHGRSHS SPC/CL*SRTSSVVDGEVCSNTL |
| 2306 | 7803 | A | 2509 | 274 | 488 | SGDKTMQLRGPCGGWGSCPAGLGT CTAGSP*LCHHKGHCSIHSTSCFCLA TVSPCAIFNSTSKAGRGRAQP |
| 2307 | 7804 | A | 2510 | 83 | 442 | NFTMVMYTDHILRNAHLMTYTSGR RLSVPKIACHITDHSLTHTCYMPYL RD*Y*TMFSQGFHYAPYLHLHT*EH PFEC LLAGRTFTDALFEPTYPTLTL LTPSHWQDGPPLTGSQMPG |
| 2308 | 7805 | A | 2511 | 2 | 270 | ARLGLPKCFFCVFVFKTASRSVSQA GVQRCDHNSLQP*PPGLKRSSLASR VAWTTGSHHHAQLIWLCLFKQYFV SSGFYLLVALWWGG |
| 2309 | 7806 | A | 2512 | 234 | 409 | KGFYAHEKNARTWWLTPIPTLSEA *GGKMA*ARSLRPAWATIRDPISAK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SKKKKKKS |
| 2310 | 7807 | A | 2513 | 78 | 460 | NVCRKMPPSDRLAGAYILQCNPVE VVGPEREDAPQNRVQVRHGCVAW PLLAPPPRHLQGEGLTSARKRVLR LGVTSGL*RTDSHNPPGPPQREQTE PRARPPALEHRAQQ*PGPGLGGHRG AGCHQ |
| 2311 | 7808 | A | 2514 | 67 | 279 | SHRVS RDAACGAAPAAARLAGGQR NGRAISGRPGLSS*GAGGGNVFKVC LLLNKNRTGGGRGHGYLYSLQR |
| 2312 | 7809 | A | 2515 | 683 | 933 | YTSELIGKIISGQEVVVGAWCEDLG *GPRKSRGREGKG*G*EGSGNAGRI VGFKQGRGEDAHSWSQRGRQEFV FYLKSTRNW |
| 2313 | 7810 | A | 2516 | 2 | 208 | SKIALLVHLK*ENRHQLFFELIPTVF FLFIFETGSHSVTLQECSGVIMVHCT LTSWAQASSPLSLPTA |
| 2314 | 7811 | A | 2517 | 426 | 601 | PSFRIFTQYSSFLKNSLKRLGAVAH VCNLSTMGG*GGRTA*AQEFETSLV NVVRPPSL |
| 2315 | 7812 | A | 2518 | 55 | 489 | HSALIQASVWFRYKYPGCGYLGASLP TN*GKKGSQVGSSAHFATTFTIPNG DNA*GAKSGSGCPGGECHPG*GPIS SCPLSEGQTCALNPLSCGSPGPDWLI LGKLGPLGCSKPKGSHFAFPLVVPF HPCSKTKLFPREELFVVR |
| 2316 | 7813 | A | 2519 | 52 | 286 | MMPCLRQRQRQREKREKREKREH MRTQRKQLK*WITRFKNSSKRQR TEKNSKKPPVPHRGAGHSNGKLNC FRPAAS |
| 2317 | 7814 | A | 2520 | 3 | 296 | TNTRYTIGDPALQDMNSRRAHSH TYGHTLLWEGICDLTRPPKLGSCRE KECPRPHPSLDR*SSGFWDPAGRGE LMQWEMPQPCSPQPLPKPCRSSI |
| 2318 | 7815 | B | 2521 | 83 | 241 | SEWQKKLTPEQFYVTREKGTPEPPFS GIYLNKEAGMYHCVCCDSPLFSV KLI* |
| 2319 | 7816 | A | 2522 | 19 | 629 | YFVLISPLLTFSTHGFDLCYLICNTV HKTPCVFRSLWDIQKEVFSIKGSRSP SPSKGNGFDSEGPVRTIPGGLTVE*L GMGSGRGEWDRILLPGTTHRGTSW HVNDSVISSCSIVYVFHSSEKKYCSG TGWPSFSEAHTSGSDESHTGILRR LDTSLGSARTEVVCKQCEAHLGHV FHDGPGPNGQRF CINSVALKFKPRK H |
| 2320 | 7817 | A | 2523 | 1 | 707 | MGAGAETGRGQRAAAPERRHGRL LWLLRGLTLGTAPRAVRGQAGGG GPGTGPGGLGEAGSLATCELPLAK\SE WQKKLTPEQFYVTREKGTPEPPFSG IYLNKEAGMYHCVCCDSPLFSSE KK\YCSG\TGWPSFSEAHTSGSDE\ SHTGILRRLDTS\LGSA RTEVVCKA /QCESSILGHVFPDGP\GPNGQRF CI NQCWLWKFKPKGNHWTIFQESAFP CHPFHVAPSIFHNSLE |
| 2321 | 7818 | A | 2524 | 303 | 743 | TGAQWGRGLGHVCWSMGFVSWEE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | CSGNGLSQAGLVKLLIILHSTVQK GLTPRWGGMLNTQLPGGVGGP*FP KMPGATL*PFEGKSPAPQLFPCQPW AGAAHGGAGGPSSGSPGPPQCPV KALPVLRA GWATQPPGSFLWPTPS D |
| 2322 | 7819 | A | 2525 | 102 | 421 | VQYGSNWNKPYWNRVGP*SHTTG ELKKRWPHPRSCCPHGAAGQGAER CGRERGPEDTSDLLNK*QW*RRFPS GPAECGAAVAGL*GAAGCRGRSRP LKS RDAGLKS |
| 2323 | 7820 | A | 2526 | 225 | 448 | TQEGRGIDFGPWWPQLLPSSPSPG L*SPATPPQAWVPPLPSSSSSPALILS GPNRKPEPPPGIPPQFYLTSL |
| 2324 | 7821 | A | 2527 | 43 | 390 | GDVPTVTGECPPSYRAMSPSYR*MS PQL*GKSPQL*GDVHQL*GNVPPVT GLCPPITGQCPLIVSPSYTVLSPHYK VVSPVTR*CPPVTG*CPPIAGQCPL *CPQAISWSPVTG |
| 2325 | 7822 | A | 2528 | 525 | 635 | HIQGQLWWPMPVISALWEA*EGGL LDPRSLRPAWAT |
| 2326 | 7823 | A | 2529 | 66 | 432 | TRGSWHKHALAPT VHRAGLWGGK AGTQASPGAADNVPPPY*TSGF CG WKAGTDFPTSKKPCPFLPHPNPPLP PCKWQKGLSLFVISHSLICKVGMQL PRGSQVRLLLTKIQIHRLSLGRAE |
| 2327 | 7824 | A | 2530 | 5 | 95 | |
| 2328 | 7825 | A | 2531 | 1 | 123 | |
| 2329 | 7826 | A | 2532 | 118 | 363 | |
| 2330 | 7827 | A | 2533 | 23 | 250 | YLIVVWICISIGLYTY*LIIRALYILR KLTLFKYIPISH*SLSFIVIFCSLVYIY MYIYIYVYIYIYIYIYIY |
| 2331 | 7828 | A | 2534 | 346 | 611 | TSVEAQDATDRLWPDSCCPAHGAC TRTVWPKKPPYFPVKKMESCSVAQ AGVQ*CVLSSLQPPSPRFK*SPASAS GVAGITDFQKLFCQ |
| 2332 | 7829 | A | 2535 | 267 | 682 | HFSSLRMQARPPSFRPYLVLHPKNC WIFILINDSWMVLF EASLPTVPSLV QTTIFLLGILQQPLTDLPSSSTPFF*S LHLSAV*VVFRKFLSWPGMVAHTC NLNTWGG*GGRTA*AQEFDTSLGNI VRPCLQKKKSR |
| 2333 | 7830 | A | 2536 | 45 | 280 | |
| 2334 | 7831 | A | 2537 | 1560 | 1885 | QLGVLLAGPFTSSPYGGVSPGLKRP WPAPRSYPLPAL*PLPAPYGVQ RSG LPNPKLGKNPLGPISSQKPPCGGPV KTSIVAHNYSALSLSLLPQPGSA PQALSL |
| 2335 | 7832 | A | 2538 | 60 | 341 | VTLHSLVILFSAHICRIKLNITNLQM YSVVHPNFHLDVTIPKIVVALCFRK KYAFFCFMQQKYRM*SEIH YIFILS VVLNVNEINSIIQMY |
| 2336 | 7833 | A | 2539 | 442 | 686 | TSYNNLLNNLNKNIETFRKELSSLSHL CNRGQGILKSLIAWLGA AAHAGNP STLGGRGRRIA*AQEFKTS LGNLRP VSPKK |
| 2337 | 7834 | A | 2540 | 459 | 603 | GFLLEIIDKAEGGAHACNPSAFGGQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DGRTT*GQEFKTSLSNVTRPHLY |
| 2338 | 7835 | A | 2541 | 1 | 188 | PEQVLWQTKVTYSGKKKKKATKRP GAVAHTCSPSTLGG*GGWIT*GQEF KTS LANMVKPCLY |
| 2339 | 7836 | A | 2542 | 582 | 825 | GLSNMVHLWIEHHPAARSRDCHSG RLRREACLG YRKIS*HWPGMVAHA CNP GTLGG*GRRIT*GQEFKTS LAN MVKLCLY |
| 2340 | 7837 | A | 2543 | 775 | 1019 | DRSSPKKPPDDLPEFTEPQWFTLKHI KQCFSDISRLRVGPGMVAHA YGVA YLSTLGG*GRRIT*GQEFETS LANM VKLCLY |
| 2341 | 7838 | A | 2544 | 303 | 429 | AACVLPSPPSAHSSTHTTGSTHLG* GPPCSGPAPTWGSWKT |
| 2342 | 7839 | A | 2545 | 853 | 867 | NP*NLACFCVLLEFPSSF*RGFRRLG AVANICNPNTLGGQDGWITSGREFE TSLGNMVKPCIY |
| 2343 | 7840 | A | 2546 | 357 | 560 | KGSLVGLSLEERIFVAVQPSLFHK KCLWQGTVAHTSNPSTLGGQGRSV A*PQEFKTS LGNIVRPCL |
| 2344 | 7841 | C | 2547 | 486 | 728 | MWVGWVEVFSGVVLGWGVPVML QSDGSWKLPVHLHELLPFHMSWYP PQDDPNISLKLGLPGCPPLSLC DVS YMVSSA* |
| 2345 | 7842 | C | 2548 | 240 | 332 | MACFSFSAQLKDRLLRSPATHTPL LNAPL* |
| 2346 | 7843 | A | 2549 | 2 | 603 | SLPYLPQPHPLEFGPLNLHRDQRAG AQTLTQPM SLCCSKSLQLPNALTDK RPCWVLFPA GLSSLLRND SAKLPFR NKSGFP PAQGLCPGGSRLTTWHLSF HGLFLLHQ RSAQRSTS QIPSNTHLT *CPTVTTETVCLK*PRLSVVSVCFC SGSP*RALQCTPPGKPS PFLS QLSLT DPLPSTNLLFHPVGT PRAPGWA |
| 2347 | 7844 | A | 2550 | 132 | 419 | |
| 2348 | 7845 | A | 2551 | 1083 | 1563 | PENQSSLYFLPANLLKMPFCFFVFF* DGVSLCCPGSAVAQLQPPAS*VQSD SPAFSLTSRWDCRRVPPRPANFCIFS SDRGFSMLVRLVSNRPQVIHLSQP PKVLGLQVETGPQKREWVPRELTA SGQWKGQEPDQGEDSGTEGRWLPL LPSAGHSGED |
| 2349 | 7846 | C | 2552 | 173 | 501 | MPSPSAPSIVPVLHGCWVHICQADV YHTLLKGFLFLRQSPTLSRLECS GTILTHSNLRLQGSSDPAALASQEA GLKLLVSSDPPTSASXXXSAXLXCQ TGV SXXRP* |
| 2350 | 7847 | A | 2553 | 174 | 364 | YDAEFPRCSFGLIYPRLSVKEASRLS AVAHTCNPSTLGGQGRWIT*GQEFE IS LANMVKLHLY |
| 2351 | 7848 | A | 2554 | 61 | 283 | GGRIA*TQHSILDNRVRLHLKKKKK KKQYLKKVHLPGA VAH/TYNPSTL GGQGGWIT*GQEFETS LANMAKLC LY |
| 2352 | 7849 | A | 2555 | 1140 | 1313 | HVENSEGASGERKLTQRLGVVAL ACNPSTLGGQGRIT*GQEFETS LA NMAKPHLY |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2353 | 7850 | A | 2556 | 99 | 296 | WVLIVHVISSKCLVLEICVYRLGAV AHACNPSTLGGQGRWIT*GQEFETS LTNMVKSSLYLKYN |
| 2354 | 7851 | A | 2557 | 175 | 332 | RNPIFSLRKWPLRPGGVAHACNPST LGGQGWIT*GQEFETSLANTVKP RLY |
| 2355 | 7852 | A | 2558 | 667 | 772 | ARCTNPSTLGGQGRWIT*GQEFENS LANMAKNRLY |
| 2356 | 7853 | A | 2559 | 7155 | 7302 | IMKLKMYIWP GAVAPACNPSTLGG RGGWIT*GQEFETSLANMVKLRLY |
| 2357 | 7854 | A | 2560 | 227 | 410 | FQVDPDTWLFIEVTLFIFMAIFYLW QVLLVFHFTAVR*CSLFQGSYGIFGI EGRIPYSEL |
| 2358 | 7855 | A | 2561 | 275 | 685 | LKPLFTPSPGPAGVPRGLCWKEAPT PGSLLGEEETELNVY*GPPPGSLRPA SHWAPPEGLRPTSPLFVAATSTIGPL PVLVTLGPHLSPLFGQFINKGRDDT VLLPPQSPGCRESLACQGEETSRLCF VSHTSPSSL |
| 2359 | 7856 | A | 2562 | 20 | 354 | PLYSQSFPPIYPFITLLPE*SF*NNNYC SfVNIPSLTPSHQLYKVHSPHPHPVF HTWAHPAPALCSSWVAMLTVYQG AVLYQCLSTAVSVQGPLRLLGFSNR DTLPSKGLS |
| 2360 | 7857 | A | 2563 | 374 | 585 | GNLINC*LHTHTHTHTHTHTHTHTHTH NLTNYPDFLYLLVTFPGDIVIQESAF IFFTKSPKHCGLGAAIRNA |
| 2361 | 7858 | A | 2565 | 918 | 1096 | HCHSNSEFDTETLGMVAHTCNPSTS GDCGKQII*TQEFGTSLGNMVKPHL YQKKKKKSR |
| 2362 | 7859 | A | 2566 | 101 | 327 | LVKNQQSTQKLAKHGWACL*SOLL ERLREENHLNAGGGGCSEL*RPCT PAWATETVDSLPIMLCLVLQPFSL SR |
| 2363 | 7860 | A | 2567 | 347 | 478 | RDHCRLGTVAHAYNPSILGGQGRR A*DQQLETSGINTVRPCLY |
| 2364 | 7861 | A | 2568 | 622 | 761 | KSVEVFYLSIGQEECLPHIQFIFHAT IFIIGRAQWLTPGIPAFWETEAQEFK CIHICMQVWWHTSV*SVRNKSLYE ELLQARDPGKFVILHYHYWLFHGK A |
| 2365 | 7862 | A | 2569 | 70 | 316 | ISHPSPSTRWEAVTWALG*LFPCPC HLQGGRQAPLPLPYPLPIVVAPPLI SRLNPDGDL SAKTILDVTLYISSTTV GGSWG |
| 2366 | 7863 | A | 2571 | 145 | 331 | IFHSKMPISEWKL*TLWQFFKELKI ELPFDPAIPLLG*PKFQRLKNTNGIC HYFYM |
| 2367 | 7864 | A | 2572 | 918 | 1135 | GFISASLCNWILTHLKFFKEMGSRC VAQAGVQWLLTGAVMAHCNLKLL GSSNPLASAH*VAGAICMYDHWHA |
| 2368 | 7865 | A | 2573 | 590 | 936 | QLAACGGSC*SQHFERPR*EDCLN PGVQDQPEQNRETPISTKILKSWA WWHIPVVP GTWRADVGLPEPSRP KATVSCDCATALQPGRRRARLCLK NKYIKYSVQKCVIFFLF |
| 2369 | 7866 | C | 2574 | 34 | 670 | MXVFLSSAGNMPVTCWCWEAPRC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NQKCTDPAARRPDPQTCASQDRLR CAPCTCHQPLXSRYTQHPGLVPLPH HDRQSVPPQGPRVVQTDAAAXMVE VSVXVVLEGWGXPTTRRMKLSLLG IKMLRRGGTVRGAPGAGSALRCGW RWRPPAWRPQMSTSRTSVGVQARS TSSSPXPXXSGXLWVHVLLXLAQL DSQQGFDLLLAGRRXSGSNLI* |
| 2370 | 7867 | B | 2575 | 70 | 165 | EQIEALLESLRQAQQNMDPKAAEE QEEKEE* |
| 2371 | 7868 | A | 2576 | 1 | 390 | FFFFFVLPVFLDFHVCVFCWK HAGYMLVLGSAAVQPEMHRPSRPP PRPI*RRQTQK*LWFEPDVSWLQGR WVENQHFINRVLTCLERV*NRIYYG TSSSSPLRSGSEGVGPGAFSRPLYPC LGPPN |
| 2372 | 7869 | A | 2577 | 435 | 861 | RASLITVCVPGHLQAADQKNLHPLR AHVVGPCLAGSSCARRPSRA/RGPP RPTPPEHGSRLPQPS/CAAASV*TTR GP*GTLCLS*WGKGTSPGCCGIERP KAGGKCTGHSGVCPVTRKSNHSLC ARSPTSCRPKFAPAAAGPRGGALPG RVILCSKAISGTGPPRPTPPEHGSRLP QPSWLRRLSEPRGGLEGRFVCRDG ARAQVLDVVCIERPKAGGKCTGHS GVCPVTRKSEGLGGGRLGLCISGCT AALPSTNM |
| 2373 | 7870 | A | 2578 | 38 | 398 | PVLFLDFHVWLVFCWKHAGYML VLGSAAVQPEMHRPSRPPNYIAK MCKLSILSLSFLKEGAGDKNSSEPN LG*VP*FSLHPCLSNQMTLGNKQA ESMSLCGFFLPDCFFLTykRIYL |
| 2374 | 7871 | C | 2579 | 42 | 443 | MKPAHSAVCPGHLASCETKEFAPR CGPTWLGPCPGRVILCSEAXSGTGP PRPTPPEHGSRLPQPSWXRRLSEPR GGLEGRFVCRDGARAQVLDVVCIE RPKAGGKCTGHSGVCPVTRKSEGL PAEDKKTNMKV* |
| 2375 | 7872 | A | 2580 | 871 | 1253 | PRLPPGLPGADRSPAGSQACA\GPA EHGPQGRRGGRGGGGGGGPGLPHP PTCGTWTSEGA\SRRAPPPPAKGG AGPRCSPD\$PSSPEHFDTQKGKLHS PCCWLFFPLLFPSSISDLSKRKRLPK NCL |
| 2376 | 7873 | A | 2581 | 222 | 754 | YPP*HVAPHPAPLPWQVQGPPDW PRYLWKVPPASLWPRGTEKSPCWA WLVGAGLGLPPFSLPNLSDLGTS FPLPQTLPLCPAPQGDLLKPKLGPK KGGSVLSTSPSSFPRGLVGGEAPPN LSPSHTHLGSNVCWTKKQEHTLLV PTFSQSSQNPLPSPSPIGAVKALFAS TMG |
| 2377 | 7874 | A | 2582 | 2 | 431 | PEGAAPAAMAVTALAARTWLGWV GVRTMQA\RGFGSDQS\ENVDRGA GSIREA\GGAFGKREQAEEERYFR/ ALQVML*DLFGVKD*N*TLSHRVL VEAQSREQLAALKKHHEEE\VHHK \KEIERLQKRNL SRHK\QKDSKLLKH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2378 | 7875 | A | 2583 | 1 | 232 | RETACCGRDARGAAPAAVATL AARTWLGWGVRTMQARGFGSDQ SENVDRGAGSIREAGGAFGKREQA EEERYFR*GSDQSENVDRGAGSIRE AGGAFGKREQAEEERYFR |
| 2379 | 7876 | A | 2584 | 3 | 399 | LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGVRV/WGVRTMQA \RGFGSDQSENFPTGPRAPHP/RKAG GALGKREQAEEERYFRAQSREQLA ALKKHHEEEN\VHHKKE\ERLAEEK FERHKQK\KMLKH |
| 2380 | 7877 | A | 2585 | 3 | 316 | LLQILGTEPQKAVIVLVENFY*YVS KYSLVKNKMSKSSFREMLQKELNH MLSDTGNRKAADKLIQNLDANHDG RISFDEYWTLLGGITGPIAKLIHEQEQ QSSS |
| 2381 | 7878 | A | 2586 | 3 | 469 | |
| 2382 | 7879 | A | 2587 | 434 | 815 | TQVDWTQRARPGPWRHPHPFPDD DSLCTGCTSHLPPHGD*L*NPSSNGA NPRLSPAPPPPREAQTPPGAGHR TPLSRACLGLAFPAQPVRLRRDTR DGRKEQRETVPPTFPDARGTRLIL RHK |
| 2383 | 7880 | C | 2588 | 204 | 354 | MWLQMTRAVLSSNLDPYVCRRRA RGRSSPSGSLXXKGEESWGPRHCY SP* |
| 2384 | 7881 | A | 2589 | 390 | 681 | RERGRAGRRRETAVRSREKERER EGLDRSSRKR*PELVKGSRAH*PQ SGRWSHRPRPAIVPTSFQPCDVRA QPNGPSDLPDHLPTRRRKACDRR |
| 2385 | 7882 | A | 2590 | 598 | 769 | YPQCPTPCQAARVWWDShLAIPAL LGGRGRWII*GQEFETSLANMAKPH FYQKKKKK |
| 2386 | 7883 | A | 2591 | 359 | 775 | KKTQPLHQGYPKINFRSPSPPIPVV PLLALPK*GHSPFVSPPLQKIPPKG SPHDPTRQRPSIAEGRAGTQLSSPL WMAGTLTEALHHKNRQYPLGSHN QLNLGSTGRFTSKRGKDGPFDAGQ LQGHLLKGTFFF |
| 2387 | 7884 | A | 2592 | 585 | 780 | TFSLPRLDFFFLKARKPRIKNTKNRP GVVAHACNPSTLRGQGRRIT*VQEF ETSLANMVKHHL |
| 2388 | 7885 | A | 2593 | 436 | 1645 | GMSALVQSRVSHLHRVSLTRLTA RAQETSSPNTVTPPNQTLSTAQNK RTIPGPARE*VTLTRLSKEPLLVEK AAPTPHPQ*GPAPRPLQASALPLYE QHRRAPSSSEDPRPLTPPSH*GVS TWTP |
| 2389 | 7886 | A | 2594 | 1 | 373 | TCSCPWLAPLTLQKNCPPHCHILSL LRKTKQNDAPKKSPRGSLPAVSGM KQDTVTLGRMEKPPRSIPQRPQWD GEATRSIPRRPRVPPVEPNPGHWQ NSPPG/EDQSILSTSNPRGPTPFKSGS |
| 2390 | 7887 | A | 2595 | 502 | 798 | SPKVQRHSSQAALRQAGGALSLLWG CLPSQRRPPRTVSSREGPHPGKGV* GGVQRSKGPPLPTCPQGLTCLTPT DPGSAWNPPTPT*NEKGNSEIIRH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2391 | 7888 | A | 2596 | 1 | 136 | HPCVHEPMSFEWPWQYRFPFFFT*G SDPKKHGWASLPSPGPWAQP |
| 2392 | 7889 | A | 2597 | 429 | 1003 | VAYVIGFKSNMPAKHMIKNTSVRV FICPPSMEGKHG*SQPR*NNSPLSPQ NNLSPTLCPLFLPQLKQESMC*SFFN FYQPALAFSLYSIIPSDVLPSSPFE TRVSWEQFAYLLLESAYLLVQAIE *ASSFFLLKHSTSLWIPLHCLFYITFD ICWSLYMNIFFRGSHCSLQYDPGFL TLSNAPSITI |
| 2393 | 7890 | A | 2598 | 367 | 463 | SGHGAHAYNPNTLGGRGRIA*SQE FNTRLN |
| 2394 | 7891 | A | 2599 | 436 | 833 | CLTSALLGCVYVYFFSPHPALFFLRI RTSAYNLLKQLFFRYWNSAKSDLS GHSKTLMLCPKSGGGKACAVEPSC SLDTYLCPEIICQALFFICLVHLL FYCYWRGHEL*YSYCP*FNVKLIM MNSIACY |
| 2395 | 7892 | A | 2600 | 53 | 95 | DSILLTQAGMQWCELGSLOP*TRP PIVCFCLFIYLLRQHLAPHPSWNAV V |
| 2396 | 7893 | A | 2601 | 432 | 825 | NFKDTAKGFLHFDHQKILDPCPLPG SRARFGTYPECPHVPSVTEAQETGL SVPSFGFHFHFLTYLLLEYFYFH*G TLYLHLDLHOK*HCQAMRNFLYKS RIQRHHIYHSLDAYANLGHDAKDPF FSLDF |
| 2397 | 7894 | A | 2602 | 83 | 111 | |
| 2398 | 7895 | A | 2603 | 1 | 71 | |
| 2399 | 7896 | A | 2604 | 215 | 758 | LPLQYHRKNIHANTVALADARAPR TASRNRLGVRASGLASSPRLGLQ GSISSASRGRPAQHVPGRPATLSPP AGAGPSR*ERSRAGARGRWVLLDH AGERPAVRELSRPDRQVSFGPRNIS EIGQVLSPETSSCELPGIGDLLWQL EYVDARKHSLVGPESLSHRELGSPA GGRRP |
| 2400 | 7897 | A | 2605 | 211 | 323 | LDSLIQHSASTLAQHSASKPWKPDS FHTQFFHTVWKLSQWCRAVVPATQ EGDAGGSLEPRSLRL*CVAGTTALH HCDSFHTVWKNCVWKLSGFHGFE AECCASVEAEC |
| 2401 | 7898 | A | 2606 | 75 | 232 | TQPGHKGETPFFPKTPKISPERWWG PIPASWGVKAGKLF*PRGERFPLIW F |
| 2402 | 7899 | A | 2607 | 325 | 566 | FNDKYFYYPGRQIQCHITLFLNLKI TSDDFFCFKKTG*VAHTCNPSTLGD *GGGIA*AQEFKTS LGT**DPIYKN |
| 2403 | 7900 | A | 2608 | 1114 | 1367 | AIARTLIIMINLTVNFSAINENCTTT *RYFDLL*YTTGMFRKIVRKLKVTH LKWNN*SKYTFKCIRKFNNLSEPF NHVCKVF |
| 2404 | 7901 | A | 2609 | 100 | 450 | FLEENYKVKFSCFSPFEELKKKGRL N**NFIS*I*IGPKIFSQTNS*NSNFYQ YLCILSGLIQDK*NFKILS*FYK*V GNFDILYIHTCVCVCVCVCVCVCVF VCLWSTLRMTDTV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2405 | 7902 | B | 2610 | 50 | 382 | XGEQLVRQDL DAGVSEHSGDWLD QDSVSDQFSVEFEVESL DSE DYSLS EEGQELSD EDDDEVYQVT VYQAGES DTDSFEEDPEISLADYWKCTSCNEM NPPLPSHCNRCWAHX* |
| 2406 | 7903 | A | 2611 | 1665 | 1787 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 2407 | 7904 | A | 2612 | 1431 | 1553 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 2408 | 7905 | A | 2613 | 1 | 752 | DLDAGVSEHSGDWLDQDSVSDQFS VEFEVESL DSE DYSPSEGGQELSDE DDEVYQVT VYQAGESDTDSFEEDP EISLADYWKCTSCNEMNPPLPSHCN RCWALRENWLPEDTGKDKGEISEK AKLENSTQAEEGFDPDCKKTIVND SRESCVEENDDKITQASQSQESDY SQPSTSSSIYSSQEDVKEFEREETQD KEESVESSLPLNAIEPCVICQ/GST*K WLHCPWQNRTSYGLLYMCKEAKE KE |
| 2409 | 7906 | A | 2614 | 426 | 813 | SSRRFVWRAKLLCERAQSGTVYEI* QCAHRHPRHRHPGCCRHRLGYAGT AGPLAGYRPFRRQHRQSLWRAASAI CVDAISMRTSRSTVRPLWPPPSPA RFATWSHYRLRDHGDHTRPVDLPT SQFTILL |
| 2410 | 7907 | A | 2615 | 1740 | 1862 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 2411 | 7908 | A | 2616 | 1174 | 1354 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPLRPAGLFKH SPGLYSQPILT |
| 2412 | 7909 | A | 2617 | 2271 | 2393 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 2413 | 7910 | A | 2618 | 1029 | 1197 | FFFFFFFFGFLVETGFHRVSQDSDL LLTS*SSRLGLPKCWDYRHEPPRPA EEGI |
| 2414 | 7911 | A | 2619 | 402 | 990 | |
| 2415 | 7912 | A | 2620 | 1326 | 1716 | KAKKKKRLFFFCIFLCFLWGLPASL LEPGNVWKHLVWNSLHWSTARVL SSPHLTSCNSWQKHPEHPKGAPKN HLKAGCSGSCL*SQHFGRRLRQEDGL RQGV*GCSKP*LHHCTPAWDKHL KNSNNSNH |
| 2416 | 7913 | A | 2621 | 148 | 420 | LSLSLCRFLGRFCSSGSSSIFVLFHF SFL*FMFSFSLETQKFHTSCVCVC VCVCVCVT*RILSFGIK*SSIQI*AQH LINFIFLSEKWR |
| 2417 | 7914 | A | 2622 | 565 | 916 | VPRARTQHSREKGRAGAWFGLHY QGSIIICGSNSTW*NPPQRGPKLLVRL MS*GHCPPSSTQSGSTTTGKEEVKS SSGSDVALALYNDYFSLFCSSSVSKI KREPQLYKQTERETGHT |
| 2418 | 7915 | A | 2623 | 1132 | 1245 | KWHLGKIQNYSTGKCNRIYIYI*I YLF*CHLSIGNC |
| 2419 | 7916 | A | 2624 | 209 | 326 | |
| 2420 | 7917 | A | 2625 | 808 | 1010 | EETEGRARWLTPVNPNTLGGRGRW IT*GREFETSLTNKEKPPSLLKNAKK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KKKRKKEIKPGMVATCL |
| 2421 | 7918 | A | 2626 | 1602 | 1940 | PSGNTSETSKGLNIRSHTRLFEDIKG VNHRSSQLFQKKPKNRDRIFQERYV RSLLSK*VHPCDICKRPTSFLTTL*Q QKHHHF*QKALENIKEEQTDKLILS CKRVLPFVKK |
| 2422 | 7919 | A | 2627 | 2565 | 2748 | KSLKLGMSLKIKFIFLIKGH LGFPHF LKICPKTNSIFNTHVS*YIYVCVYIY VYTYTHIY |
| 2423 | 7920 | A | 2628 | 1032 | 1292 | MYIPLNNGTVGVDSQMHL DVQIDY RVLFSYDDWCRNV*FGWAFTSCLP LHGNIGGFFKMCVSYFFWEGELFSS VYFLESSYRKPNL |
| 2424 | 7921 | A | 2629 | 1640 | 1815 | NSKGESSAPLFLPD SHLEKRKSYGT HPLYISLLKNYEK*NNSNLKAVIFK ALLKNKQT |
| 2425 | 7922 | A | 2630 | 1089 | 1226 | IQIQNKLLKKECPSWVW*HMPVISAT QEGEVGRSLQPRSLRSAWAT |
| 2426 | 7923 | A | 2631 | 197 | 430 | SSFLLVYFFIFYFILFFETESRSVSRLE YSGAISAHCCLRFLGSSDSSCLSYSE G*GGSIDRAQEVKAAASCRTTAL |
| 2427 | 7924 | A | 2632 | 343 | 596 | GYSLLYIQKQPTPLKTKARIGCSYY VNCIFLWNFWKAHTSCFPLCSFVGD FMYICCLERNPEVGSAQ*DNGKQM PCYYRAASEG |
| 2428 | 7925 | A | 2633 | 1143 | 1553 | QCRRVPRGKRLELGVHSSTG*QAPL LPSASATSSGFLADRRVGTGLRTPL RSRRSAGPYLARPASSAARGPPVGR RGPPWGWAAASAAISARSSPPSAAGS GPDWRRPGKRHSRPTAAASAHTS PSQSPAIPAGGR |
| 2429 | 7926 | A | 2634 | 158 | 585 | ALTWVHLSSVSFFFPDLKLTPSRSP ANPSTQQPPHPPHPAPKP*WEAGRI AAS*LPSKAGSWKPLL VNP KAKLW SHVGRMEGDLQCPLCLWLHLPILW FFGGSCFPQTEHSPVQSPDGLI IAWN CPASDAGIKDCLPKYFC |
| 2430 | 7927 | A | 2635 | 1348 | 1540 | SCCWACE*QCNWYVYISVCACVYT YICISTHIYIYTYIHVHLMGYVKIKQ LFNACDSMEHLQAH |
| 2431 | 7928 | A | 2636 | 263 | 615 | LVNSEGNIWVKLCHELQHGPLNSSP FLILLSHSEKINRASIMLKRYKLIN NYILSAFNPPPGKIHTHTHTHTHTHT HTHTESQKVKST*EIT*IFPQQYTNL CQREEHCYFLSHSE |
| 2432 | 7929 | A | 2637 | 270 | 665 | KLKGVAVHPYCQPARTLAPRLALS EGSFRATCPG*ELSGLRCSPICCPPRS PPALPLCPLKTKLPKC*KTQTYPGS GF*PSHPSCSGPKPLMGCP TPGGG QVDEWIVIYNKIYGRNTGLRRLHRP LYQFK |
| 2433 | 7930 | A | 2638 | 54 | 311 | SQHFRPRQVHHLRSGVRDQPGQH GEMPSLLKIQKLAGHGATHL*SOLL GRLRQENHLNLGGRGCSEPEIVPLH FSLGKQSEALS |
| 2434 | 7931 | A | 2639 | 26 | 229 | CRMTMSRLVTMGVAVFLVVCERC DAVCPSGQSPSPAPWASPPECCRDH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ICPHPVGPPGPPSLALPAW |
| 2435 | 7932 | A | 2640 | 133 | 586 | THVMLCAQVGSHHPALPWASPEC CRDHICPHPVGPPGPPSLALPAWDT HTHTHTHTHTHARTRATHAHILPS HAVFYFDFVQSGSLAGSPYPRGGG GGWFLGGAKKGRECPGG*MGPP MTPSSFQKQLLLPPSQGPTPKPPEGG PCLQ |
| 2436 | 7933 | A | 2641 | 186 | 609 | RVGHHPPSVRHPHQHGWLRDPV QLHLWSSCVAFPPGGAPAGLPPSDQ DPGPPLAISPTHWPPPCGQPKTIAA HGNGHTRTGGR*RPRL*SRPAEWP SAPKGRSGGLPGSFQEPADSYPGCG TWCSSACKGRQPSYS |
| 2437 | 7934 | A | 2642 | 989 | 1790 | NYTPFLPCSASAEFCELWGRPLVV FCYFYFQPPLAVEPFNVIVICCWVR VKVGPGAFPRGLRRDVQRADFSRS SEGLLMGWVRDFDNHQSTCALDPF SGGIGSLLVPGGSDLQIGCFQKSFQA LIEN*CLNRHNSLG*TPKRSIKILWA E*ISRAGLCNSSPEHPACGHPPPR*G QWEAGPTAARTCFSPPTSNPPPSNG PQAHEAQVSGDHSIGGS*GSPSPPL AYNLSTRKAQPKCGKKCMVLPSTC KNCTYCKPFALWNCMP |
| 2438 | 7935 | A | 2643 | 92 | 330 | RQVCLPPSERNVASLRTPHPRGAQ KSQEGPPGRQSPSELKSRYWCVENS TWVSRAPQGTGWPGWALPFPHQG* GWLGP |
| 2439 | 7936 | A | 2644 | 1137 | 1290 | HGQINQMEVNLPMDRKV*THHTHT THHTHTHTHSSTSCPYTLKRNVK S |
| 2440 | 7937 | A | 2645 | 96 | 357 | |
| 2441 | 7938 | A | 2646 | 2648 | 2953 | DWGYLPFKTLTPGMVCHCLPLKS FPLFFPPLFSK*WMGPKLYPPKPHL YQNISPQYLCQKTPQTKMPILKKG VFFPFRM*APQESGTNVFCMFLCPS TL |
| 2442 | 7939 | A | 2647 | 201 | 377 | QTVFVKLCVYTHIYN*VYMLIHI*A PLSVY*YAYI*AHILSYTYVHLVYI TEKYDF |
| 2443 | 7940 | A | 2648 | 1917 | 2056 | QSHAKEWIFLLTCFIF*KLLRNIIYI YIYTHTHAYIYIYIYIYFQ |
| 2444 | 7941 | A | 2649 | 246 | 717 | KRQSEEGVFSCCQGWNESLLLKSK VLEYP*FLHFPSFSFDLYLFNYVFIY LFIYFCSIQSQTQSKAERAYIYIYLY MCCRQNTVNFTTTTQKQFCHLNIH LRRRNEKRWGCHFLVYAFEARSMF IYFFSLCINENDPEWRLAERSMYWS KHHKSC |
| 2445 | 7942 | A | 2650 | 191 | 657 | SGGERNSSAPSAMSPSGSATTSPG T*PRIIDERTPAFHARASTVKPPAGI NTREHPPLPCTPKPCTKTHFTAPP PQRCTHTSSPPRNLIQIFTRDTHPPPT HTHRHTHTQEPGWWSFDWVGCLR GFSFECTHFHFPQNKGTFFKMSYIA TY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2446 | 7943 | A | 2651 | 1108 | 1282 | PPLWAPAPAILFLQERKRGNDPNW DARRGN*TKNKNKNKNKNKKTETL LRRPVFGAAN |
| 2447 | 7944 | A | 2652 | 2 | 479 | FIIAHPDVLGELSYFVTEKMISIHLE CSCNVWRVLYYGFNLYIYIRYIICN YIS*YILYIK*YT*VFF*TMGVYYKIN NNMQTVVPVYLNVIQVCCY*QIYL TFIYYGSHFLIELRNY*TRMHMLLYI DLLPVFTLPLPFMLSMMLNMGGIFN GPNF |
| 2448 | 7945 | A | 2653 | 341 | 622 | YQNRLFNPQCFTCLLVWLWDSPAP PPRPWQPPQGF AHT*DRKEEGDPI GIWAPEGKSCPTKPPPPSLPRTSPGW KRALQKGDTCGPGPSTAST |
| 2449 | 7946 | A | 2654 | 597 | 785 | NNSPSQ*CHFGTDSIICILKQRLGAV AYACTLSTLGG*GGRIA*AQEF EAS LGNIVRPCLYI |
| 2450 | 7947 | A | 2655 | 237 | 656 | RGQGWVGDSSQGRGGAKEGLLP SH GLPTPNPIHPTSPIPPENYVQRNTEK SWSWREGGRWKEIGRGRMRGKPS P VLPPPGDRVMEGGPPTPLLQHRSPH PGERHGF S*SKFPPPPGSRPQKERR KGQRGM CVRVGQIN |
| 2451 | 7948 | A | 2656 | 109 | 290 | NKLLNIYMD**IICQILLKLYLVPIKL MDTVYMSIYLSLELCFVISPFLLTGI YLNLYIY |
| 2452 | 7949 | A | 2657 | 122 | 359 | |
| 2453 | 7950 | C | 2658 | 133 | 315 | MQWLYIATLIPFFWTQRKGTFS GK SQLILDFLQGALAILSPDPHPGILHR SLWAHLPA* |
| 2454 | 7951 | A | 2659 | 1399 | 1644 | CERGLPGPFSPMAHQG*TRAGDTG QPASSLPLGLTAGPYFPSPGCLGPFT LDGCGLSPPPLYLPVFFPGGLLKSSR PLSCLN |
| 2455 | 7952 | A | 2660 | 592 | 943 | RTGCGQTLTVSHPDQARHWP GPGF ALILLYYPAQGFHLLPEAGPEGRG SLLTEEGSREANSRSSLISAAQLPPA APPQGLGV*MQESSRWGGKGRSKG SLPINLGLNSKLLKKTTPP |
| 2456 | 7953 | A | 2661 | 181 | 401 | |
| 2457 | 7954 | A | 2662 | 1163 | 1457 | HPRICWHHSDLHTTTKTS HST*SESQ NPHSESPGPRGCEPPGPRGSEPPSLL *LSLPPPLPFAFCSSCPGLMAGFPK QALSITGPFSPSVALWLGHC |
| 2458 | 7955 | C | 2663 | 275 | 327 | MPFRLSQDCHHSAGAQQ* |
| 2459 | 7956 | A | 2664 | 70 | 191 | DLLQKPQV*DPSRTECVSM*CFLSPP *AETTSILPCFPRI |
| 2460 | 7957 | A | 2665 | 40 | 142 | THIHILGFLI*G*GLAMLPSLVNSW AQVILLPQH PKVLQLQAGSTVNQPA HRC |
| 2461 | 7958 | A | 2666 | 479 | 722 | YCHIFLGGFFCCCSQHILNVFLCLAS FFE*MISQL*KILLGLGAVAYACNPS TLGV*GGRIT*GKKFKTSLGNIVRA HLC |
| 2462 | 7959 | A | 2667 | 265 | 518 | VKTVFLSGLDPLSLNENNMVLIMTS IVIFSHPLHFRFETLIGEWPFLLLG QV*WLTPLIPGLWEAKVGG SLEPRS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LRTAWET |
| 2463 | 7960 | A | 2668 | 626 | 695 | GPAARARPGKGIRPFRL**HHFGCS LWMGWKMGSQCRSPVESIPLGRAR WLTLPVPLREAEAGGSLEPRGSIPG WATRVPRPLYIEKKKKK |
| 2464 | 7961 | A | 2669 | 66 | 610 | TNNGSKSFCLKEHRGSCGCCSSKDF GVPQRLVLGLVLEDLILGELQVLA FGALSGSISIFPSIPPHSAIKKNSHLR KIPPVPPRQPFRVWTSGPPAPRAS PSFCFSPPLAPRPPGLRTRPPPS*APA APQSRRTGGPARCPRGVPQRSQPE *TPCKKNFLMEKISYDFHSQRSSD |
| 2465 | 7962 | A | 2670 | 1077 | 1598 | YVCHTSLYTSKSAHSSPWKFSWDV NPTPLAIHVTTSTKTVSFHTEEV RVW SVHSTLKRFGFGAGGGE*GISEKGG HMAQTGTSRRPIAGRDPGPGRPGL LAERYRPGEEAEVAPEPEDPH*CH HQHTGGPQAPSAQVKVQSSPRRPH QLPVSVPWPWPGGCRGPITTVGTS |
| 2466 | 7963 | C | 2671 | 40 | 180 | MSFEAEIVLSPDRTTALHPGLQIETL SHIIILILSTISFHQLLH* |
| 2467 | 7964 | A | 2672 | 1818 | 2154 | PTPVFVPSLFP SHKHL PQALCGLCG LMSMATKGLSPYTSPLNLWRDTH QRLDFSSSYIIFKTNRLGAVAHTCDP STLGG*AGKIV*G*EFETSPCKKRDL VSKIIFKKEQK |
| 2468 | 7965 | A | 2673 | 137 | 1610 | EENIKSYKEYKCHNLYVIRKELLGG GAVAHACNPSTLGLQV*AIPQKIKK YLNFKL |
| 2469 | 7966 | A | 2674 | 1 | 490 | GNRSRARRLASSPGSAAAA YRRPLP AGPSVYPQHERPCASTARRATGFRE IKVPSKSEVTRILDGKRIQYQLVDIS QDNALRDEMRALEQPQGHPTPDL STGDQYCGDYELLSWRLWKQNN AGVS*KLGLKSSPVPEFPLAGTPITN TPPQPFNLANERTF |
| 2470 | 7967 | A | 2677 | 2 | 215 | |
| 2471 | 7968 | B | 2678 | 63 | 203 | SFRRPMASASTHPAALSAEQAKVV LAEVIQAFSAPENAVRMDEAPG* |
| 2472 | 7969 | A | 2679 | 433 | 895 | VFHLPSAEPRASDALMASASTPNRR PLSAEQAK\VVLAEVIQGVSPRRJA VAHGTKARDNAC\ND\MGKMLQF\ VLP\VA\TPRSQQEVIK\A\YGFQLPTG EGVP*SFAPIWSSSYEA\QD\PEIRQA LSGKLEGACFCRP*TLPTPWGLLVG GSVAAS |
| 2473 | 7970 | A | 2680 | 235 | 442 | RPTFFYIPFKISKIKPSKIST*RPPSLL VG*KSKEKASTQKCLTKIPVPSANL KDPLPKHDEKREL RH |
| 2474 | 7971 | A | 2681 | 199 | 1061 | RRSEPKGWNRAFAFPKVGCGCVW EKTGMGDQNPEETALPSSLHVSISQ RSPRSTQASPPTRGHPVQPRRVYTP FKAGRPRRQKQVTHGQTAATLQVE *ATLPTNT*TS\TRAPCENQRGGKQ RSGWLRATKPH\TAERRPSLNRPLTP TEPNCKTTELKSYSLQSKTWRNKS* VKTCRSKG**VMER*WSGKHSVKI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VSTFPPSPRGSSSRLKPEARVARKY GPSPQLKPRRWREKHKGPREMGR SEKSESLEWDRSLPVLRLMVDGFS KQNRNGQGRGAQSMW |
| 2475 | 7972 | A | 2682 | 415 | 575 | ISGWGVGGSCLSQHFGRTREQEDHL NLGVRDQPGQHSENVSIKKKKRN VISI |
| 2476 | 7973 | A | 2683 | 457 | 549 | VSTGNKVVPQGQKVKAICI**KVLLK MQIAFTFCPGTLLPVD*TKVTHL NECNILASLWWLKHDLVFQLLATW LHFNLSISSENASAPSYCPTGVA LSKPIFNYPHFIPFLHFSHMTLS*PY LAFFLSPCNSKRNLDSHMVAIEAN RCLAN*NKNYDL*TADVSSFQNILQ FIVNHKIKLPT |
| 2477 | 7974 | A | 2684 | 291 | 364 | RLKL*SPHLRSYFEKSKEQLASRT TGQS |
| 2478 | 7975 | A | 2685 | 2 | 361 | TETLARPPSPLVTNMKLLAETVLLL TICSLEGALVRRQAKEPCVESLV SQYFQTVTDYGKDLMEKVKSP ELQAEAKSYFEKSKEQLTPLIQ EGLGTGTWFNFFELFSVGT LGTTAWPPS |
| 2479 | 7976 | A | 2686 | 425 | 678 | LLGAISWELWGTQPCHPVEGVP GPFGLSNPQAGAFREQPTGPV P*SSSFEKSKEQLTPLIKKAG TELVNFLSYFVELGTQPATQ |
| 2480 | 7977 | A | 2687 | 64 | 287 | RQMA LLKANKDLISAGLKEFS VLLNQQVFNDPLVSEEDMATV VEHSMN*YMSYYSLQATGEP QDLRPCSCALL |
| 2481 | 7978 | A | 2688 | 983 | 1386 | QEVRYRKVETLRCLLFSSCLV PVCAASPVSRRPGCRFLRSS LHWPTGRLVFRQRGETFLV PEKTVLRGVASAPAKAAGR TPVPGRRPRDARLRADARS* SC*RAARPRRGASGAVGAR CGPRGPFPLRSSGGIFV |
| 2482 | 7979 | A | 2689 | 473 | 706 | NLTASKISLKYCKQYLWILFR KRLWPGVVAHVCNPRTLGGR GGQTT*TQEFETILGNMVK PISTKYQKKKKKKRAAA |
| 2483 | 7980 | A | 2690 | 1400 | 1600 | VGGGSGRSSKFPPLP*CP PPSCCSLPISSPPCLSTP GPSLLHVSKGTRRISRL LDKRISKRFTNH |
| 2484 | 7981 | A | 2691 | 6133 | 7646 | YMLFLFLSTKGWTVIQNRQD GSVDFGRKWDYPYKQGF GNVATNTDGKNYCGLPGNE QACKIKSFYWKWDF* LKNIH CWKPV LGS*EE FPDKNVEAKDKGRKAV FSFPKFYFW*EILFCFS RVEYWLGN DKISQLTR MGPTLLIEMEDWKGD KVKAHYGGFTVQNEAN KYQISV N KYRGTA GNALMDGASHLMG ENRDHDPFHNGHGS FQPPYDARDNDG WYVWHSLLL*KSH*Y HYESLTIFLIATT SWALTVSHCPKLF MHHSKAFQL*GRH SYSHFTDEI*RDY VICPMSHNYPEIK LEFEHSYFLNNEH LDKYL YLYILKCV* KLSFSFPGFSDT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KGCKSYYSIK*QTQSLDGLPQRPS YLSFLL*GTGGLWCISVTLCIAPK GK TTVHTSVAVFYG*SAKRNLTTVVLF LITPNTFSFRLTSDPRKQCSKEDGGG WWYNRCHAANPNGRYYWGGQYT WDMAKHGTDDGVVWMNWKGSW YSMRKMSMKIRPFFPQQ |
| 2485 | 7982 | A | 2692 | 711 | 865 | VTMKTFSLRHKACGQVKNTLTI*Q PNSSIQPTSHYYPHCQPN TGMLIRK G |
| 2486 | 7983 | A | 2693 | 26 | 351 | ASLPDVTNMKLRAATVLLLTICSLE GALNRTQATDPCSENLC SQYFQTVT DYGKDLMEKDMSPELQAEAKSYFE NSKEQLTPLITKAVT*LGNFLSYFV* LGIQPASQ |
| 2487 | 7984 | C | 2694 | 10 | 123 | MSTDRHQGQRRWLGRPPHCYQHE AARSNCATPHHLQP* |
| 2488 | 7985 | A | 2695 | 6 | 409 | FCPALSSSTALFFLRGLWFRGKRLG STDLT LHKPFNLTPQFLHWYEMG ESHIDPKMLKPESGRSKSLFPSAAFL DLQSSFLPSFLVVFPPPLSGSCRSLSL PSGTNPLLQLVPLPPSILLPLSTVLF* RATKG |
| 2489 | 7986 | A | 2696 | 736 | 927 | SVAHSSCVSHTHMHTLLGRRATINC LFRNGRGQVQWLTS AVPALRKADV GG*LEPRSSRP AWAT |
| 2490 | 7987 | A | 2697 | 2 | 251 | FFLKPCLOTVATSGGCNFWPQAI FL SWPPNSISYRTQPTIFFQYNINILQAL A*FTLFACNPSSLGG*G*WIMWPRS RHCTPV |
| 2491 | 7988 | A | 2698 | 1278 | 1515 | SMVIRIMKVNHPMGLLTKRAKRS LNEMLNVDGKSGGYILGAVAHTCN PSALGGRGGWIT*GQEFKTSLSNME KPLLY |
| 2492 | 7989 | A | 2699 | 139 | 260 | |
| 2493 | 7990 | A | 2700 | 268 | 388 | |
| 2494 | 7991 | A | 2701 | 233 | 400 | HFLRAKVSVTQARVQWLDNGSLQP PTSM LK*SSYLSLSKCWDYRHVPM APRHFNK |
| 2495 | 7992 | A | 2702 | 602 | 758 | IICLSVI*NPRYTLGTVAHTCNPSTFG G*GTWNS*GQKFETSLTNMAKL CF Y |
| 2496 | 7993 | A | 2703 | 379 | 1160 | LVDMLQLWPPVFHENKCCLGPPPQT TH*RPAPAVPTPQAGPGTQGLATAS SVSMLCSDKLFPSDQPRV*PGDAE LSVLGVGRSSRKESPDDQAPPLPVIC ELSFARVGGAPGEPLQRPV VLS*TP GTLWSKEIA*LQAVLGQY*HEGCAT IMPADP*GRPGPENSGSVTAQGQPL PGRP*NRTHLFFVPHPGQAASQSQS SSSPP*QSERRA*IVSPNSGQRYFFPE TEARRQ*GEPRGEGGGDLPQPFQPV LLAALVHI |
| 2497 | 7994 | A | 2704 | 178 | 412 | LLHSSLGHVARLPTLQNMKTLARD GSVCFQSHLLGRLRQEDHGCSKP*L HHCTPAWVTEQDPILLKTEIGIPVCS FKR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2498 | 7995 | A | 2705 | 67 | 398 | ISLTLGRHHGKINVYFLYLKMQG*Y FCCTFVSVVNCSDCLSGHSRRKTEG DKVRKEKQEA*AWCKTCETTLKTF PILLFTKKQAGHITPLMLPFLILHTV VTPYFNLEAD |
| 2499 | 7996 | A | 2706 | 264 | 612 | KHFSYNFFSFSFFLEGGRVLLCPSG WSLAQCSLQLLGSSNPPTLAS*VAG TTGVCQRAWLILKFFCRDRVSLCCP GWSGNS*LQMILSPRPKILGFQASA TALGPLTPFCLIV |
| 2500 | 7997 | A | 2707 | 179 | 472 | |
| 2501 | 7998 | A | 2708 | 498 | 849 | GSLLSRAPIPYPLNWVSFFIPEVRTPP DIHTIGSEFPRFLKYLKPTREKILVPA LSPPVQPGPSVPFPLPLSQDSSGQAK APWPSSLMH*PGALPLRTTSTQKCD SPSEQTSDASG |
| 2502 | 7999 | A | 2709 | 768 | 1073 | GVETGFDLIAFEDLHAVPRDSGISLF LQATSAPPPPGTARPHQESPLASHK* QARQAPEPLGYA*ARQAQRMEATK ARPRPKSSGARVGREPTCSKPAPRR |
| 2503 | 8000 | A | 2710 | 5451 | 5678 | |
| 2504 | 8001 | A | 2711 | 396 | 687 | TFCPRCGCPSGLAMRLFLSLPVLVV VLSIVLEGPAPA*GAPEVSNPFDGLE ELGKTLEDYTREFINRITQSELPAM WDWFSETFRKVKEKLKTD |
| 2505 | 8002 | A | 2712 | 1 | 93 | LPKRWNSCHEPLVPLFSPLLVNAV GVLGSK*GKKIKDNEIGEEIKLSLFA YEMILFVLL*NPYS*PKNFTVKLL YQSLRK*SDTRLKSTIYLYTSNKLK LRELYSE*PKRWNSCHEPLVPLFSPL LVNAVLGVLGSK |
| 2506 | 8003 | A | 2713 | 376 | 469 | NQLPGERWLTPIPTLWEARA*GL FEPRSL |
| 2507 | 8004 | A | 2714 | 715 | 1050 | |
| 2508 | 8005 | A | 2715 | 404 | 559 | VNIFHFKTFYLGPGAVAHTCNPSTL GG*GGQIT*GQEFKTSANMMEPHL Y |
| 2509 | 8006 | A | 2716 | 3 | 180 | FFFIGVLTLLPRLECSGAITAHCSLD LLGPGVYTT*TLQVLGITGVCHHGQ LIYFYFL |
| 2510 | 8007 | A | 2717 | 1825 | 1958 | LWTISVFWKAGVPLPC*QSPRWTKS ECLSFTPMFLNKS NFKKRI |
| 2511 | 8008 | C | 2718 | 23 | 349 | MPGRGSTAQRGFSKRYSRSGARSL CSLFLFLAKSLSRAMTSFSNISGAGL ASKKNAVFQHSPLSALIEQAGSFGF YGFISLLPWRQRDFNHVLLGICWA VTSVEASE* |
| 2512 | 8009 | A | 2719 | 41 | 298 | ASKVICQQRWHAGFAWLLSLEASL PREGTAGEAVVLAHCLSPSVLKEKR QPAVRAVRKASRPP*ILQRHSRQNE GHRQEWCGHTA |
| 2513 | 8010 | A | 2720 | 277 | 651 | KPSRARLLYESKKEGEMLENCQFFL CLFAKEHLQAH*QKSS*TSMDRLIN EPSNDWDIYYWGHRS*TSPRNIWK MKSWALLERLCLKTKTKRQRLRGP SFWSTSLEKPRWSCAPRPGHGG SVC GW |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2514 | 8011 | A | 2721 | 76 | 185 | VWQCLPLYPLPNTLRAVAFRFLAIG YAFPLSCLCALWIFPQNLTSLVTDY *FGWSK*DPQ*FVICLCVCVCVCVC VCVISKLCSSSTDSSR |
| 2515 | 8012 | A | 2722 | 1685 | 2124 | |
| 2516 | 8013 | C | 2723 | 299 | 577 | MFCFDQSSLGSIVLESWITVKPLTLI SSTLMRRDDNFICCHAGRLFLTTP YRWHTLSGVALFPGPCCGIFFCHSG FQCGRLLPYRVHAPQG* |
| 2517 | 8014 | A | 2724 | 14 | 213 | VDMGSHRVSQDGLELMTP*SARLS LPKCWDYRRDTPRLALLVLLNLPV PLGASHVGHCLLSYFCS |
| 2518 | 8015 | A | 2725 | 1169 | 1404 | SFLYFNGLMNFPRPGQAFEDSHEFKY KY*K*ARL*IAHTCNPSILENQGGQI P*AQVFETSLDHTPRPCIYPPKKKKK K |
| 2519 | 8016 | A | 2726 | 44 | 417 | CGCGLGEICLSHGVAQHNRGSNCQ KALFNAEPKCASSSSSGKGG/TILVP PAGGKGPNI*WNP GPPGARGFPGL TPPRGGKKGRAQPPENLVF*EKTG FPIVQRGGLKPPPGPPKGGE*RGPP |
| 2520 | 8017 | A | 2727 | 624 | 1023 | CWLWSRGILPAPWSCAAQPWLQLP EGSF*C*TKMCSSSSSPKREFPFGPP AGRQGPQSNKREPPAPRVKGIPPPPP PKTGEKEDGPTTPINLGFPSSSRVPP VTGGGYKPPRPPKGGEKTGGTPGT HHRAL |
| 2521 | 8018 | A | 2728 | 36 | 211 | KTKNISQL*WHTPIVAATWEARAR GSPEPRSLRPAVSLQTAPTALQPSRL EMFVRRYP |
| 2522 | 8019 | A | 2729 | 640 | 898 | VLLTCLVCLVSSKTKPNITKQHTKI KFPQSSRARWLTPVIPKFWEA*AGG SPEVRSLRPAAGLEFLVSHLGPRKC WDYRHKPPCLA |
| 2523 | 8020 | A | 2730 | 707 | 1164 | SCIFLNQVFNKNLYFLFFKIKNNLYF LCCMRILICAYNG*RFYLCGMK*GL *SWF*CFSLSLFTAVKFIKCFSVVF CSLSFTGYFFMYTFRIFCLLYPVVQ MISYILQMPFQFLFSFSIKLPSCPNVQ FVSVCVCVCVCVNLIK SARLPI |
| 2524 | 8021 | C | 2731 | 270 | 371 | MQNLQCFRAFELLTHNSASELPLSA PVTYTEDD* |
| 2525 | 8022 | A | 2732 | 2553 | 2764 | GIGPGWGIRPKRTRPRQVNSNVLKA QEWQAEYPGIFQRPYPSYEQSFPP* TPPNPIKTSFPPRNCNSP |
| 2526 | 8023 | C | 2733 | 25 | 288 | MSKVQTWGRQKTSHTRLSLHTWK VAQRPGRGAPHLPDGVAARQRCSS LSTRVCCHHVSPQPNLGWAASVG DHSQLACSHGPLQSPS* |
| 2527 | 8024 | A | 2734 | 1043 | 1207 | NMMTHTLKKVGTGGRARWAHTC NASTLGG*GWWIT*GQEFETSLAN MVKLHLY |
| 2528 | 8025 | A | 2735 | 74 | 233 | MVTFNCFLNH*TVTKGFTRLIV |
| 2529 | 8026 | A | 2736 | 11 | 151 | ICHDAVDRPR/CCRSAMTPWIDRDL PGRPTRPEPAVQRMISYDDKNRMG SDDVCIFLILE |
| 2530 | 8027 | A | 2737 | 214 | 369 | QKDSPD*SCDCVLKENEISNLRCPIQ |

MISSING AT THE TIME OF PUBLICATION

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2554 | 8051 | A | 2767 | 108 | 279 | |
| 2555 | 8052 | A | 2768 | 3 | 314 | LLALVKEGPVPLFLLMKEREGVSSV RSLDTHGILSSTPPVHLPKTG/TEAS GSSWGPADPQDAEKSCRIPTSPTLGG GVPACVRCACVLLCCHGALSRLAA SLFFL |
| 2556 | 8053 | A | 2769 | 1 | 465 | |
| 2557 | 8054 | A | 2770 | 192 | 400 | |
| 2558 | 8055 | A | 2771 | 1414 | 1597 | SGVYKRCKGGGRFVFLECATSGLSL ISSGLSWG/RLWGHGGCRLAGGWG GGGGSGGGMALL |
| 2559 | 8056 | A | 2772 | 673 | 988 | |
| 2560 | 8057 | A | 2773 | 749 | 1169 | |
| 2561 | 8058 | A | 2774 | 2 | 290 | |
| 2562 | 8059 | A | 2775 | 3 | 520 | HERRVVAWAGRGFVCCARSSRSRV IFCSAPAGMAHKQI*YSDKYFEEH YEYRFVMLPRELSKQVPKTHLMSE EEWRRRLGVQK/SLGWVHY\MIHE PEPHILLFR\RLPKSSTKMKFISGIV KSCFKFNVYVYKVVVFQWNTWRN GYKSFHPYLCMSCILHSNRARVKC NCK |
| 2563 | 8060 | A | 2776 | 1134 | 1312 | |
| 2564 | 8061 | C | 2777 | 49 | 282 | MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAARRPDPQTXESQDRLR CAPCTXHQPLPLDTHNRTL VHNRL NIPQKL* |
| 2565 | 8062 | A | 2778 | 1 | 306 | |
| 2566 | 8063 | C | 2779 | 54 | 212 | MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAALIFLAPMPVQSDDSGK RQTG* |
| 2567 | 8064 | A | 2780 | 34 | 308 | |
| 2568 | 8065 | A | 2781 | 35 | 407 | |
| 2569 | 8066 | A | 2782 | 41 | 360 | |
| 2570 | 8067 | C | 2783 | 105 | 302 | MXNLKRLQISMKPAHSGVCPVTRX SEGLGGGRLGLCIXWLQRGASQHQ HVTGMFPAEDKKTNMKV* |
| 2571 | 8068 | A | 2784 | 3007 | 3541 | KRVDYWGKSSIICTLLPHRSGLC KYYFFFLSLSFKDSFWVIFFFCLSQR WKGERAKEKTTNNKENEAFPSGYQ NAPGEEGTVRGAPGAGSALRCGWR WRPP/SRCGWRWRPPAWRLRCPRP ARRWVCKPGPPPPPLPPRRPWGP CSAGPGAGLTPSRASICSWQARRQS GSHLITLERKRVRR |
| 2572 | 8069 | A | 2785 | 272 | 801 | |
| 2573 | 8070 | A | 2786 | 659 | 842 | |
| 2574 | 8071 | A | 2787 | 156 | 203 | |
| 2575 | 8072 | A | 2788 | 441 | 785 | |
| 2576 | 8073 | A | 2789 | 2 | 28 | |
| 2577 | 8074 | A | 2790 | 5 | 1049 | LRVAVLVAFKMSTKNFRVSDGDWI CPDKKCGNVNFARRTSCNRCGREK TTEAKMMKAGGTEIGKTLAEKSRG LFSANDWQCKTCSNVNWARRSEC NMCNTPKYAKLEERTGYGGGFNER ENVEYIEREESDGEYDEFGRKKKKY RGKAVGPASILKEVEDKESEGEED |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | EDEDLSKYKLDEDEDEDDADLSKY NLDASEEEDSNKKKSNRRSRSKSRS SHSRSSSRSSSPSSSRSRSRSRSS SSQSRSSSRERSRSGSKSRSSRS VTGALLPHEKDLIQVHLLLRGTERE VVDLLHLVIAKKDEQDHGHPKDA TGHHLDPILVPVQVQKRNNVLKF TS |
| 2578 | 8075 | A | 2791 | 971 | 1106 | |
| 2579 | 8076 | C | 2792 | 291 | 444 | MGCFFPNSWVRAGVLIPVPVICLSV RLTWGREAQROGWVCRCSQNWVI FAP* |
| 2580 | 8077 | A | 2793 | 1 | 672 | |
| 2581 | 8078 | A | 2794 | 1 | 691 | MDFLLSWVHWSLALLLYLHHAKW SQAAPMAEGGGQNHHEVVKFMDV YQRSYCHPIETLVDIFQEYPDEIEYIF KPSCVPLMRCGGCCNDEGLECVPT EESNITMQIMRIKPHQGQHIGEMSFL QHMKCECRPKKDRARQENGSAQA KRDNVRSRQLPTSSRP*SRRWRSW STSRPAPVTPRASPLRATSSRPSSRT SASRSREASRPWWATTSWARSR AAAARTCC |
| 2582 | 8079 | A | 2795 | 312 | 394 | |
| 2583 | 8080 | A | 2796 | 490 | 2890 | PVALTDRQTDAPSPSYHLLPGRRR TVDAAASRGQGPEPAPGGGVEGVG ARGVALKLFVQLGCSRFGGAVVR AGEAEPGAARSASSGREEPQPEG EEEEKEEERGQPWRLGARKPGSW TGEAAVCADSAPAARAPQALARAS GRGGRVARRGAEESGPPHSPSRGS ASRAGPGRASETMNFLLSWVHWSL ALLLYLHHAKWSQAAPMAEGGGQ NHHEVVKFMDVYQRSYCHPIETLV DIFQEYPDEIEYIFKPSCVPLMRCGG CCNDEGLEC/VVPTEESNIPMQIMRI KPHQGQHIGEMSFLQPNKCECRPK KDRARQEKKSVRGKGKGQKRKRK KSRYKSWSVPCGPCSERRKHLFVQ DPQTCKCCKNTDSRCKARQLELN ERTCRCDGSALAQRDNVLFQAAT DEQPAVIKTLEKLVNIETGTGDAEGI AAAGNFLEAELKNLGFTVTRSKSA GLVVGDNIVGKIKGRGGKNLLMS HMDTVYLGILAKAPFRVEGDKAY GPGIADDKGGNAVILHTLKLKEYG VRDYGTITVLFNTDEEKGSFGSRDLI QEEAKLADYVLSFEPTSAGDEKLSL GTSGIAYVQVQITGKASHAGAAPEL GVNALVEASDLVLRMTNIDDKAKN LRFQWTIAKAGQVSNIIPASATLNA DVR YARNEDFDAAMKTLEERAQQ KKLPEADV KVVIVTRGRPAFNAGEG GKKLVDKAVAYYKEAGGTLGVEE RTGGGTDAAYAALSGKPVIESLGLP GFGYHSDKA EYVDISAIPRRL YMAA RLIMDLGAGKEFH HHHHHAS |
| 2584 | 8081 | A | 2797 | 326 | 1280 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2585 | 8082 | A | 2798 | 356 | 518 | |
| 2586 | 8083 | A | 2799 | 27 | 225 | |
| 2587 | 8084 | A | 2800 | 470 | 754 | |
| 2588 | 8085 | A | 2801 | 707 | 907 | |
| 2589 | 8086 | A | 2802 | 2 | 502 | VLSPEEDKATITSLWAKVNVEANAG RKKPLGKAPLVVLPPWTPRGFLWN SFGKTLASALLAPSMGKTPQKSK ATLAKKGA*TSLGEDAVKAPLDDSP RATFCPSLSELHCDKLHVDPENFK A/LLGNVLVTVLAHFGKEFTPEVQ ASWQKMVTGVA\SALA\SRYP |
| 2590 | 8087 | A | 2803 | 921 | 1146 | |
| 2591 | 8088 | A | 2804 | 1170 | 1482 | |
| 2592 | 8089 | A | 2805 | 1492 | 1853 | |
| 2593 | 8090 | A | 2806 | 909 | 1180 | |
| 2594 | 8091 | A | 2807 | 105 | 248 | CTCSRVSHPNAPRNSLVSMVFRMHH PPPLDTFRQ/PQPSFNL*YP*PNYP |
| 2595 | 8092 | A | 2808 | 662 | 843 | |
| 2596 | 8093 | A | 2809 | 263 | 408 | |
| 2597 | 8094 | A | 2810 | 701 | 950 | |
| 2598 | 8095 | A | 2812 | 1426 | 1525 | |
| 2599 | 8096 | A | 2813 | 1 | 1416 | |
| 2600 | 8097 | A | 2814 | 108 | 520 | |
| 2601 | 8098 | A | 2815 | 3 | 201 | GRGLRSPDVTQQRGRSPSAAER *PTRPGVLRALPAPA*GKHCPWPRP GARRPPSSPAARPCP |
| 2602 | 8099 | A | 2816 | 318 | 428 | |
| 2603 | 8100 | A | 2817 | 448 | 647 | |
| 2604 | 8101 | A | 2818 | 42 | 191 | |
| 2605 | 8102 | A | 2819 | 3 | 452 | |
| 2606 | 8103 | A | 2820 | 25 | 519 | EFHRLRENPPMVAVSCPTKTNVKA\ AWG\KVGAAHVRSMCAEALERMF LSFPT\TKTYFPFHD\SHGFAQV*G ATGKKVADALTNAVAHVDDMPN\ ALSALSDLHAHKLRVDPVNF\KLLS HCLLG*PWAHLPRPSSTPGGCTPS LGTNFLGFLKLRCLNLPNNL |
| 2607 | 8104 | A | 2821 | 270 | 453 | |
| 2608 | 8105 | A | 2822 | 115 | 427 | |
| 2609 | 8106 | A | 2823 | 1 | 1656 | |
| 2610 | 8107 | A | 2824 | 1 | 1188 | |
| 2611 | 8108 | A | 2825 | 1091 | 1764 | SIAYQPKRVQDQTDSPILPELISNF SKVSGYKIN/AKKSQAFLYTNNRQT ESQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTKKWK NIPCSWVGRINIVKMAILPKVIYRFN APIKLPMPPFTELEKTTLKFIWNQK RVRIAKSILSQKNKAGGVTLPDFKL YYKATVTKTAWYQNSMVLVPK QRYRSMEQNRALRNNAAYLQLSDL |
| 2612 | 8109 | A | 2826 | 1 | 1449 | |
| 2613 | 8110 | A | 2827 | 2 | 1675 | |
| 2614 | 8111 | A | 2828 | 301 | 453 | |
| 2615 | 8112 | A | 2829 | 1 | 2139 | |
| 2616 | 8113 | A | 2830 | 83 | 1257 | WQQTAVVDGGLKRLSLLNCRDGD CPSPQEPGPNSGRFQPAATDWLEFQ ARRRMKLKAILSKLTQEQKTKHH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MFSLISGS*KMRIHGHK/VGEHHSPG PVEGVSMPTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENYKPLLNE IKEDTNKWKNIPCSWVGRINIVKMA ILPKGIYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIAKSILSQKNKAG GITLPNFKLYYKATVTKTAWYWYQ NRDIDQWKRTEPSEIMPHIYNYLIFD KPEKDKQWGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVRFKTIKTLEENLGITMRDIGMG KDFMSKTPKAMATKAKIDKWDLIK LKCFC TAKETTIRVNRQPTK |
| 2617 | 8114 | A | 2831 | 1 | 1383 | |
| 2618 | 8115 | A | 2832 | 2 | 153 | |
| 2619 | 8116 | A | 2833 | 1 | 2436 | |
| 2620 | 8117 | A | 2834 | 1569 | 1835 | |
| 2621 | 8118 | A | 2835 | 933 | 2812 | |
| 2622 | 8119 | A | 2836 | 56 | 1692 | KSKSKQHSKASRRQEITKIRAELEKEI EIQKTLQKINESRSWFFERINKIDRP LARLIKKKREKNLIDAIKTDKGDITT NPTEIQTIREYYKHL YANKLENRE EMDKFLDTYTL PRLNEEEVESL NTP ITGSEIVAINSLPTKKSPGPDGFTAE LYQRYKEELVPFLKLFQSIEKEGIL PNSFYEASIIIPKPGRDTTKKENFRP ISLMNIDAKILNKILAKGIQQHIKKLI HHDQVGFIPGMQGRFNIRKSINVIQ HINRTKDKNHMIISIDAEKAFDKIQQ PFMLKTLNKL GIDGTYFKIIRAIYDK PTASII L NGQKLEAFRLKTGTRQGCP LSPLL FNIVFEILARAIROEKEIKGIQ LGKEEVKLS\LFADDMIVYVENPLP SQPQNLL*GWLSNFSK/MSSGYKIY KIDVQKS\QAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIHLTRDVKDL\F KETYPKLLNEIK\EDTNKWKNIPCS WVGRINIVK\MAILPKVNYRFNAIPI KLPMTVFTELEKNYFKVHMEPKKE PALPSQS |
| 2623 | 8120 | A | 2837 | 2 | 433 | |
| 2624 | 8121 | A | 2838 | 371 | 452 | |
| 2625 | 8122 | A | 2839 | 307 | 497 | |
| 2626 | 8123 | A | 2840 | 95 | 314 | |
| 2627 | 8124 | A | 2842 | 2 | 311 | |
| 2628 | 8125 | A | 2843 | 1 | 602 | |
| 2629 | 8126 | A | 2845 | 571 | 690 | CQQGFSFLQAYGPAQHAIS\MRKFK AKYPDYEV TWANDGY |
| 2630 | 8127 | A | 2846 | 130 | 943 | |
| 2631 | 8128 | A | 2847 | 45 | 405 | GIPGRRNMAVADLDLIPDV\IDIDSD GVFKYVLIPSPLGIPAPGIRPAESKEI VRGYKWA\GHHADIYDKSVGATCR KQGLRTVSILGGGRIS/HTKSPGQER FTVY\GYSMGLWSCPRTPIST |
| 2632 | 8129 | A | 2848 | 1340 | 1504 | |
| 2633 | 8130 | A | 2849 | 3 | 200 | GSCACAGSCKCKCKCTSCCKKSEC GAISRN LGLWLR\CCSCCPLGCAKC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AQGCICKGASEKCSCCA |
| 2634 | 8131 | B | 2850 | 1 | 384 | MWESVELPRDLLSGFAQNADSDMD NKVQVSDGDKELVGNWSKEKELPT VALHHALHVFHWLFSSRLGTPVSPR VAMEPKWSCEAGCCSCCPVGCACK AQVLRRLQRGIGEVQLLCLMWEQLF SQNCNT* |
| 2635 | 8132 | A | 2851 | 1 | 2880 | |
| 2636 | 8133 | A | 2852 | 584 | 1253 | |
| 2637 | 8134 | A | 2853 | 1 | 2736 | QSRARADQRITESRQVVELAVKEH KAEILALQQALKEQKLKAESLSDKL NDLEKKHAMLEMNARSLQQKLETE RELKQRLLEEQAQLQQQMDLQKN HIFRLTQGLQEALDRADLLKTERSD LEYQLENIQVLYSHEKVKMEGTISQ QTKLIDFLQAKMDQPAKKKKVPLQ YNELKLALEKEKARCAELEELQK TRIELRSAREEAAHRKATDHPHPST PATARQQIAMSAIVRSPEHQPSAMS LLAPPSSRRKESSTPEEFSRRLKERM HHNIPHRFNVGLNMRATKCAVCLD TVHFGRQASKCLECQVMCHPKCST CLPATCGLPAEYATHFTEAFCRDK MNSPGLQTKEPSSSLHLEGWMKVP RNNKRGQGWDRKYIVLEGSKVLI YDNEAREAGQRPVEEFELCLPDGD VSIHGA VGASELANTAKADVPIYLK MESHPTTCWPGRTL YLLAPSPFDK QRWVTALLESVVAGGRVSREKAEA DAKLLGNSLLKLEGDDRLLDMNCTL PFSDQVVLVGTEGLYALNVLKNS LTHVPGIGAVFQIYIHKDLEKLLMIA GEERALCLVDVKKVKQSLAQSHLP AQPDISPNIFEAVKGCHLFGAGKIEN GLCICAAMPSKVILRYNENLSKYC IRKEIETSEPCSCIHFTNYSILIGTNKF YEIDMKQYTLEEFLDKNDHSLAPA VFAASSNSFPVSIVQVNSAGQREEY LLCFHEFGVFVDSYGRRSRTDDLK WSRLPLAFAYREPYLFVTHFNSLEV IEIQARSSAGTPARAYLDIPNPRYL PAISSGA IYLASSYQDKLRVICCKGN LVKESGTEHHRGPSTSRSSPNKRGP PTYNEHITKRVASSPAPPEGPSHPRE PSHPTATARGGPSCAGTS PWPPPG AREVPRPDAQHAERAVPREAV |
| 2638 | 8135 | A | 2864 | 426 | 539 | |
| 2639 | 8136 | A | 2865 | 1 | 1134 | |
| 2640 | 8137 | A | 2866 | 766 | 1115 | SARQIATFFNNGIKHLAIMGGDILH VAHIFVTPFNLEGAYTSINQRAEVG SLIVIFHRQQMFFIGNHPPLIV/YSMC MANGTPASNRHGWRYAPDR*RSVR RCDGDPLHPDVRRRSG |
| 2641 | 8138 | A | 2867 | 61 | 390 | |
| 2642 | 8139 | A | 2868 | 627 | 1324 | |
| 2643 | 8140 | A | 2869 | 343 | 452 | |
| 2644 | 8141 | A | 2870 | 589 | 672 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2645 | 8142 | A | 2871 | 1 | 3000 | |
| 2646 | 8143 | A | 2872 | 2 | 191 | |
| 2647 | 8144 | A | 2873 | 251 | 505 | GSSSRLGQRTD*ATASRRHFKNKV PGEAKNCSPEDDEIFLYLKGGVAD ALLYRATHMILTVGGTICSIPYYEL AVASFPKKAGS |
| 2648 | 8145 | A | 2874 | 1780 | 1914 | |
| 2649 | 8146 | A | 2875 | 1154 | 1256 | |
| 2650 | 8147 | A | 2876 | 1 | 2629 | |
| 2651 | 8148 | A | 2877 | 334 | 468 | YEEEEEDYD*EEEESEPPLDENDL EEDVVFQPPQIEGEAVYDA |
| 2652 | 8149 | A | 2878 | 2 | 416 | |
| 2653 | 8150 | A | 2879 | 1 | 4116 | |
| 2654 | 8151 | A | 2880 | 3 | 3080 | EELEASKSFGPGNEEEKEEKEYE EEEEEDYDEEEESSEAGNQRLOQV MHAADPLEIQADVHWTHIREREE ERMAPASESSASGAPLDENDLEEDV DSEPAIEGEEAENGHPGDTGAELD DNQHWYDSPSDADRELRLPCPAEG EAELELRVSEDEEKLPASPKHQERG PSQATSPIRSPQESALLFIPVHSPSTE GPQLPPVPAATQEKSPERLFPEPLL PKEKPKADAPSDLKAVHSPIRSQPV TLPEARTPVSPGSPQPRPPVAASTPP PSPLPICSQPQPSTEATVPSTQSPIRF QPAPAKTSTPLAPLPVQSQSDTKDR LGSPLAVDEALRRSDLVEEFWMKS AEIRRSGLTPVDRSKGPEPSFPTPA FRPVSLKSYSVEKSPQDEGLHLLKP LSIPKRLGLPKPEGEPLSLPTPRSPSD RELRS AQEERRELSSSSGLGLHGSSS NMKTLGSQSFNSTSDSAMLTPSSPP PPPPGEEPATLRRKLREAPNASV VPPPLPATWMRPPREPAQPPREEVR KSFVESVEEIPFADDVEDTYDDKTE DSSLQEKFFTPPSCWPRPEKPRHPPL AKENGRLPALGTLQPKRGLPLVS AEAKELAEERMAREKSVKSQALR DAMARQLSRMQMELASGAPRPR KASSAPSQGKERRPDSPTRTLRS EEPTLKHEATSEEVLSPPSDGGPDG SFTSSEGGSSGSKKRSSLFSPRRNKK EKKSKEGGRPEKPPSNLLEAAAK PKSLWKS VFSGYKKDKKKKADDK SCPSTPFSGATVDSGKHRVLPVVR AELQLRRQLSFSESDSLSSDDVLEK SSQKSRREPRTYTEELNAKLTRRV QKAARRQAKQEELKRLHRAQIIQR QLQQVEERQRRLEERGVAVEKALR GEAGMGKKDDPKLMQEWFKLVQE KNAMVRYEELMIFARELELEDQRS RLQQELRERMAVEDHLKTEEELSEE KQILNEMLEVVEQRDSLVALLEEQR LREREEDKDLEAAML SKGFSLNWS |
| 2655 | 8152 | A | 2881 | 1 | 4132 | |
| 2656 | 8153 | A | 2885 | 1898 | 2056 | |
| 2657 | 8154 | A | 2886 | 1 | 233 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2658 | 8155 | A | 2887 | 1092 | 1339 | |
| 2659 | 8156 | A | 2888 | 363 | 512 | EPLEGLLCLEGKGVEIVTILQAETPG EPLPP*KPHS*PGLCLR YRGHTL |
| 2660 | 8157 | A | 2889 | 1 | 136 | |
| 2661 | 8158 | C | 2890 | 12 | 236 | MTPGGLFLPYHSLPQPDFLASCPT HLSTPFLVADNELRLPKGQICPLHV FVLANRVVLKLCANSVWEHSGIT * |
| 2662 | 8159 | A | 2891 | 1548 | 1849 | |
| 2663 | 8160 | A | 2893 | 1 | 1441 | |
| 2664 | 8161 | A | 2894 | 954 | 1194 | |
| 2665 | 8162 | A | 2895 | 2039 | 2207 | |
| 2666 | 8163 | A | 2896 | 680 | 757 | |
| 2667 | 8164 | A | 2897 | 361 | 476 | |
| 2668 | 8165 | A | 2898 | 226 | 293 | |
| 2669 | 8166 | A | 2905 | 265 | 396 | |
| 2670 | 8167 | A | 2906 | 250 | 447 | |
| 2671 | 8168 | A | 2907 | 632 | 1038 | |
| 2672 | 8169 | A | 2908 | 3 | 363 | VKDDPNDHEQGKRGHKPFLRELPR ATIFFLINL*VIAEVEVQDSCIDQAES EMLLRSGAPDPGVPL*GCFALVIT HTHSSRAAMAFVPTGKKASCYSQE PS*WQNSPNDTQDHSNDLSE |
| 2673 | 8170 | A | 2909 | 57 | 448 | |
| 2674 | 8171 | A | 2910 | 62 | 371 | |
| 2675 | 8172 | A | 2911 | 398 | 789 | VTGAPLMLPVLPKPGMPLAALVTG LSGLLWPCCAELVGTEFKLPALVHL PHCFFASLLESPVSPRLAMEPNCSC AAGVSCTCAGSCKCKECKCTSCCK SECCSCCPVGC\SKCAQG\CVCKG ASEKCSCCD |
| 2676 | 8173 | A | 2912 | 577 | 896 | |
| 2677 | 8174 | A | 2913 | 2 | 184 | |
| 2678 | 8175 | A | 2914 | 1 | 459 | SSNTMNGWFWIDKCSLWLSQSLPY TRATQVTIKIPNPATGV/SSGFVD*F WIDKCSLWLSQSLPYTRATQVTIKIP PNPATGVRRALWIDSDLRCAPLGLS TGGGKSRIKLGLGVPKFRGSDRNR VLIGAFYNPLAGYRALIGAFYNPLP PHLLQLLLSVLLQPLLCCGKCKL KAPEGEETEFYVSPKAAV |
| 2679 | 8176 | A | 2915 | 440 | 620 | |
| 2680 | 8177 | A | 2916 | 2 | 987 | FGLRWPRGAVRRWQLWEEAAWK AEGAQARTNPHVSWAATVTRCSVP GKRNPAGWAAEPESGTWSPPGAE IRMFRFMRDVEPEDPMFL\MDPFAI HRQH\MSRMF\SGGF\WILAPFLSITD WQHCQGTRP\ASRR\MQQAGSCSPL FG\MCLGIFGWFSWDMFWGLME*H DLGNMEHMTAGGNCQTFSSSTVIS YSNTGDGAPKVYQETSEMRSAPGG IRETRRTVRDSDSGLEQMSIGHIRD RAHILQRSRNHRTGDQEERQDYINL DESEAAAFDDEWRRETSRFRQORP LEFRRLSSGAGGRRAEGPPRLAIQ GPEDSPSRQSRRYDW |
| 2681 | 8178 | A | 2917 | 121 | 329 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2682 | 8179 | A | 2918 | 323 | 457 | |
| 2683 | 8180 | A | 2919 | 1 | 243 | |
| 2684 | 8181 | A | 2920 | 147 | 321 | |
| 2685 | 8182 | A | 2921 | 1 | 2310 | |
| 2686 | 8183 | A | 2922 | 319 | 773 | |
| 2687 | 8184 | A | 2923 | 85 | 369 | |
| 2688 | 8185 | A | 2924 | 1 | 681 | |
| 2689 | 8186 | A | 2925 | 1556 | 1953 | HGVAAASLPSSAGRLSRARGPGSEE PAAAPAPRWQHPRGPGGPVSRR RRPPHGGTPTGTVRRGGGGDPAAPG SGCPSPAVVPPRPCPGAPLRRATLPP ACCGSLACSPLTL*PAPS/TPPL*ADD SCSVGLPT |
| 2690 | 8187 | A | 2926 | 322 | 376 | |
| 2691 | 8188 | A | 2927 | 365 | 666 | |
| 2692 | 8189 | A | 2928 | 310 | 448 | |
| 2693 | 8190 | A | 2929 | 908 | 1189 | |
| 2694 | 8191 | A | 2930 | 761 | 913 | |
| 2695 | 8192 | A | 2931 | 1188 | 1373 | EPHLKKKKKISRWWCIPVVPVTW KAEVGGSLPRRWRLQ*AEITPAHS SLGNGLTLLKKKK |
| 2696 | 8193 | A | 2932 | 240 | 475 | |
| 2697 | 8194 | A | 2933 | 1212 | 1424 | |
| 2698 | 8195 | A | 2934 | 403 | 539 | |
| 2699 | 8196 | A | 2935 | 436 | 594 | |
| 2700 | 8197 | A | 2936 | 1 | 570 | |
| 2701 | 8198 | A | 2937 | 1086 | 1359 | |
| 2702 | 8199 | A | 2939 | 40 | 361 | |
| 2703 | 8200 | A | 2940 | 12 | 337 | |
| 2704 | 8201 | A | 2941 | 232 | 339 | |
| 2705 | 8202 | A | 2942 | 951 | 1069 | |
| 2706 | 8203 | A | 2943 | 286 | 621 | |
| 2707 | 8204 | A | 2944 | 299 | 513 | HKCYFTLAHVHLIISFCAATLE*A*P SWGTCNSTPNFVNTTPTLTLAYYLGL WRSLRPFSDSVSFSFCSGIL |
| 2708 | 8205 | A | 2945 | 97 | 258 | |
| 2709 | 8206 | A | 2946 | 5 | 464 | |
| 2710 | 8207 | A | 2947 | 1 | 522 | |
| 2711 | 8208 | A | 2948 | 76 | 488 | |
| 2712 | 8209 | A | 2949 | 619 | 746 | |
| 2713 | 8210 | A | 2950 | 125 | 279 | |
| 2714 | 8211 | A | 2951 | 1300 | 1410 | |
| 2715 | 8212 | A | 2952 | 1867 | 1947 | |
| 2716 | 8213 | A | 2953 | 2 | 52 | |
| 2717 | 8214 | A | 2954 | 352 | 538 | |
| 2718 | 8215 | A | 2955 | 3 | 313 | QFEGTRICPAACFPLESGTPGFSLAS KWTPNCSCSPVGS\CACAGS\CK\CN RVANRTVLTQTSCCSC\CPVGCAVA LPRGCICKGTS\DKCRSRCLDARDSC ALQM |
| 2719 | 8216 | A | 2956 | 1172 | 1914 | HFSAQPWASPCS/SLLLLGLEGGIV GSLPEVLQAPVGSSILVQCHYRLQD VKAQKVWCRFLPEGCQPLVSSAVD RRAPAGRRTFLTDLGGGLLQVEMV TLQEEDAGEYGCMVDGARGPQILH RVSLNILPPGAVEDDVQAGRWRVA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SRDDVACGSEEEEETHKIGSLAENA FSDPAGSANPLEPSQDEKSIPLIWGA VLLVGLLVAAVVLFAVMAKRKQV TIQLLQGNPTALAKSKEELSMPKS YQY |
| 2720 | 8217 | A | 2957 | 3 | 632 | |
| 2721 | 8218 | A | 2958 | 3 | 728 | |
| 2722 | 8219 | A | 2959 | 194 | 451 | |
| 2723 | 8220 | A | 2960 | 2 | 484 | NVLTSHQTQPNQRGKAATVTPALWR LTDVRLVTKYKIHFERNVGSFENSM KGNSIYF*GPGHDP LLNMNIVY*KS LTNNHMHKIT*ESL TEVLFSQGIFS VTNPHPEIFLVARIEKVLQGNITHCA EPYIKNSDPVKTAQKVHRTAKQVC SRLGQYRMPFA |
| 2724 | 8221 | B | 2961 | 65 | 391 | MAEVRKFTKRLSKPGTAAELRQSV SEAVRGSVVLEKAKVVEPLDYENVI AQRKTQIYSDPLRDLLMFPMEDISIS VIGRQRRTVQSTVPEDA EKRAQSLF VKECIKTY* |
| 2725 | 8222 | A | 2962 | 1 | 2148 | |
| 2726 | 8223 | A | 2963 | 816 | 1014 | |
| 2727 | 8224 | A | 2964 | 2 | 358 | |
| 2728 | 8225 | A | 2965 | 84 | 176 | |
| 2729 | 8226 | A | 2966 | 137 | 426 | QACIMREYKLVVLGSGGVGKSALT VQFVQGIFVEKYDPTIEDS\YRKQV EVDAQQCMLEILGYLPGTEQFTSNE GFIHEKWTRICISLFHHSTVHI |
| 2730 | 8227 | A | 2967 | 449 | 602 | |
| 2731 | 8228 | A | 2968 | 203 | 535 | |
| 2732 | 8229 | A | 2969 | 2 | 446 | |
| 2733 | 8230 | A | 2970 | 3 | 240 | |
| 2734 | 8231 | A | 2971 | 914 | 1291 | |
| 2735 | 8232 | A | 2972 | 188 | 266 | |
| 2736 | 8233 | A | 2973 | 191 | 306 | |
| 2737 | 8234 | A | 2978 | 1 | 440 | |
| 2738 | 8235 | A | 2979 | 3 | 670 | TSRGRVGTQAGEPRDLRPPPCPSSPL RVAVV\CLEQPERGAWEAHNIPQP NGDSAVRSFGVTGTHVKLP GPAPD\ NPNVYDFKTTYDQMYNDLLRKDK \ELFTQNGILHIAGRNKRIKP\GPERF QNCKDLFDLILTCEERVYDRVGWK I*ISR\EQGDLPSVHVVNLDIQDNH EEATLG/ARFLICE\VCQCIQHT EYM HNEIDELLQEFEEKSGRTFLHTVCF Y |
| 2739 | 8236 | A | 2987 | 367 | 492 | |
| 2740 | 8237 | A | 2988 | 49 | 332 | |
| 2741 | 8238 | A | 2989 | 582 | 923 | |
| 2742 | 8239 | A | 2990 | 523 | 668 | |
| 2743 | 8240 | A | 2991 | 942 | 1513 | |
| 2744 | 8241 | A | 2992 | 176 | 362 | |
| 2745 | 8242 | A | 2993 | 4937 | 5137 | |
| 2746 | 8243 | A | 2994 | 651 | 836 | |
| 2747 | 8244 | A | 2995 | 1686 | 1883 | |
| 2748 | 8245 | A | 2996 | 415 | 635 | |
| 2749 | 8246 | A | 2997 | 2 | 308 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2750 | 8247 | A | 2998 | 57 | 598 | |
| 2751 | 8248 | A | 2999 | 802 | 923 | |
| 2752 | 8249 | A | 3002 | 119 | 297 | |
| 2753 | 8250 | A | 3003 | 950 | 1314 | |
| 2754 | 8251 | A | 3004 | 1 | 579 | |
| 2755 | 8252 | A | 3005 | 27 | 483 | RDAEDAIYGRNGYDYGQCRLRVEF PRTYGGRRGGWPRGGRNGPPTRRS FRVLVS/GWQ/DLKDHMREAGDVC YADVQKDGVMVEYLKEDMEYA LRKLDDTKFRSHEGETSYIRVYPER STSYGYSRSRSGSRGRDSPYQSRGS PHYFSPFRPY |
| 2756 | 8253 | C | 3006 | 34 | 171 | MPKSFRVIAERSMHSWYVCFLICFIL HISITLHSLVMVFVTWREY* |
| 2757 | 8254 | A | 3007 | 1688 | 1871 | |
| 2758 | 8255 | A | 3008 | 1 | 688 | MSGWADERGGEGDGRIYVGNLPTD VREKDLEDLFYKYGRIREIELKNRH GLVPFAFVRFEDPRDAEDAIYGRNG YDYGQCRLRVEFPRTYGGRRGGWPR GGRNGPPTRRSDFRVLVSGPSPASG SWQDLKDHMREAGDVCYADVHK DGVGMVEYLKEDMEYALRKL *PPKFRSHEGETSLHRRFIPERSNQL MATSPVSGLGSRGRLSIPKARGSP HYFSSFPGPT |
| 2759 | 8256 | A | 3009 | 428 | 579 | |
| 2760 | 8257 | A | 3010 | 1924 | 2043 | |
| 2761 | 8258 | A | 3011 | 131 | 395 | |
| 2762 | 8259 | A | 3012 | 910 | 1173 | |
| 2763 | 8260 | A | 3013 | 1295 | 1489 | |
| 2764 | 8261 | A | 3014 | 1477 | 1604 | |
| 2765 | 8262 | A | 3015 | 443 | 805 | |
| 2766 | 8263 | A | 3016 | 1 | 2109 | |
| 2767 | 8264 | A | 3017 | 1297 | 1408 | |
| 2768 | 8265 | A | 3018 | 3 | 314 | |
| 2769 | 8266 | A | 3019 | 5 | 340 | GSGTSAKAFRSIWGPLPPVHRHGSP RSSVQR/DGPGLGTGEPRVYIRNKV ANTGVPGAPGPSIGGVTA PATDYCH RIAPILAARRRRRRRRRRRRRRRG GGGGVAGGGGGGG |
| 2770 | 8267 | A | 3020 | 1 | 1973 | DGGARARGRAAARRRRRPRRRRRR RRRRRRRRRRRRRRRRRLGLERP QPTSRGRAPGASRAEEKMEELVVE VRGSNGAFYKAFVKDVHEDSITVA FENNWQPDRQIPFHDVRFPPVGYN KDINESDEVEVYSRANEKEPCCWW LAKVRMIKGEFYVIEYAACDATYN EIVTIERLRVNPKNPATKDTFHKIK LDVPEDLRQMCAKEAAHKDFKKA VGAFSVTYDPENYQLVILSINEVTS KRAHMLIDMHFRSLRTKLSLIMRNE EASKQLESSRQLASRFHEQFVREDL MGLAIGHTGANIQQARKVPGVTAI DLDEDTCTFHYYGEDQDAVKKARS FLEFAEDVIQVPRNLVVIGKNGKLI QEIVDKSGVVRVRIEAENEKNVPQE EEIMPPNSLPSNNSRVGPNAPEEKK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HLDIKENSTHFSQPNSTKVQRGMVP FVFGTKDSIANATVLLDYHLNYL KEVDQLRLERLQIDEQLRQIGASSR PPNRTDKEKSYVTDDGQGMGRGS RPYRNRGHGRRGPGYTSGTNSEAS NASETESDHRDELSDWSLAPTEEER ESFLRRGDGRRRGGGGKG\QGGRG RGGGFKGNDDHSRTDNRPRNPREA KGRTTDGSLQNTSSEGSRLRTGKDR NQKKEKPDSDVGQQPLVNGVP |
| 2771 | 8268 | A | 3021 | 1 | 2116 | |
| 2772 | 8269 | A | 3022 | 656 | 883 | |
| 2773 | 8270 | A | 3023 | 303 | 589 | |
| 2774 | 8271 | A | 3024 | 2 | 478 | MAGKQAVSASGKWL MGIRKWYY NAAEFNKLGLMRDDTIYEDEDVKE AIRRLPENLYNDRMFRIKRALDLNL KHQILPKEQWTKYE/EGLCCSSSAL CFLLR*KDQPIECPSRSQEELL*SKLS PL*TAFET*AKENFYLEPYLKAEVIRE RKERE EWAKK |
| 2775 | 8272 | A | 3025 | 323 | 400 | |
| 2776 | 8273 | A | 3026 | 2 | 396 | RPPTTTKFAAARQMAGKQAV*STQ AKGLNG/IFKKWYYNAARIQNKLGL LMRDDTIYEDEDVKRSP*EDFPEN LYNDRMFRH*EGHWTLNLKHQILP KEQWTNFEEKNFY\LEPYLKE/VLF RERKERE EWAKK |
| 2777 | 8274 | C | 3027 | 144 | 341 | MYHSLEKFSSCFKHIPDNFLKMTKI KQNIYRDHFLNFLSFQGXQHKKNK TGQHFTSKCTEPFLQD* |
| 2778 | 8275 | A | 3028 | 1070 | 1335 | |
| 2779 | 8276 | A | 3029 | 2 | 303 | |
| 2780 | 8277 | A | 3030 | 149 | 244 | |
| 2781 | 8278 | A | 3031 | 1642 | 1797 | |
| 2782 | 8279 | A | 3032 | 1115 | 1320 | |
| 2783 | 8280 | A | 3033 | 1240 | 1408 | |
| 2784 | 8281 | A | 3034 | 539 | 669 | |
| 2785 | 8282 | A | 3035 | 1155 | 1579 | |
| 2786 | 8283 | A | 3036 | 437 | 666 | |
| 2787 | 8284 | A | 3037 | 51 | 279 | IKGRWEPPPLASFFLTSQGHCS DGP GP*GWGEAVSPRGRNTLSSSSWHW VPYSELRGRGVACRKEVYKIVQNT QH |
| 2788 | 8285 | A | 3038 | 3 | 300 | |
| 2789 | 8286 | A | 3039 | 451 | 760 | |
| 2790 | 8287 | A | 3040 | 183 | 410 | |
| 2791 | 8288 | A | 3041 | 602 | 1145 | |
| 2792 | 8289 | A | 3042 | 2 | 496 | |
| 2793 | 8290 | A | 3043 | 710 | 896 | |
| 2794 | 8291 | A | 3044 | 143 | 601 | |
| 2795 | 8292 | A | 3046 | 120 | 280 | |
| 2796 | 8293 | A | 3047 | 2 | 424 | |
| 2797 | 8294 | A | 3048 | 3 | 452 | |
| 2798 | 8295 | B | 3049 | 240 | 420 | XLKGHGQRKVAERADPKPLPQRGR TCPKRRCPLSDPARCTSFRVDPVN FQASLSHCLAW* |
| 2799 | 8296 | A | 3050 | 310 | 401 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; †=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2800 | 8297 | A | 3051 | 544 | 700 | |
| 2801 | 8298 | A | 3052 | 1 | 568 | |
| 2802 | 8299 | A | 3053 | 686 | 787 | |
| 2803 | 8300 | A | 3054 | 8 | 182 | |
| 2804 | 8301 | A | 3055 | 227 | 547 | |
| 2805 | 8302 | A | 3056 | 1 | 523 | ESLRKQLGQEPFFDMHMMVSKPE QWVKPMAVAGANQYTFHLEATEN PGALIKDIRENGMKVGLAIKPGTSV EYLAPWANQIDMALVMTVEPGFGG QKFMEDMMPKVHWLRTQFPSLDI* VDGGVGPDTVHKCAEAGANMIVS GSAIMRSEDPRSVINLLRNVCSSCS RNRSP |
| 2806 | 8303 | A | 3057 | 919 | 1100 | |
| 2807 | 8304 | A | 3059 | 429 | 780 | |
| 2808 | 8305 | A | 3061 | 567 | 682 | |
| 2809 | 8306 | A | 3062 | 148 | 372 | |
| 2810 | 8307 | A | 3063 | 113 | 303 | |
| 2811 | 8308 | A | 3064 | 367 | 449 | |
| 2812 | 8309 | A | 3065 | 48 | 369 | |
| 2813 | 8310 | A | 3066 | 979 | 1254 | |
| 2814 | 8311 | A | 3067 | 173 | 776 | |
| 2815 | 8312 | A | 3068 | 1 | 111 | |
| 2816 | 8313 | A | 3069 | 33 | 494 | |
| 2817 | 8314 | B | 3070 | 100 | 154 | MVHLTPVERVCRCYCPVGQX* |
| 2818 | 8315 | A | 3071 | 559 | 775 | |
| 2819 | 8316 | A | 3072 | 744 | 940 | |
| 2820 | 8317 | A | 3073 | 1 | 255 | |
| 2821 | 8318 | A | 3074 | 1 | 1206 | |
| 2822 | 8319 | A | 3075 | 905 | 1823 | |
| 2823 | 8320 | A | 3076 | 36 | 689 | |
| 2824 | 8321 | C | 3077 | 215 | 325 | MSVYPLDHIQKRIARRSSLTSCMRG TIAWPTNSLTT* |
| 2825 | 8322 | A | 3078 | 1 | 831 | |
| 2826 | 8323 | A | 3079 | 97 | 236 | |
| 2827 | 8324 | A | 3080 | 409 | 602 | |
| 2828 | 8325 | A | 3081 | 818 | 1095 | |
| 2829 | 8326 | A | 3082 | 528 | 714 | |
| 2830 | 8327 | A | 3084 | 91 | 242 | |
| 2831 | 8328 | A | 3085 | 75 | 430 | VSPGLPAARLFQVAYLDSHLKCPGC QHVPMTVTFISSKEKP*PRTVPRPP WMRLGHVILFSFLIPSNLSFSPVIFFL CGPFKVVICTELQNVSRSPQTTLAT VYCNKITSYICKKKK |
| 2832 | 8329 | A | 3086 | 1000 | 1145 | |
| 2833 | 8330 | A | 3087 | 225 | 324 | |
| 2834 | 8331 | A | 3088 | 3 | 54 | IIHYSLLIIV*CWVQF |
| 2835 | 8332 | A | 3089 | 461 | 658 | |
| 2836 | 8333 | A | 3090 | 337 | 408 | GIQDRASHCTQGPPPPPS*VPQASPA AGEGPCDPPGRYPLRDSGQSVTLH AGSSATTIQEPRGA |
| 2837 | 8334 | C | 3091 | 155 | 453 | MLGALGAEELSLDSLPEGLLNFSKP GSEGGRLGLVPAAGEGPCDPPGR YPLRDSGQSVTLHAGSSATTIQEPR GAGHALASXQECQWSRDRAAQAG E* |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2838 | 8335 | C | 3092 | 121 | 393 | MALPGRLPHRKLAGGTLEAPWPGIP SGAVRRHQPOPPTTLXXWLGVKK PLRKRIEAKFLCAEGPEHIRQGSAA VPGGGGRSRNCEQCLI* |
| 2839 | 8336 | A | 3093 | 270 | 573 | |
| 2840 | 8337 | A | 3094 | 15 | 297 | |
| 2841 | 8338 | A | 3095 | 970 | 1098 | |
| 2842 | 8339 | A | 3096 | 127 | 296 | |
| 2843 | 8340 | A | 3097 | 875 | 1075 | |
| 2844 | 8341 | A | 3098 | 171 | 404 | |
| 2845 | 8342 | A | 3099 | 186 | 392 | |
| 2846 | 8343 | A | 3100 | 2 | 202 | |
| 2847 | 8344 | A | 3101 | 2 | 242 | ARGNMAAATLTSKLDSELLFRRTSTF ALTIIVGVMMFFERAFFDQADAYFT DHINNEGVRPCAIPDLGTRLRGDSGV EKL |
| 2848 | 8345 | A | 3102 | 79 | 1137 | |
| 2849 | 8346 | A | 3103 | 374 | 519 | LDSRRK**C*LESRPHE*TS/DLSSGS LLI*GIWSILFYPMFAF*KFQKEN |
| 2850 | 8347 | A | 3104 | 1 | 1214 | |
| 2851 | 8348 | A | 3105 | 105 | 379 | |
| 2852 | 8349 | A | 3106 | 260 | 421 | LLYGDCTWTSFHLQRLQLHCQVSQ PCREL*LVSSVLCFPFISEELHCVTG HF |
| 2853 | 8350 | A | 3107 | 420 | 848 | |
| 2854 | 8351 | A | 3108 | 664 | 1059 | |
| 2855 | 8352 | A | 3109 | 73 | 269 | |
| 2856 | 8353 | A | 3110 | 307 | 566 | |
| 2857 | 8354 | A | 3112 | 316 | 410 | |
| 2858 | 8355 | A | 3113 | 200 | 403 | |
| 2859 | 8356 | A | 3114 | 258 | 377 | |
| 2860 | 8357 | A | 3115 | 1767 | 1893 | |
| 2861 | 8358 | A | 3116 | 1 | 389 | |
| 2862 | 8359 | A | 3117 | 3 | 569 | RHGEERLQTRTLRAAELSARAPSHS LPAPRSAPTWQKFSSPTEVERCVES L/LAVFQKYAGKIDGYNYNSLPRPE F/L*AFMNTLAAFTKNQEGPWVSL DRMMEETGTPNSDGSARISSGISLI WIGWALAMGLAWNFLPSRAVPFPR KAGPGGDPLGPGGFQTPPPFSFPGLS VLHLPQAHPSLEAH |
| 2863 | 8360 | A | 3118 | 362 | 712 | |
| 2864 | 8361 | A | 3119 | 2 | 152 | |
| 2865 | 8362 | A | 3120 | 134 | 760 | |
| 2866 | 8363 | A | 3121 | 670 | 891 | |
| 2867 | 8364 | A | 3122 | 44 | 63 | SPSNRNTTEEGTLTNIIHNLGMYVFL HAVKGTPTFETP*PG*KARAP*PPLGN NWDYGDRTSFTGSFTTSPHLYFL ASFYTKYDPTHFILNHSFSS*VVLNS PKWPQLHGVRIFGN*KSKQQEH |
| 2868 | 8365 | A | 3123 | 88 | 207 | |
| 2869 | 8366 | A | 3124 | 2 | 191 | |
| 2870 | 8367 | A | 3125 | 145 | 865 | |
| 2871 | 8368 | A | 3126 | 69 | 118 | |
| 2872 | 8369 | A | 3127 | 1148 | 1323 | |
| 2873 | 8370 | A | 3128 | 197 | 327 | PLGKKFSCSKSLRLLGPFLQL*SLRF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RKTTY |
| 2874 | 8371 | A | 3129 | 154 | 303 | |
| 2875 | 8372 | A | 3130 | 3 | 158 | |
| 2876 | 8373 | B | 3131 | 144 | 274 | XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL* |
| 2877 | 8374 | A | 3132 | 383 | 529 | |
| 2878 | 8375 | A | 3133 | 1981 | 2132 | EKENEDQKLIHLFFFFSLGVKPTPCL KNINFFNHFASFLCASINKKWKRI |
| 2879 | 8376 | B | 3134 | 144 | 274 | XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL* |
| 2880 | 8377 | A | 3135 | 383 | 529 | |
| 2881 | 8378 | A | 3136 | 1979 | 2131 | EKENEDQKLIHLFFFFSLGVKPTPCL KNINFFNHFASFLCASINKKWKRI |
| 2882 | 8379 | A | 3137 | 296 | 592 | |
| 2883 | 8380 | A | 3139 | 224 | 700 | VLLPPTGKRYPKVYIGVFKGPRKM GSSEIPFQNPFSIFSKEGYFLCREDFP NGAQISLLEEPFQIHLKLTfMFKNTT NFIFTAELCDQCQGL*NLIHLSSSP* KKRHLT/HNQTHPHIKTDFHC*FIHY LVV*KSQSTSQHLFKSTMGKDQRQI DNNIMN |
| 2884 | 8381 | A | 3140 | 761 | 963 | |
| 2885 | 8382 | A | 3141 | 475 | 715 | |
| 2886 | 8383 | A | 3142 | 381 | 698 | |
| 2887 | 8384 | A | 3143 | 2 | 235 | YASLEPPDRPQVGASCGPGTYV*GA VPPSPAGVGREGVAGKGTGGCTCDK PLSPCSLAG\RRGSFRRPSWTSPL LCW |
| 2888 | 8385 | A | 3144 | 49 | 353 | |
| 2889 | 8386 | A | 3145 | 174 | 495 | |
| 2890 | 8387 | A | 3146 | 73 | 226 | |
| 2891 | 8388 | A | 3147 | 326 | 421 | |
| 2892 | 8389 | A | 3148 | 1306 | 1444 | |
| 2893 | 8390 | A | 3149 | 53 | 246 | |
| 2894 | 8391 | A | 3150 | 228 | 271 | |
| 2895 | 8392 | A | 3151 | 419 | 599 | |
| 2896 | 8393 | A | 3152 | 1 | 322 | |
| 2897 | 8394 | A | 3153 | 151 | 375 | |
| 2898 | 8395 | A | 3154 | 2017 | 2191 | |
| 2899 | 8396 | A | 3155 | 3 | 234 | LWSASSAQDATWADSQELSMARLP HVRKCVVVVLLLQGLSLELLDFPP L/CLGPGCPCHLAHQHPCPRPLFQ LSGR |
| 2900 | 8397 | A | 3156 | 43 | 408 | |
| 2901 | 8398 | A | 3157 | 3 | 374 | |
| 2902 | 8399 | A | 3158 | 1 | 823 | MAVVAPRTL L L L L LSGALALTQTWA GSHSMRYFSTSVSRPGSGEPRFIAV GYVDDTQFVRFDSDAASQRMEPRA PWMEQEEPEYWDRQTEISKNAQI DLESLRIALRYYNQSED/VPPPKTH MTHHPISDHEATLRCWALSFPYPAEI TLTWQRDGEDQTQDTEL VETRPAG DGTFQKWASVVVPSGQEQRYTCHV QHEGLPKPLTLRWEPSSQPTIPIVGIL AGLVLF GAVIAGAVVAAMWRRK SSDRKGGSYSQAASSDSAQGS DVSL TACKV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2903 | 8400 | A | 3159 | 1 | 1264 | MAVMAPRTL L L L L S G A L A L T Q T W A G S H S M R Y F F T S V S R P G R G E P R F I A V G Y V D D T Q F V R F D S D A A S Q R M E P R A P W I E Q E G P E Y W D Q E T R N V K A Q S Q T D R E N L R I A L P L T Y N Q S E A G S H T L Q M M Y G L G R G G S D G A L S F R G L P P V T A Y D G K D N I A L N E D L R S W T A A D M A A Q I T Q R K W E T / A A H E A E Q W R A Y L E G R C V E W \ L R R Y L E N G K E T L Q R T D P P \ K T H M T H H P I S D H E A T L R C \ W A L S F Y P A E I T L T W Q R D G E D Q T Q \ D T K L V Q T R P A G D G T F \ H K G A S C V G P L G E E Q R Y T C \ H V Q H E \ G L P K \ P S T M \ R W * P S S Q P T H P P S W G I H C L A L V L L W K L * S L E A V V A A C E C G R R K S S D R K \ G G S Y T \ Q A A K P V T S A Q G S D V S L T A C K S V R Q L P C V G L R G K S C F L P F P L V D L E E P W T L F P A K G T L H V S V F M |
| 2904 | 8401 | A | 3162 | 1 | 342 | G S R T V P S P S P S S G L A S P G S P T H R S L G P T T P P M A S A T E D P V L E R Y F K G H K A A I T S L D L S P N G K Q L A T A S W D T F L M L W N F K P H A R A Y R Y D G H K D V V T S V Q F S P Y G Y L M A A G / S R D L S V R L W I P V ** E Y S * N G K Q L A T A S W D T F L M L W N F K P H A R A Y R Y D G H K D V V T S V Q F S P Y G Y L M A A G L E T Y P |
| 2905 | 8402 | A | 3163 | 1 | 583 | D M E S R S V T Q P G V Q W C Y L G * L Q P P P P R F * R F S C L S L P G S W D Y R C V P P H P A N F F I F S R D G V S H H V G Q A G L E L L V S S D P P A S A S Q S A G I T G L S H H A R P D / Y T F L L T V F E P F H G T H V R P P V T C G T L A S N W T P T A F I S L A E N T K V L K V A L K E V P F G F D I A I S K A S G T V Q I R A M S F M K T T F L S P S F V R E C H T H D H V T L L Q S |
| 2906 | 8403 | A | 3164 | 1 | 347 | F F I L F F L R Q S H S V A * A G V Q W H N L D S L Q P L P P G F K Q F S / L S L P S S W D Y R R M P P R P A N F \ * F L V E T G F R H V G Q A G L E L L T S G D P P A S T S Q S A G I T G V S H G A Q S C P L L Y I E F P L S I L A A T |
| 2907 | 8404 | C | 3165 | 13 | 399 | M E K I P V L F R V A N L I S I I P A P N K S R L C G K T R I S R S A K S K A N T R V F L A C R F G L A G D N A I A N V H A P D A D L E A Q S D V E R T M D L K P C I W V P D T L G E A E Q T A P A D R L S M H T Q H F G R P R R A D H E V R R P R P S W L I W * |
| 2908 | 8405 | A | 3166 | 168 | 414 | N P L L L P N T F P A N G N T I L I K E K V L F L F F * D G S P V L S P R P D C G L Q W R N L G A S L Q S P P P G F T P F S C L S L P S S W D Y R H P P L R P A N F F L Y F L V E T G F H R A S Q G \ G L D L L T S R S / I P P R A S Q S A / R G L Q G V S H P R P A Y M S L R Y N K P A H V P L K I K V K K |
| 2909 | 8406 | A | 3168 | 28 | 123 | |
| 2910 | 8407 | A | 3169 | 2 | 123 | E N R L M A G G E / H M L A A I L L F T A L R C L C K V K H K P G L H A H * G T A P |
| 2911 | 8408 | A | 3170 | 1 | 402 | Q G F S P P \ E S L R Y G \ S W E G K A L T F P Q P D T H K G S V L E D * * K R K A S L Q L R * E E G I C L \ C L S L G M E C L G V K P / V A Y I L F T E I G E S R L M A G G K / H M L A A I L L F T A L R C |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LGKVKHKSGLRAHRGTAPFLKLIY DTEFAHMFSC |
| 2912 | 8409 | A | 3171 | 1 | 399 | SSSLQPPPPGFK*FSCIGLPTS RDYR CVPPRPAANFVFSVETGFHHVQGAG LELLTSGDPSTSASQSAGMTGVTTV PRPVLLISEAHFWSCKNSLFTGENVI EANQNLLALRFISAMD LQSLRIVRN QTFFF |
| 2913 | 8410 | A | 3172 | 1 | 451 | LYGEGWSFALVAQAGVQWCDLRL LQPLLPGFKYSPASASRVAG/HYR WSL/DSVTQAGVQWHNLGSLQPPPP SFKRFSCLSLPSS*DYRCTPPGLA*/F FIFLVEMGF\SLLARLVSNS*PSGDPS TLGLPKVLGLQGVSHHALVPHLLIL QKR |
| 2914 | 8411 | A | 3173 | 2 | 346 | |
| 2915 | 8412 | A | 3174 | 1 | 2430 | |
| 2916 | 8413 | A | 3175 | 576 | 983 | GRSFIVSFLLVNSGKVPTDK/ERLFD RMMNSNWG/RSFAKKVNSNLST*Q FKYKNKGICAAACQFSLFPLK*PIPRL FFAGEHTIRNYPATVHGALLSGLRE AG\RIADQFLGAMYTLPRQATPGVP AQQFPKACETDAF |
| 2917 | 8414 | A | 3176 | 1 | 2930 | RRAGSVKRGEARLFGPTERQSERPL RPSAARRPEMLSGKKA AAAAAAAAAA AAATGTEAGPGTAGGSENGSEVAA QPAGLSGPAEVGPGAVGERTPRKK EPPRASPPGGLAEPPGSAGPQAGPT VVPGSATPMETGIAETPEGRRTSRR KRAKVEYREMDLANLSEDEYY EEERNAKAEKEKKLPPPPQAPPEE ENESEPEEPSGVEGA AFQSRLPHDR MTSQEAACFPDIISGPQQTQKVFLFI RNRTLQLWLDNPKIQLTFEATLQQL EAPYNSDTVLVHRVHSYLERHGLIN FGIYKRIKPLPTKKTGKVIIIGSGVSG LAAARQLQSFGMDVTLLEARDRVG GRVATFRKGNVYVADLGAMVVTGL GGNPM AVVSKQVNMELAKIKQKC PLYEANGQAVPKEKDEMVEQEFNR LLEATSYLSHQ LDFNV LNNKPVSLG QALEVVIQLQEKHVKDEQIEHWKKI VKTQEELKELLNK MVNLKEKIKEL HQQYKEASEVKPPRDITAEFLVKSK HRDLTALCKEYDELAETQGKLEEK LQELEANPPSDVYLSSRDRQILDWH FANLEFANATPLSTLSLKHWDQDD DFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVN TRSTSQTFIYKCD AVLCTLPLGVLK QPPAVQFVPPLPEWKTS AVQRMG FGNLNKVVLCFDRVFWDPVNLFG HVGSTTASRGELFLFWNLYKAPILL ALVAGEAAGIMENISDDVIVGRCLA ILKGIFRS\SAVPQPKETVVS R WRA DPWGRGS*SY\VAQGS\SGNDYDL MAQPYHSWAPSIPGAPQPIPRLLC GENITIRNYP/TPVHGALAEVGSRE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AGKEIARPSFWGAMY/TRLPRQVATP GCFLAQVVPQACETRCIPKGRGPM CPVSCPCKEGSSSNTRSPLEKSTPGI WAPDQLMELPDLTKGACLLNDLE HQGGTCPLVWNCVLRKD |
| 2918 | 8415 | A | 3177 | 62 | 447 | GDRAEESAEPRAWSHSDNSHRYTT LFICLTHTHVHNPNVHSHTHTHTHT HTHTHTHTVSYRHTETPPLLLKQTG LKFY*NSRDDTPRSRPGSSGLQRLSS SPPVPFQPGTVEASADFCGDDLLTT VRLQ |
| 2919 | 8416 | C | 3178 | 90 | 233 | MRIGYKVKDGTFLDLQMGGPLPGXX XXSRPKRNHQLSKGEREINLGKL* |
| 2920 | 8417 | A | 3179 | 462 | 929 | SLFHTWKADGFFLTGNSSSRPGNNT ICKSKKCPILYLISNPHPQIMPLFF CDGSFTLVGPGWEWQWCDLSSLQP PTPR/FN*FCSLSLPSSWDHRHPPSCP ANFLYF**RLGFHHVGQAGLELLAS SDPPASASHSVGITGVSHHTWPMPL LLLI |
| 2921 | 8418 | A | 3180 | 160 | 272 | FFL*DRALLCLPDWSAVV*SWLTAA LA\YRRKRSSYLSLPSSWDYRHLPP CPANFSYFL*RQSLTVLPRLVSNSW TQVSLLTQPSVLGLQA |
| 2922 | 8419 | A | 3181 | 6 | 270 | RDRVLLCHTDWSIAV\ESQLTASSN SWVK*SSCLSLQRTDRDYRHEPPYL ANF*IFCRD/RGLTMLPRLV*NSWPQ GILPPWPPKSLGLQV |
| 2923 | 8420 | A | 3182 | 92 | 549 | VWQGLHPQLHPHFASQNLISLALS LKAGVQWHDLSLQPPRRFKPFS CLSLPSSWDYRRAPLCPANFFLYF** RQGFTMLARLVSNY*PRDPPASASQ SAAITGVSHCARPRLSSLLQCFSNSS RLEHTDGIHFLSEAMSAIHESFPHI |
| 2924 | 8421 | A | 3183 | 16 | 661 | DRVSVTQAGVQWCNLGSLQPLPPR FR*FCSLSLLSSWDYRRPPRPANFC IFSRD/MAFTTLARLVSNS*PQ/CDPP TSASQSAEITGVSHRAWVLSPPQPF FFFDMESHAITQAGVQWRHLGSLQ PPPPMFK*SSCLSLSSWDYRRPPPR PANFFVFL*RDGVSPC*PGWSRSPD LVIHPPWSPKSAGITGLSHCAQPYP QFSKHKDLRVSGKA |
| 2925 | 8422 | A | 3184 | 288 | 489 | CGLILELEKLLLWVIQQIQMSLNKA TI*SNDFCPLST*NQVWCVFKGRSL HFEQKVVPSSNKVTG |
| 2926 | 8423 | A | 3185 | 3 | 166 | WLYSANVAHAPYRGSALWCLRDS RPPAQYWSAFQHYSL*PTQFPLEFT TKSLLS |
| 2927 | 8424 | A | 3186 | 3 | 725 | LALLGRVYDVLSDARD/YVELGPQYS VSKMTQRRSHVYTTRLNT/ADIYDS DLVPLCPQLSAVPLHSRNSAPYPYN PLYSVP/LPG/VVTGRFYGEDGLPTP ALTQVEAAITRGLEANKLQLQEKQ TFPPCNAEWSSARGSLWCSQKSPK DADDTSIYMFYQKVGDNDSIDSWKN AGRVFKDSDKFDANDPILKDQTQE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WSGSATFTSDGKIRLFYTDYSGKHY GKQSLTTAQNGVKPEGTTETTMK |
| 2928 | 8425 | A | 3187 | 1 | 1988 | |
| 2929 | 8426 | A | 3188 | 134 | 944 | MLRCGGRGLLLGLAVAAAAMAA RLMGWWGPRAGFRLFIPEELSR YRGRPR\DPGA*YLALLGRVYDD/DPP GRRHYEPGSHYSGFAGRDASRA FVTGDCSEAGLVDDVSDLSAAEML TLHNWLSFYEKNYVCVGRVTGRFY GEDGLPTALTQVEACDSTRGFGGQ TNYKLQEKQTFPPCNAGGGAQPGAA RLWCSQKSGGVSRDW/ALAVPRKL YKPGAKEPRCVCVVRTTGPPSGQMP DNPPHRNRGDLADHPNLAEYTGCP PLAITCSFPL |
| 2930 | 8427 | A | 3189 | 1 | 312 | AQPGVQ*RNLHSLQPPPPGSKRLSC LSLPSS*DHRPPPCPANF/SVFLVE MGFHHVGQAGLELPTSGDPPASAS QSAGITGASHRTRPES*FY*LRLGIII FR |
| 2931 | 8428 | A | 3190 | 2 | 176 | |
| 2932 | 8429 | A | 3191 | 3 | 67 | |
| 2933 | 8430 | B | 3192 | 1 | 1587 | MVKLSIVLTPQFLSHDQGQLTKELQ QHVKSVTCPCEYLRKVINTLADHH HRGTDGFGGSPWLHVIIAFPTSYKVVI TLWIVYLWVSLKTIWFSRNGHDG STDVQQRAWRSNRRRQEGRLSICM HTKKRVSSFRGNKIVLKDVTILRRH VETKVRAKIRKRKVTTKINHHDKIN GKRKTARKQLSQHSISHVLAFS DPP FCKKGSLLQAPP SADDNIKIPAERLR IPLPPSADDNLKTPSERQLTPLPPSAP PSADDNIKTPAERLRGPLPPSADDN LKTPSERQLTPLPPSAPPSADDNIKT PAERLRGPLPPSADDNLKTPSERQL TPLPPSAPPSADDNIKTPAERLRGPL PPSADDNLKTPSERQLTALPPSAPPS ADDNIKTPAERLRGPLPPSADDNLK TPPLATQEA EAEKPRKPKRQRAAE MEPPPEPKRRRVGDVEPSRKP KRRR AADVEPSSPEPKRRRVGDVEPSRKP KRRRAADVEPSSPEPKRRRVGDVEP SRKPKRRRAADVEPSLPEPKRRRLS * |
| 2934 | 8431 | A | 3193 | 792 | 1024 | SHRKM FQRAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKALCNW RMIISRHLPSVVLHVPLYQPRTRPRT LH |
| 2935 | 8432 | A | 3194 | 1 | 1656 | |
| 2936 | 8433 | A | 3195 | 112 | 368 | SHRKM FQRAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKPLCNW VSLLVFLAFEHSLPGQDMDTFFSLQ LCAQARTGRSD |
| 2937 | 8434 | A | 3196 | 1 | 1353 | |
| 2938 | 8435 | A | 3197 | 1 | 452 | |
| 2939 | 8436 | A | 3198 | 1 | 510 | |
| 2940 | 8437 | A | 3199 | 2159 | 2958 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2941 | 8438 | A | 3200 | 350 | 927 | LFLVSPLKTISGSRNGHDGSRDVQQ RA*SSNRRRQ\KKRVSSFRGNKIVLK DVITLRRHVETKVR\AKIRKRVTTK INHDKINGKRKTARKQKMFQRAQ ELRRRAEDYHKCKIPPSARKPLCNW VSLFVFLAFEHSLPGQDMDTFFSLQ LCAQALQREMAERKAA\YRHHSPIP VGNRVVQKHLH\PHPVGPLI |
| 2942 | 8439 | A | 3201 | 1 | 277 | FFFF*ERIWLCCPGWSALARTWLT AAPNSWAQTILPHSWG\YR\RLPPCP AFILFYLF/CRDK/SLAML\PRLVLNS\ WAQVILPLQPPKVLGLQA |
| 2943 | 8440 | A | 3202 | 1 | 340 | SIHLPKAPPPNHSTGVWVQHRNFFL RWHLTQC/*PGWSAVAQSLLTATST SR\VKQSSHLSLLSSWDHRCAPP\HL ANFLYF**RRDFTVLLRLVSNS*A*V ICPRWPPKVLGLQM |
| 2944 | 8441 | A | 3203 | 2 | 354 | ESLTGVQWHEFASLKPL/PCLSLPR GWDYRRAPPRPAYF/*FLVETGFHHI GRAGLKLLTSDDPVSASQSAGITG MSHRAWPLLKYFSALQTLN\ILQKN KNKNLIKTYFISLHV\KIF |
| 2945 | 8442 | A | 3204 | 166 | 373 | EGALFCSQASELLSCGLLAVFTRFK LRGPHCCCAKKVYSLPRMGPH\TTL H/TALNI*SCPCCLFIFLVC |
| 2946 | 8443 | A | 3205 | 2 | 775 | LHHLPGGGSVSHNKPALCGAVPAG RPDTGDNPAVPGRSNGSALTPVWV LIAKQSPPIVKILKFGWFPIILAMVIS SFGGLILSKTVSKQQYKGMAIFTPVI CGVGGNLVAIQTS\RISTYLHMWSA\ LGVLPLLMMKKFCPNPRSTFC\SQKL NSMSCSRLLLLLGGSQGH\LIFFYIIY LGGGVVSQ*S/T/TPDLCGCSNLLGRA* SRVTNPAVTGA\VELVRLTWHQGL \DPDNHCIPYLTGLGDLLGTGPPGDS AFSLTGY |
| 2947 | 8444 | A | 3206 | 2 | 348 | IAFGRYELDTWYHSPWP\EEYARLG RL\HMC\EF*IKYMNSLTILTMH\MVN CAFDPP\LG\LPKELSLETRMETFFPAL PSFH\SIHCPLCVQPELGKAFGCLSVG AWGCRTHLRFTGLH |
| 2948 | 8445 | A | 3207 | 1 | 1503 | |
| 2949 | 8446 | A | 3208 | 1 | 635 | |
| 2950 | 8447 | A | 3209 | 1 | 665 | MQA\IKCAGGWKAEAVGKTCLLISY T\TNA\FPGEYIPTVFDN\YSA\NVMV DGK\PVN\WGLWDT\SGQKDYDRVT PPYPYPA/QADVFLICFSLVSPASFE NVR\AKWYLNVRHHCPN\TP\IILVGT V\LDLRDDKD/TRIEKLKEK\KLTPIT YPQGLAHG*GRLGAVKYLG/CAPA AHTSEGLKTVFDEAIRA\VLCPPPVK ERGRENCLPVVNV\SAPSFLGPVPLE PL |
| 2951 | 8448 | B | 3210 | 1 | 693 | MYGVSAFVVLSP\TGRLPSVLQKEN QQQGV\PNSPPLHEQM\QMDTGLCRL TPGLTLAGQWTRGSDSLPGAGEAG RTSFLPMYNANSAASSATHTGAAS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RESCGERECVQFSQRTARDRWCIRG RAELEQDILDSAAVTIIQKWHIKGRP ALHPAGVLGHVEAPFSLVLQLERSR FLKNRWESAGARYPGREEGNEIRH RGCGDRGSQEAAVRCKGPPTRPV ELPPRLPVLS* |
| 2952 | 8449 | A | 3211 | 1 | 627 | FFFGKSILLFKKINVTFDIEKDILKMF LKGLKRHLFWPGMVAPAC*SQHSG RPRRMDHLRSGVRDQPGQ\QGETPS LLKNIKKISRAWWQAPVIPATREG*/ E*GESPEPGEGKVCRRAEIAATCTP AWGVQSETLSSKKKKSFVLNVPHH PRQASVSFHCFFHKNQWGSPLWKKA RTFLLGNGWLSCPHLSTQGNSLSA PHLAEAQTLSP |
| 2953 | 8450 | A | 3212 | 114 | 411 | EREFRLFVPQVELQGPDLG*LNLLLP RLKQFFGLTFQRIWNYKLAPPPVN LEFWAKTGFSHVNQVGFELLT*GDP P/AWASQRVKMTGPTHQAHLGNF F |
| 2954 | 8451 | A | 3213 | 48 | 1400 | HPMTPI*STPLLYPL/PVTSGLASLSS LTLQNSDS\LLQPLTSAM/PPSAIPTP QRTSTPGLALFPGLPSPVANSTSTPL TLPVQSPLATAASASTSVPVSCGSS ASLLRGPHPGTSDLHISSTPAATTLP VMIKTEPTSPTPSAFKGPSHSGNPSH GTLGLSGTLGRAYTSTSVPISSLAC LNPALSGLSSLSTPLNGSNPLSSISLP PHGSSTPIAPVFTALPSFTSLTNNFPL TGNPSLNPSVSLPGSLIATSSTAATS TSLPHPSSTA AVLSGAFCFSTSPAAP FPLNLSTAVPSLFSVTQGPLSSSNPS YPGFSVSNTPSVTPALPSFPGLQAPS TVAAVTPLPVGWPQHPQLPVLPGF GSAFSFHFNSRSLHKGPFIIWDFK AGRQFWFFRAFGPSRVSLGFLRLH NHPCKNYSIMRLHSQHCYSRSIQLR LWESYPAQPDGVS |
| 2955 | 8452 | A | 3214 | 2 | 694 | QLLNYAPGPGGPRYVDCDLF*NGY HL\WYHD\YGHLEFTRLQLATQFEN WYMKYQSPHQTKEYG\AETVSGFPR DPPSDVPVRCPRKSLLEQ\YHLGLDS KPQKNTCLESPLWNFADFMTAQSP \TKVLGNKKGIFTRAETTQQSAAFL LRERY\WKIAQ*NP GIPHSVARSQCL ENTACCSLSKTDTHLRVPSSPGGQR LPQQQNKCLLDCSRQTRTFSGLGfV VIYSSREH |
| 2956 | 8453 | A | 3215 | 2434 | 2765 | GIILFWAQLFPASFFFFFFF*DGVS LC CPGWSA VVRSQLTASSASRVQAILC LSLPSSWDYRHLPPCLANFFVFL/CR DGGFTMLARLVLS*AS*VHPPWPP QSAGDYQA |
| 2957 | 8454 | A | 3216 | 2 | 481 | LFLFLRHSFTLSPSLDVQWRDLGSL QPPPPRFK*FSCLTLPSSWYYRHVPL CLANF*FLVETGFCHVGQSGLELLT SGDLPASASQSVWITGMSHGARLH GHFLGSWENWTCQAPGSSKSDCS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PHMANAVSAGGPGTLLIPSAPSCPC NLAGGRCPLR |
| 2958 | 8455 | A | 3217 | 126 | 364 | RAWANLS*LKVLPPGLKGFSGTL PSTGNNGLVPPRVNFGSFSKNGVS PCGP/GWF*TTALRELGPLSLLEIGIN PFFL |
| 2959 | 8456 | A | 3218 | 132 | 342 | SLSSLKNMYICLWNVFLFVFGYRAF LCHPGWSTVAQS*LT/IPGT/LWVKP SSLLVLPKRWDYRHEPLRPDLK |
| 2960 | 8457 | A | 3219 | 2 | 264 | QLTATPPPTGFKQFSCLSHPSSWD\Y RYVPPRPAKFCIFS/VRRGFTMLAR MVSIS*PCDLPTSASQSAGITGVSHR AWPVL*FVFLVETGFHHVGQDGLN LLTLRSAHLSPKCWDYRRKPPGLA CFMILNSYLV |
| 2961 | 8458 | B | 3220 | 134 | 3038 | PGMEDGSDDMDTSVEDIGGRSCVT RFVRTLLIMEHGVKPHSKHLTEYF AFLYEFAMGEEESQFLLSLQAIST MVHFYMGTKGPENPQVEVLSEEEG EEEEEEEDILSLAEKYPAALEKMI ALVALLVEQSRSERHLTSLQTDMA ALTGGKGFPLFQHIRDGINIRQTCN LIFSLCRYNNRLAEHIVSMLFTSIK LTPEAANPFFKLLTMLMEFAGGPPG MPPFASYILQRIWEVIEYNPSQCLD WLA VQTPRNKLAHSWVLQNMEN WVERFLLAHNYPRVRTSAAYLLVS LIPSNFRQMFSTRSLHIPTRDPLS PDTTVVLHQVYNVLLGLLSRAKLY VDAAVHGTTKLVPYFSFMTYCLISK TEKLMFSTYFMDLWNLFPKLSEP AIATNHNKQALLSFWYNVCADCPE NIRLIVQNPVVTKNIAFNILADHD DQDVVLFNRGMLPAYYGILRLCCE QSPAFTRLASHQNIQWAFKNLTPH ASQYPGAVEELFNLMLQFIAQRPD MREEELEDIKQFKKTTISCYLRCLD GRSCWTTLISAFRILLEDEDRLLVV FNRGLILMTESFNTLHMMYHEATA CHVTGDLVELLSIFLSVLKSTRPYLQ RKDVKQALIQWQERIEFAHKLLTLL NSYSPPELRNACIDVLKELVLLSPH DFLHTLVPFLQHNHCTYHHSNIPMS LGPYFPCRENIKLIGGKSNIRPPPEL NMCLLPTMVETSKGKDDVYDRML LDYFFSYHQFIHLLCRVAINCEKFTE TLVKLSVLVAYEGSKSKCFLEANC GQFGSALFITNLISQYQNLQSDFSNR VEISKASASLNGDLRALAFAPVSTH SQTVPSSNSNSARAFKQMQLDSA TEKLTPRGKKPKERKTKDDEGGNS HLKGRAC* |
| 2962 | 8459 | A | 3221 | 2170 | 3139 | DLRALALLSVHTPKQLNPALIPTL QELLSKCRCTCLQQRNSLQEQEAKER KTKALALWTTIITFRVGGGSNTLGV TGLRVVCSAEPPKYKC*KQN*LPTS PPNVILMTFREVSLLACVFTDDEGA TPIKRRRVSSDEEHTVDSCISDMKTE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TREVLTPSTSDNETRDSSIIDPGTE QDLPSPESSVKEYRMEVPSSFSED MSNIRSQAEEQSNNGRYDDCKEF KDLH\CSKDSTLA\EEEESEFPSTSISA VLSDLADLRSCDGOALPSQDPEVAL SLSCGHSRGLFSHMQQHDILDTLCR TIESTIHVVTRISGKGNQAAS |
| 2963 | 8460 | A | 3222 | 3 | 344 | PESHSAQAQGVQWPDLGSLQLSLP AFKQFSCLSLPSSRDYRRASPRPANF *FLVETGFCHVSQAGLKLLASSDPP VSASQTARITGVSHHAQPRATFYRH KSVLVLP LLKSPQ |
| 2964 | 8461 | A | 3223 | 1411 | 1741 | GYLQFSFSFFLFFFFFFFFFLGESHSV T/RGLECSSVISTHCNLR L PGSSDSR ASASRVARTRGMHHHTRQIFVFLV QMGFHHVQGAGL/DSS*PSVVHPP\ RPPKVLGLQA |
| 2965 | 8462 | A | 3224 | 361 | 462 | RHFLSTETCYCNSFF/RHSSSKNYTK LKRYE*VS |
| 2966 | 8463 | A | 3225 | 3 | 89 | |
| 2967 | 8464 | A | 3226 | 1 | 336 | VCQVCGFRSRLHTNVNRHLLLNKP KIFPHVCDDCGKGFSSMLEYCKHL NSHLSEGIYLCQYCEYSTGQIEDLKI HLD FKHSADLPHKCSDCLMRFGNE RELISHLPVHETT |
| 2968 | 8465 | A | 3227 | 951 | 2075 | RTANLNFCKILDKSQALNVNCPAET GL*LRANSRWP/PINCELCFNSKYF SDLKQHMILKHKRTDSNVC RVCKE SFSTNMLLIEHAKLHEEDP/N/YVCK YCEYKPVIFENISRHIADTHFR\DPPI HWCEQCDVQFSSSEL YLHFQEHSC DEQYLCQFCEHETNDPEELA*\HVG K*GMHVN**ELSDKV/CNNGWNMG QYSLLSKITFDKCKNFFVCQVCGFR SRLHTNVNRHVAIEHTKIFPHVCDD CGKGF SNNTWKRKR GQGKTFPLLI NLELSTSLTNYRGSPWASELSTSVE VSMAMLPAAEAETQGHDSGEREPF SQTPGLMQPFSIPVQITLQGSRRRQG RLPVLGDWRPFKLTCS SPALIIAQPI VGAQE |
| 2969 | 8466 | A | 3228 | 2 | 415 | LDPGSLAGFTSYIQFMYDEFVEEYE PTKADSYRKK/VAQDGEEVQIYIINT AGQEDYTAIKDNYFHC VFSITEMES FAATVDFKEQ/ILRVKKDENIPFLLV GNKSDLEDKRQVSIEEAKNRAD*W NVIYVETSPKT*AN |
| 2970 | 8467 | A | 3229 | 607 | 1317 | |
| 2971 | 8468 | A | 3230 | 260 | 535 | |
| 2972 | 8469 | A | 3231 | 246 | 985 | KLRHKMAANKPKGONSLALHKVI MVGSGGVGKSALT LQFMYDEFVED YEPTKADSYRKKVVLDGEEVQIDIL DTAGQEDYAAIRDNYFRSGEGFLC VFSITEMESFAATADFREQILRVKED ENVPFLLVGNKSDLEDKRQVSVEE AKNRAEQWNVNYVETSAKTRANV D/KEWPFLKTRWWNTCKYISSHCPR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PAPVSRKTAHWAEVFFDLMREIRARKMEDSKEKNGKKKRKSLAKRIRERCCIL |
| 2973 | 8470 | A | 3232 | 1 | 634 | MAANKPKGQNSLALHKVIMVGS GVGKSALT\QFMYDEFVED*EPTK ADSSRKKVVLDGEEV\QIGYPLDTA G\QED\YAAIRD\NYFRSGEGFLCVFS ITEMESFAATAEFREQILRVKEDEN VPFLLVGNKSDLEDKRPGL*EEAK\NRAEQWNVNYVETSAKTRANVDK VFFDLMREIRARKMEFEFYLYNGTK NTKRLAERIREGGCIL |
| 2974 | 8471 | A | 3233 | 314 | 373 | |
| 2975 | 8472 | A | 3234 | 1 | 2129 | PSVAGAATLWFHVTLPFCARLCGR RSCTHSGIITEFHFFHL/PFRPIILAC GNDDCRIHIFAQQNDQFQVLSLCG HEDWIRGVWAAFGRLLLASCSQ DCLIRIWKLYIKSTSLETQDDDNIRL KENTFTIENESVKIAFAVTLETVLAG HENWVNAVHWQPVFYKDGVLQQP MRLLSASMDKTMILWAPDEESGV WLEQVRVGEVGGNTLGFYDCQFNE DGSMIIAHAFHGALHLWKQNTVNP REWTPEIVISGHFDGVQDLVWDPEG EFITVGTDTTTRLFAPWKRKDQSQ VTWHEIARSQIHGYDLKWLAMINR FQFVSGADEKVLRVFSAPRNFVGKF LCHYR\KSLNHVLCNQDSDLPEGAT \APALGLSNKAVF/LREDKAPQPPDE EELLTSTGFEYQQVAFQPSILTEPPT EDHLLQNTLWPEVQKLYGHGYEIF CVTCNSSKTLASACKAAKKEHAAI ILWEITTSWKQVQNLVFHSLTVTQ MGLLT**GSFLLGCFPEDSNLVIVEK AWIQS/TPEFEPVFSLFAFTNKITSVH SRIIWSCDWSPDSKYFFTGSRDKKV VWGECDSTDDCIEHNIGPLPPSVL DRGWGCDQLSASAQCSHPSQRYVV AVGLECGKDLLIYL GKRLIKFQK*M T/ATHCVGNKSKPKVIHWAIQKIYC WEGICSGKT*TRREGRRRC*VVYTFA SCG*DHTVKIHRVNBKCAL |
| 2976 | 8473 | A | 3235 | 451 | 778 | GSGRWKSRSVARAGMQISGAHLQL NCKPPPPGLKADPPWLSL\PSSWDP QMCPPTPWLLFVCLVETGFTMLPQ AALQLLS*SDLSA*ASQNAGITGMS HHAGPDTVPLF |
| 2977 | 8474 | A | 3236 | 1 | 186 | FFFEMESRTVTQAGVQWHDLGSL QPPPPG\SSDSPVSASHVAEITGAHH HTWLIFIFLFL*GVQWHDLGTLTAT SSLLGSSDSPVSASHVAEITGAHHH TWLIFIFLFL |
| 2978 | 8475 | A | 3237 | 1 | 353 | KIWLFFVFKTDVSILVHPRLECSGAI SAHCNLHLPGLSDSHTSAFRVAGTT GARHQAQLIFTFLVEMGFHHVGH GLKLPT*EIRPPRPPEVLGLHACAT VPGHKYVNEPIKMVLLK |
| 2979 | 8476 | A | 3238 | 3 | 453 | GQTGTWQGNTGQRPQLPPHPPPIH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LVSRRHRGKLRHGFRLRPMPEPRGLES GKTGSARGVAACTSP*GRSG\QGGG PRDIAQQGGCRGSACGRRSHEALRP RVWCGEGPQWTW\CAVCPNRSAP GAGLADRQHPGESRAWGETRLCE AGGAE |
| 2980 | 8477 | A | 3239 | 232 | 472 | LHSFIHSFIHLFIYLFDRVLLCCPDW STVERSQTTLKSRVVK*SSCLS/LP SSWGYRSVPPCPANYFYFL*RQRLT TLPS |
| 2981 | 8478 | A | 3240 | 2 | 345 | MVHVAVAGLNGTHSCPPASSSVLTF GHPAPHEQLQQSVGPTSPHSPLL*PL SSLEVLGWGSEGVGGLQEIQKCSK ALPCKTPCGCFCIYLIFSPTQGDFIPH DPAPPLLSASWV |
| 2982 | 8479 | A | 3241 | 205 | 361 | DAHSPAPAVSTPGQAWAAVLAMFP PGPWGEGSGRL\PHDPAPPLLSAS WV |
| 2983 | 8480 | A | 3242 | 137 | 959 | IPFPVMLDPAGRQQQRWGRIMGY KVSLGGA*NLGRCKNIHKGSCREGL CLISLRAWEGRVLGEGFAQN*HTA HPEPGKSSHS*KIPFQRESGL*PATH PVPSKTPPLPGESSRARAWCLKGE DPCPRKPPAP*SLPPGPWGE/P*QGL QPRLGL*TPGLGYEHLKPFP/PSA PAA*PPG\PAKAQAPRKSCAPTIVTH ALLPPNPLPTQLGWKWISADQSQSN PFPRAYP/REPSLFPSNAPLSPSPHP TTFPEFPCSPTPPPQIPHPQDFPRS |
| 2984 | 8481 | A | 3243 | 23 | 438 | SRHLGLPKCWDYRQEPLCLALSFFF RVRVS\SVAQVVQWHDGRSLQPQ TPGPK\YPPATAS*VAGARLIFFK*FL *RWDLTIMPKAGLKL PATGDPPACL LLSFSLIPTGGFTRFEPTRHSLLEV GLSPMLVRHWLWA |
| 2985 | 8482 | A | 3244 | 1 | 1061 | ASRRALQLFGIPVRQLQKGACPLGL HQLSSPRYKFNFIADVLFKIAPAVV HIELFLRHPLFGRNVPLSSGSGFIMS EAGLIITNAHVSSNSAAPGRQQLK VQLQNGDSYEATIKDIDKKS DIATIK IHPKKKLPVLLLGHSDRTCRPGEVL WVAIRQIPSP*QNTV\TTGIVSTAQR EGRELGLRDSMDY\QTDAI\NYG NSGGPLVNLDGEVIGINTLKVTAGIS FAIPSDRITRFLTEFQDKQIKDWKKR FIGIRMRTITPSLVDELKASNSDFPE VSSGIYVQEVVPNSPSQRGGIQQGDI IVKVNGRPLVDSELQEAVLTESPL LLEVRRGNDLLFSIAPEVVM |
| 2986 | 8483 | A | 3245 | 1 | 268 | QGSPSRDPSPLGGPNGGIFLAP/AGP NPP/RGTRGNPVFS*NSKICPGWGGP PVGPGS/RGELG*RAALAPGGPGGL DWAPGP*PGGQRGAPF |
| 2987 | 8484 | A | 3246 | 20 | 353 | KEVGRLTHSVNHSGGREKYVWHP GNAL*Y\GKLPVLPPIFIVNR*VQ*P *PERHVMVTRGSGMNVWIMP/PGKPP RPAEVPVEVEGHLEWTAEDSSNHC QLQG*DQLQWGRWL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2988 | 8485 | A | 3247 | 2 | 322 | KLDNSSKWLENGTFDLSILQDLDNF C*KMGKWSEVPYVQAFFSIHSLPSL CSQCHL/CPDFPSFSP/YPLLLSPPQT QSPLNPPFPLTPLTSLLPRLLLARLN QVPILP |
| 2989 | 8486 | A | 3248 | 141 | 924 | PFSSQTVKLSGGATRNPVSSPKASG GQPSEGWEVALEGDSCAALMRQQ CPGLLKSRK/RAPGNPTASGS\APGA TKRSLGGRRARRGLEFVVSRRFFGGGR AQSSLGNAHPHSGTIPKAPHASQQG LGLRLGGLEPSTPPWVHPPARPRAS PDPSRVAGSPRSLPNPPAAGKGGRG SGEEARYFDLS*ILKSLPYPGHERVY QEPQRGVKTSCSCSPF/HLPLLLFQS SPPPSTLVGAGLKIGFLRCPVGGILI GKGFFFNCLHST |
| 2990 | 8487 | A | 3249 | 1 | 363 | QVSLVINWDLPTNR*NYIHR*AYIW NTPLPLHTWPSLGLKLLIFLIPFLEFQ \IGRGGRLDRKGGAINKGTEYDERT LRDIETFYNTSIEEMPFNVADHMLM GCPATQPLSGLIIGASDQY |
| 2991 | 8488 | A | 3250 | 1 | 87 | LNETVLLWHSGWMSTVVQTQLLPA ASTW\VKQSSHLSSLNSWDHSR\VP PHWANFLIFCR/DRSFAMLPKLVS PWAQAVLPPLPIVL*LNETVLLWH SGWMSTVVQTQLLPAASTWA |
| 2992 | 8489 | A | 3251 | 3 | 270 | CFNSAWTEPGARSPPRPAHSQPSV TSSPHPR\TAPRPPPLQR\PS*\SPP*R PRPP/PHVRHNYPSGLKSHH*SAE*P GPLGPIPTVY |
| 2993 | 8490 | A | 3252 | 3 | 452 | |
| 2994 | 8491 | A | 3253 | 1 | 477 | TLLVPQDSERTHPWCLSPADKTNV KA\AWGKVGAHAGEYGAEALERM FLSFP\TTKTYFPHFD\LSHG\SAQG* RAHGKKVADALTKAVAHVDDMP KRRCPP*SDLHGAQAFGWDPVQLQ SS*SHLPCLGEPWAAHLPRPSFNPW RLQRLPWGQISWGFC |
| 2995 | 8492 | A | 3254 | 3 | 295 | LFLFFFFFF*MESHVTRLECSGTIW AH*NLHLPGSSDSPALASRVAGTTG MCHHIQLIFFVFLVEKGFHHVG*/D MSLSLDLVIHPPWPPKVLGLQA |
| 2996 | 8493 | A | 3255 | 306 | 519 | GTRVERHSRERPSCHLLCEPSQRYS PLLFLVGL*CPPASPGKSPRTKENNF TADSKSQGQSEKSLWVTLA |
| 2997 | 8494 | A | 3256 | 453 | 626 | HGSCLLHHREQVPIPPGIPNLSDSIL* FPVLRIWMLCLYTSCMWFSQSFWI AVMYFV |
| 2998 | 8495 | A | 3257 | 1537 | 1909 | NVLTVEDHPIPIPSKNRPFHNLLPVN LAFFFFFLNRVSF\CHLGWSA VARS HLTCNLLSPGFKQFSCLSLLSSWDY QACMHHTRLVFGVFSRDGGFTMLA RLVSNS*PQVILPPLPPKVLGLQA |
| 2999 | 8496 | A | 3258 | 1 | 342 | KTESHSVAQAGVQWCDLGSLLQPPP PRFKLFSCLSLLSSWDYRGALPRPT DLFA/QFLVEMGFCHVAQAGLELLS SGNLFASASQTARITGVNHHTWPVL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | *F*VKIPPSLPGLL |
| 3000 | 8497 | A | 3259 | 1 | 338 | FFLRWSL/NSVAQAGVQWRNLSSL QALPPGFRPFSCLSLPNS*DYRCPPP RLANFFLYFLVETVFHRLY*RSRMV LIS*PGDPPTSASHSAVVRILLRRRQ CLRQGLCRASVF |
| 3001 | 8498 | B | 3260 | 188 | 1504 | MRTLLPPALLTCWLLAPVNSIHPEC RFHLEIQEEETKCAELLRSQTEKHK ACSGVWDNITCWRPANVGETVTVP CPKVFSNFYSKAGNISKNCTSDGWS ETFPDFVDACGYSDPEDESKITFYIL VKAIYTLGYSVSLMSLATGSIILCLF RKLHCTRNYIHLNLFSLRAISVL VKDDVLYSSSGTLHCPDQPSWVG CKLSLVFLQYCIANFFWLLVEGL YLHTLLVAMLPPRRCLAYLLIGW GLPTVCIGAWTAARLYLEDTGWD TNDHSVPWWVIRIPILISIIVNFVLFIS IIRILLQKLTSPDVGGNDQSQYKRLA KSTLLLIPLFGVHYMVFAVFPISISSK YQILFELCLGSFQGLVVAVLYCFLN SEVQCELKRKWRRCPTPSASRDYR VCGSSFSRNGSEGALQFHRGSRAQS FLQTETSVI* |
| 3002 | 8499 | A | 3261 | 1 | 1047 | MVSIWPRDLPASASQSAGITGLIGA LVLSVGIYAEVER/HEI*NP*KCLPGS SHHPHPPGRRHVHGLLHWCAGVPP *QPPELLASRLSRGYGLVLSWLEP RYEKMISGMYLGEIVRNILIDFTKK GFLFRGQISETLKTRGIFETKFLSQIE SDRLALLQVRAILQQLGLNSTCDDS ILVKTVCVVSRRAAQLCGAGMAA VVDKIRENRGLDRLNVTGVDGTL YKLHPHFSRIMHQTVKELSPKCNVS FLLEDGSGKGAALITAVGVRLRTE ASS |
| 3003 | 8500 | A | 3262 | 178 | 568 | IFFFFFFFKMESCSVAQAGVQWWDL SSLQPLPPGFMPFCLSLPSSWDYRR PPLL PANFLYF**RRGFTVLARMVSI S*PCDPPASASQSAGITGVSHCAQLE SKFYEGRDVHLFCSPLYFQKARKLP GIE |
| 3004 | 8501 | B | 3263 | 776 | 5218 | MLGDNSSMSVTAPKTFQWDMMW RRKGLILIALCRPKEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEGEEEEEEEEEDQLDT MLWDSSTNLTNTALSKEKTMFSSR AKIVKPNGEKPDEFESGISQALLELE MNLDLKAQLWELNITAAKEIEVGG GRKAIHIFVPVPQLKSFKQKTQVQLRR ILPKPTQKCTNNKQKLPRSCTLTA VHDAILEDLVFPSEIVGKRIHVKLD GSHLIKIHLDEAQQNNVEHKVEPFS GVYKKLMGKDVNFEPFQQLMPGT PGSLEMGLLTFRDVAIEFSPEEWQC LDTAQQNLYRNVMLNRYRNLAFLG IALSKPDLITYLEQGKEPWNMKQHE MVDEPTGICPHFPQDFWPEQSMEDS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FQKVLLRKYEKCGHENLQLRKGCK SVDECKVHKEGYNKLNQCLTTAQS KVFOCGKYLKVIFYKFLNSNRHTIR HTGKKCFKCKKCVKSFCIRLHKTQ HKCVYITEKSCKCKECEKTFHWSST LTNHKEIHTEDKPYKCEECGKAFKQ LSTLTTHKIIKAKEKIYKCEECGKAF LWSSTLTRHKRIHTGEKPYKCEECG KAFSHSSTLAKHKRIHTGEKPYKCE ECGKAFSHSSALAKHKRIHTGEKPY KCKECGKAFFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTKHKIIH AGEKLYKCEECGKAFFNRSSNLTIHK FIHTGEKPYKCEECGKAFFNWSSSLT KHKRFHTREKPFKCKECGKGFIWSS TLTRHKRIHTGEKPYKCEECGKAFFR QSSTLTKHKIIHTGEKPYKFEECGK AFRQSLTLNKHKIIHSREKPYKCKE CGKAFKQFSTLTTHKIIHAGKKLYK CEECGKAFFNHSSSLSTHKIIHTGEKS YKCEECGKAFFLWSSTLRRHKRIHTG EKPYKCEECGKAFFSHSSALAKHKRI HTGEKPYKCKECGKAFFSNSSTLAN HKITHTEEKPYKCKECDKTFKRLST LTKHKIIHAGEKLYKCEECGKAFFNR SSNLTIHKFIHTGEKPYKCEECGKAFF NWSSSLTKHKRIHTREKPFKCKECG KAFFWSSTLTRHKRIHTGEKPYKCE ECGKAFFRSSTLTKHKTIHTGEKPY KCKECGKAFFKHSSALAKHKIIHAGE KLYKCEECGKAFFNQSSNLTHKIIH TKEKPSKSECDKAFFWSSTLTEHK RIHTREKPYKCEECGKAFFSQPSHLT THKRMHTGEKPYKCEECGKAFFSQS STLTTHKIIHTGEKPYKCEECGKAFFR KSSTLTEHKIIHTGEKPYKCEECGK AFSQSSTLTRHTRMHTGEKPYKCEE CGKAFFNRSSKLTTHKIIHTGEKPYK CEECGKAFFISSSTLNGHKRIHTREK PYKCEECGKAFFSQSSTLTRHKRLHTG EKPYKCGECGKAFFKESSALTKHKII HTGEKPYKCKECKKAFFNQSSILTNH KKIHTITPVIPLLWEAEAGGSRGQE METILANTVKPLLY* |
| 3005 | 8502 | A | 3264 | 1 | 208 | RDRVLF*HPHWSAVV*SKLTAASTS WVK*FSCLSFLSWCLAMLPRVLN SWPQVTLPPQPPKVLGLQV |
| 3006 | 8503 | A | 3265 | 78 | 359 | RHSSKNLGNVDSECE*T*FPDIIPFH* KKLTEGEYQKSVNH/MTNAVAHST LSSQLLLALQKTLCLFLMLLTKL PTIIHRTVDAHSLADDDVE |
| 3007 | 8504 | A | 3266 | 48 | 330 | VCGCVWMLRVLCYP\GW\SAVAQ S*LTAALISL\VNPSSSLSPSSWDHR RAPPRPANFFNL*RQELPMLRLVL/ NVWAQVILPPWPPKMLELQV |
| 3008 | 8505 | A | 3267 | 200 | 1033 | RSLAPRWHLGHKEKNVTTSVWG WPSPGRNASNSAGVGAGLPFVSTW LAVSSKNIDITEHIDFATPIQQPAME |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PLCNGNLPTSMHTLG\HLHGVSNSPS QPCTYTGESQLTEVLQNLGQR/RNI HNSRLNRLAPRM/LQSFGKEPRPSW VL/CPAWQALYWARV*RPKERRPIEL PSAQRLLHYGP\PMQKDVPLISLANIL PQLPSSGNDVIVATHGQ*SLHHTL L*TPFHLGNVYVAMEEFKALVWY ESTL\SLQPEFVPAKNRIQTIQCHLM LKKGRALLP |
| 3009 | 8506 | A | 3268 | 2 | 2956 | LADSSPSNLQIIKELLSMHHQPDPA LTKEFDYLPPVDSRSSSGFVGLRNG GATCYMNAVFFQQLYMQPGLPESLL SVDDDDTDNPDDSVFYQVQSLFGHL MESKLQYYVPENFWKIFKMWNKE LYVREQQDAYEFTSLIDQMDEYL KKMGRDQIFKNTFQGIYSDQKICKD CPHRYEREEAFMALNLGVTSCQSLE ISLDQFVRGEVLEGSNAYYCEKCKE KRITVKRTCISLPSVLVIHLMRFGF DWESGRSIKYDEQIRFPWMLNMEP YTVSGMARQDSSSEVGENGSRVDQ GGGGSPPRKKVALTENYELVGVIVH SGQAHAGHYYSFIKDRRGCGKKG WYKFNDTVIEEFDLNDETLEYECFG GEYRPKVYDQTNPYTDVRRRYWN AYMLFYQRVSDQNSPVLPPKSRVS VVRQEAEDLSLSAPSSPEISPOSSPRP HRPNNDRLSILTKLVKKGEKKGLFV EKMPARIYQMVRDENLKFMRNRD VYSSDYFSFVLSLASLNATKLKHPY YPCMAKVSLQLAIQFLFQTYLRTKK KLRVDTEEWIATIEALLSKSFDACQ WLVEYFISSEGRELIKIFLLECNVRE VRVAVATILEKTLDSALFYQDKLKS LHQLLEVLLALLDKDVPENCKNCA QYFFLFNTFVQKQGIRAGDLLLRHS ALRHMISFLLGASRQNNQIRRWSSA QA\REFGNLHNTVA\LLVLHSDVSS QRNVAPG\IFKQRPPISIAPSSPLLPL HEEVEALLFMSEGKPYLLEVFMFAL RELTGSL\ALIEM\VVYCCFCNEHF SFTMLAFHLRNQL\ETA\PPHEFKGI RFPTTFMEILVIEDPIQAERV\KVFVE TENGLLALMHHSNHVDSSRCYQCV KFLVTLAQKCPAAKEYFKENSHHW SWAVQRLHHKMSDLYWTPLSNVS NETSTGKTF*RTISDHDTLPYATALL NEKEHSGSRNGSKSRPANENGHRH LQQGSQSPLDDWVSLRSDLDDVDP |
| 3010 | 8507 | A | 3269 | 68 | 301 | NFRDLCDILCSETTRLNTINMSIL SNLTYRFSEIPF*IFRRLFVL*KL/ENS ILKYIWTCKGPRLVKTTFKNNSESW |
| 3011 | 8508 | C | 3270 | 224 | 518 | MINKGQAGANIKSNXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXX* |
| 3012 | 8509 | A | 3271 | 342 | 724 | NTYPWAVL/VFFFFFLRWSLTLVAR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LECRAGVQWCDLGSLLQPLPPQFE* FSCLSLQLALPRPAKFFVILVEM\GF TMLAKMVSIS*PCDPPALASQSARIT ILDFMLAPACPLLIPFTWTLFFRNTI |
| 3013 | 8510 | A | 3272 | 3 | 367 | |
| 3014 | 8511 | A | 3273 | 58 | 553 | VARSAPPDGAVCAGPGSRRTMAE QSDEAV\KY\YTLERFQMHN\HSKST WLILHHKG\YDLTKFLEEHPGGEEV LREQA\GGD\ATENFEDVGHSTDAR EMSKTFIIGVELHPVDRPKLNKASGT FKGCV*GNFLFTTI*FLVPSWWTNW \VIPAISAVGRRLGCIRL |
| 3015 | 8512 | A | 3274 | 41 | 400 | KRLGPRGGVGPSPNGGNQGL*GPKI FPWPSTLGTK/GEPLPSSSSSSSPQK RGFPSSPEK\APGVPPPTPKGPSPPGG GVKKKGRA*KKKPLGLWEKGPNPA PGGPGTPTFGGPPGQYPG |
| 3016 | 8513 | A | 3275 | 3 | 146 | WGVITMMVTCV/A/CTLFWLIAIL AQCNP LYRP*LKDETTWYLKHHWP |
| 3017 | 8514 | A | 3276 | 161 | 472 | |
| 3018 | 8515 | A | 3277 | 3 | 273 | AAAPGNGRASAPRLLLLFLVPLLW APAAVRAGPDEDLSHRNKEPPAP SSCSRSLWAVQGPEPARVEVSGPG WGERGCRAECAEYQAPGL |
| 3019 | 8516 | A | 3278 | 124 | 672 | FQRTKLLNGPGDVETGTSITVPQKK WLHVISPIFVQSLTLPFLAKWGDRL QLLQIELAAREVSDI*EETV*NETYL LLCSRKTLDTLKWHSIPSARLF YI**FCSCLKLAFSQFLPA\DPYGVA VGGTVGHCLCTGLAVIGGRMIAQKI SVRTVTIIGGIVFLAFAFSALFISPD S GF |
| 3020 | 8517 | A | 3279 | 2 | 991 | AAAAPGNGRASAPRLLLLFLVPLL WAPAAVRAGPDEDLSHRNKEPPAP \PSSCSRSLWAVQGPEPARVEKIFTP A\APVHTNTEDPATQT\NLGIYPMQF VAAIIQLLIVSEIGVSRTFFIAAIMA MRYNRPGPCWAGAMLCL/AGLMT CLFS/VLFGYATTVIPRGLYILMFQP VLFAIFGIRMLREGLKMSPDEGQEE LEEVQA\ELKKKDEEFQRTKLLNG\ PGDVETGTSITVPAQKKWLHFISPIF GQALTLTFLAEWGDRS*LTIVLAA REDPYGVA VGGTVGHCLCTGLAVI GGRMIAQKISVRTVTIIGGIVFLAFA FSALFISP |
| 3021 | 8518 | A | 3280 | 1 | 278 | QHDLQDVDVAFTEEE*RLAGPAQR KLYRDVIVENLRNLLSVGHPPFKQD ISPIERNQDLWIMTTATRIPGNLGKN QTVISSYSKLFICFASS |
| 3022 | 8519 | A | 3281 | 263 | 588 | DSALPQKEELKMNMFKAEVTFKDV AVAFTEEEELGLLGPAQRKLYRDV VEN\FRNLLSVGHPPFKQDVSPIER NEQLWIMTTS/TPRRQGNLDTLS\VK ALLLYDLAQT |
| 3023 | 8520 | A | 3282 | 1 | 1285 | MEDSELPSARSVLPSKRIGVVQSQQ RPPLGERHYGPTTRDGALHSAYSPT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QARCVSHPTYEKYPHVWRGWPPFS PEKERQRLENLRRKEEAEQLRRQK VEEDKRRRLKEEVKLKREERLRKVL QARERVEQMKEEKKKQIEQKFAQI DEKTEKAKEERLAEKAKKKAAAK KMEEVEARRKQEEDARRLRWLQQ VRAQ/EGNRSREVK*HLKSHEPVCS GGDSRTHPQPLVHAWSQCLP*RLL\ |
| 3024 | 8521 | A | 3283 | 3 | 262 | RVLRELQEREKALRLQKEQLQRELE EKKKKEEQQLAERQLQEEQEKKA KEAAGASKALNVTVDVQSPACTSS PITPQGHKAPPQINPHNYGMDLNSD DSTDDEAHPRKPIPTWARGTPLSQA IHHQYYQPPNLELFGTILPLDLEDIF KKSKPRYHKRTSSAVWNSPPLQGA RVPSSLAYSLKKH |
| | | | | | | FHTEERSYECTECGKA\FKHSSTLLQ HRKVHTPERRQEDRAHGKVVSC*H RVHQERSYSRKEVKESGRESAIRKK LNLAHPNTHPRE |
| 3025 | 8522 | A | 3284 | 1 | 269 | FFFFPQIGSHPI\RLCSDAITFCCSL NLPGSRDPPASAS*VAETTGLHHHA GLIF*FFVE/MGL/HQAGLELLDKVIL PPLPPKELGSQM |
| 3026 | 8523 | A | 3285 | 3 | 1191 | KSCFNAFFNFEDMQEITQHFAVCH VDAPGQQEGAP/SPFPTGYQYPTMD ELAEMLPVLTHLSLKSIIIGIGVGAG AYILSRFALNHPELVERPLCSLMVD PC/ALKGWIDWAASKLSG\TTNVV\ |
| | | | | | | EIILAHHFGQEELQANLD\LIQTYRM HIAQDINQDNLQLFLNSYNGRRDLE IERPILGQNDNKS\TLKCSTLLVVG DNSPAVEA VMADCGGLPHVVQPG KLTEAFKYFLQGMGYIPVCAAQSPE HRVST\SASMTLARSRTHSTSSSLG SGESPF\SRSVTSNQSDGTQESCESPD VLD\RHQTMEISLDDVLLSALLRNN GKSAQQKKISAKPKLEFLCPRPGTC DHGSRKFCYTVLVDPRERSKATAV ALGSFPAGGPAELSLRLGEPLTIVSE |
| 3027 | 8524 | A | 3286 | 3 | 638 | SSKLSGLTTNVVDIILAHHFGQEELQ ANLDLIQTYRMHIAQDINQDNLQLF L\KSYNGRRDLEIERPILGQNDNKS TLKG\STLLVVG\DNSPAVEA VVECN SRLNPINTTL\KLMADCGGLPPG*FS PGKLTEAFKYFLQGMGYIPLVLCYS TSGSMTSVARSR\THSTSSSLGSGES PFSRSVT\S\NQSDGT\QES\CESPDVL DRQQTMEVSC |
| 3028 | 8525 | A | 3287 | 1 | 407 | FSIETESCSVAQAGGKWHDSGSLQP QPPRFK*FSCLSLLSWDYRPAPP/* PG*LFFVFLVETGF/THVGQPGLKLL TSSDPPTSASQSAGITGLRDRAQPPP EDSNVQFENHWQRECTMLLFTLGP LKLFP\TELML |
| 3029 | 8526 | C | 3288 | 157 | 468 | MHHIHNASRTFQLIFSSFPRGNAIVF MLKMGGFLELRGPRSGMDHHRGR GEANQPF\CP\TSPAACGQNLPIKHGL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PRWSTKGETTADTDSVDLENPILYK YFQL* |
| 3030 | 8527 | A | 3289 | 14 | 348 | EFHSCRPGWSAMTQSRLTLQPPPPG FK*FSCLSLSSWDYRHTPPHPASF* LLVDTGFLHVGQAGLKLLTSGDSP TSASQSARITGVNHCARPSTFLRLQ RKAGRCSTSRL |
| 3031 | 8528 | A | 3290 | 1 | 2201 | MTNLAMVERDSEAGTAASRFPNGH AAKGKAQAHYKVRPAEVRCLKL GPEWVTLRYTIKHRPYKLCGKRQH VFFFTSRSDVGFMLTTLKPFGSVSV ESKMNNKAGSFFWNLRFSTLVST SRTMRLCCLGLCKPKIVHSNWNILN NFHNRMQSTDIIRYLFQDAFIFKSDV GFQTKGISTLTALRIERLLYAKRLFF DSKQSLVPVDKSDELKKVNLNHE VSNEVDLTKETKPNRISSRKLSEEC NSLSDVLDAFSKAPTFPSSNYFTAM WTIKRLSDDQKRFEKRLMFSPAF NQLCEHMMREAKIMQYKYLFLSLH AIVKLGIPQNTILVQTLLRVTQERIN ECDEICLSVLSTVLEAMEPCKNVHV LRTGFRILVDQQVWKIEDVFTLQVV MKCIGKDAPIALKRKLEMKALREL DRFSVLNSQHMFEVLAAMNHRSLI LLDECSKVLDNIHGCPLRIMINILQ SCKDLQYHNLDLDFKGLADYVAATF DIWKFRKVLFILFENLGRFPVGLM DLFMKRIVEDPESLNMKNILSILHTY SSLNHVYKCNKEQFVEVMASALT GYLHTISS\ENLLDAVYSFCLMNYFP LAPFNQLLQKDIISELLTSDDMKNA YKLHTLDTCLKLDDTVYLRDIALSL POLPRELPSSHTNAKVAEVLSSLLG GEGHFSKDVHLPHNYHIDFEIRMD TNR\NQVLPL/SLDVGTTSAT\DIQRL LTYISFAGLSELKS |
| 3032 | 8529 | A | 3291 | 3 | 485 | LHTLDTCLKLDDTVYLRDIALSLPQ LPRELPSSHTNAKGGQRS*AALLGG EGTPPSKDV\HLAPHNY\HIDFEIQN GTPNRNPSAYPLS\DVDTTSCLOIFK E*LCYVFPRSAAYCLGSSHPRGFLAM KMRHLNAMGFHVILVNNWEDGQT RDGRCQSPFLKT |
| 3033 | 8530 | A | 3292 | 1 | 530 | LRKTFIPNRPLILLPPGNSLATHLFF\ ETVSRVAQAGVQWHHLGLLQSPS PGFKRFSCLSLPSNWDYRHAPPRLA NFYIFS*DGVSFHHVGQAGLKLLTS GDPLTLASQSAGITGVSHCTRPLIHK FGLSYRQRIENVFLLPYTHASSLLQ LLLAPLVTNGQQGEQKPELVREVG |
| 3034 | 8531 | A | 3293 | 115 | 463 | VTKQLFNILSFIFFHTSILIFFFLKME SCSVA\RLCSGT\LAHCNLCPLGSS NSPASASRVSWDYKVCATMPG*FL YF**EQGFHHVGQAGLRTPGPQGD PARPWAPKVLGLQA |
| 3035 | 8532 | A | 3294 | 503 | 1055 | DIDFSPV*LVNVQMRRHALLMNLW DT/QDSHTSLRNAEYCSLMEEDMAP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SNKTTWLRPLTQQF*NLPQKKTLA KK*KDFTHRVLFTA*MCLPQSSSLW HL*NWKQSKCPSVGDWEH*FVQW GTPYQKEE*GTPIDKGQSTYNIMQI YICFFLKQYKDKNLKWLLWRTGVS GGSETEIDSEVISGL |
| 3036 | 8533 | A | 3295 | 3 | 304 | FFLVETEFCHAAQAGVQWCDLGSL QPPPPGLQOSSHLNLPKS*DYRCEPP MPG*FLETGFHPSCPRLVPKLLGSSS PPASAS\QSIGIS\GVSHCPEKPPF |
| 3037 | 8534 | A | 3296 | 324 | 650 | KKEHRVTCFSFWEMESRSVA*AEV Q*HDLDSLQPLPHGLKRVSCSLPSS WDYRHLPPCLTNVCIFSRNGVSLY* PGWSRTPDLVILPALAPQSAGITGG EPPCPATK |
| 3038 | 8535 | A | 3297 | 2 | 564 | FFFFPPQPPSPGFKQFSCLTLPSSWD YRCPPRPANF*FLIETGF/VHVGQA GLELLTSGDLPTPASQNAGITGVRP GTQPASCF*MWQGLIGQNKMTISLL LQSILL |
| 3039 | 8536 | A | 3298 | 352 | 392 | |
| 3040 | 8537 | A | 3299 | 20 | 200 | FTLIQNCFHEIQIEQCGLDAVAHTY NPSTLGGQGG*IA*AQEFETSLGN\M VKPHLSLKF |
| 3041 | 8538 | A | 3300 | 971 | 9082 | |
| 3042 | 8539 | A | 3301 | 1 | 15447 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSIFYSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGSFKVN SCKDHIGKSMNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSRKTSVSQTSLEAKKWLRGIFD GQPERINTADYVGNYLYENNSNSTI AENDKNHLSEKQDTYLSNSSMSNS YSYHSDEVYNDSGYLSKNKLD SGIE PVLKNVEDQKNTSFSKVISNVKDA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVGPPAFRIAS GKIRLCSHETIKKVKDIFTDSFSKVI KENNENKSKICQTKIMAGCYEALD DSEDILHNSLDNDECSMHSKVF DIQSEEILQHNQNMMSGLEKVS KISPCDVSLETS DICKCSIGKLHKS VSSANTCGIFSTASGKSVQVSDASLQ NARQVFSEIEDSTKQVFSKVL FKSNEHSDQLTREENTAIR TPEHLISQKGFSYNV VNSSAFSGFSTASGKQV SILESSLHKVKG VLEEFDLIRTEHSLHYSPTSRQ NVSKILPRVDKRNPEHC VNSEMEKTCSEFEKLSNNLN VEGGSSENNHSIKVSP YLSQFQQDKQQLVLG TKVSLVENIHVLGKEQ ASPKNVKMEIGKTETFS DVPVKTNIEVCSTY SKDSENYFETEAVEIAK AFMEDDELTD SKLPSHATHSLFTCP ENEMVLSNSRIGKRRGEPL ILVGEPSIKRNLLNEFDRIEN QEKSLKASKSTPDGTIKDRRL FMHHVSLEPITCVPFRTT KERQEIQNP NFTA PGQEFLSKSHLYEHLT LEKSSSNLAVSGHPFYQV SATRNEKMRHLITTGRPTKV FVPPFKTKSHFHRVEQCVRNINLEE NRQKQ NIDGHGSDDSKNKINDNEIH QFNKNNSNQAAA VTFTKCEEEPLDLITSLQ NARDIQDMRIKKKQ RQRFVFPQPGSLYLAKTSTLPRISL KAAVGGQVPSACSHKQLYTYG VSKHCIKINSKNAESFQFHTEDY FGKESLWTGKGIQLADGGW LIPSN DGKAGKEEFYRALCDTPG VDPKLISRIWVYNHYRWII WKLAAMECAFPKEFANRCLSPERV LLQLKYRYDTEIDRSRRSAIKKIME RDDTAAKTLVLCVSDIISLSANISET SSNKTSSADTQKVAIIELTDGWYAV KAQLDPPLLA VLKNGRLTVGQKIILHGAELV GSPDACTPLEAPESLMLKISANSTR PARWYTKLGFFPDPRPFPL PLSSLFSDGGNVGCVDVIIQRAYPIQ RMEKTSSGLYIFRNEREEEEKAAKY VEAQQRLEALFTKIQEEFEEHEEN TTKPYLPSRALTRQQVRA LQDGAELEYEAVKNAADPAYLE GYFSEEQLRALNNHRQMLNDKKQA QIQLEIRKAMESAEQKEQGLSRD VTTVWKLRIVSYSKKEKDSVILSI WRPSSDLYSLTEGKRYRIYHLAT SKSKSKSERANMPAGRTV*K*SKKQ KSFYKRRGLGCSMSPSTTFKSGIQ*Y*LSI PEKSFI*S*KCQHSYFNSYFQGC SVKPSHDF*RQRIIQNVRQAQR*QL*I* C*INQKYSHGKESRCMCFK*KL*KR* AVAT*KIHESSITFKKGTINQNTNLR VIQKNQEE TTSISKITVNP DSEELFSDNENNFVQVANERNNLALGNT KELHETDLTCVNEPIFKNSTMVLYGDTGDKQATQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; v=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | <p> VSIKKDLVYVLAEEKNSVKQHIK MTLGQDLKSDISLNIDKIKEKNNDY MNKWAGLLGPISNHSFGGSFRTAS NKEIKLSEHNIKKSKMFFKDIEEQYP TSLACVEIVNTLALDNQKKLSKPQS INTVSAHLQSSVVVSDCKNSHITPQ MLFSKQDFNSNHNLTSPQKAEITEL STILEESGSQFEFTQFRKPSYILQKST FEVPENQMTILKTTSEECRDADLHV IMNAPSIGQVDSSKQFEGTVEIKRKF AGLLKNDCKNSASGYLTDENEVGF RGFYSAHGKTLNVSTEALQKAVKL FSDIENISEETSAEVHPISLSSSKCHD SVVSMFKIENHNDKTVSEKNNKCQ LILQNNIEMTTGTFVEEITENYKRNT ENEDNKYTAASRNSHNLEFDGSDSS KNDTVCIHKDETDLLFTDQHNICKL LSGQFMKEGNTQIKEDLSDLTFLEV AKAQEACHGNTSNKEQLTATKTEQ NIKDFETSDTFFQTASGKNISVAKES FNKIVNFFDQKPEELHNFSNLSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNNDKNLVSIE TVVPPKLLSD NLCRQTENLKTSSIFLKVKVHENV EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMMSGLEKVSJIS PCDVSLETSICKCSIGKLHKSVSSEA NTCGIFSTASGKSVQVSDASLQAR QVFSEIEDSTKQVFSKVLFSNEHS DQLTREENTAIRTPHEHLISQKGSYN VVNSSAFSGFSTASGKQVSILESSLH KVKGVLEEFDLIRTEHSLHYSPTSR QNVSKILPRVDKRNPEHCVNSEME KTCSKEFKLSNNLNVEGGSSENNHS IKVSPYLSQFQQDKQQLVLGTKVSL VENIHVLGKEQASPKNVKMEIGKTE TFSDVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDELTDKLP SH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEP SIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNPNTA PGQEFLSKSHLYEHLTLEKSSS NLA VSGHPFYQVSATRNEKMRHLITTGR </p> |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PTKVFVPPFKTKSHFHRVEQCVRNI NLEENRQKQNIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPSNDBGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRSAIK KIMERDDTAAKTLVLCVSDIISLSA NISSETSSNKTSSADTQKVAIHIELDG WYAVKAQLDPPLAVLKNGRITV GQKIILHGAELVGSPDACTPLEAPES LMLKISANSTRPARWYTKLGFFPDP RPFPLPLSSLFSDGGNVGCVDVIIQR AYPQWMEKTSSGLYIFRNEREEEEK EAAKYVEAQQKRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSDEILFQI YQPREPLHFSKFLDPDFQPSCSEVDL IGFVVSVVKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASN QWRPESKSGLLTLFAGDFS VFSASP KEGHFQETFNKMKNTVENIDILCNE AENKLMHILHANDPKWSTPTKDCT SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKKRRALDF LSRLPLPPPVPICTFVSPAAQKAFQ PPRSCGTTYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSSE DYLRLLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI |
| 3043 | 8540 | A | 3302 | 1 | 2163 | |
| 3044 | 8541 | A | 3303 | 1 | 5771 | |
| 3045 | 8542 | A | 3304 | 1 | 3395 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PORDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRITKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|---|---|--------|-------------------------------------|---|--|--|
| | | | | | | FESGSDKISKEVVPSLACEWSQLTLS GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRK FAGLLKND CNKSASG YLT DENEVGFRGFYSAHG TKLNV TEALQKAVKLFS DIENISEETSAEVH PISLSSSKCHDSVVS MFKIENHNDKT VSEKNNKCQLILQNNIEMTTGT FVE EIT/EM*HAFT*GFC*HSE*RNFTT*P KYVWIGESF*NITL*C*FGNFRYM* M*YREAS*VSLICKYLWDF*HSKW KICPGIRCFITKRKTSVF*NRR*YQA SLFQSIV*K*RTRPAHKRRKYCYT YSRTFNIPKRLFI*CGKFICFLWI*YS KWKASFHFRKFLTQS*GSVRGI*FN QN*A*SSLFTYV*TKCIKNTSSC**E KPRALCKLRNGKNLQ*RI*IHK*LKC *RWFFRK*SLY*SFSISLSISTRQTTV GIRNQSLTC*EHSCFGKRTGFT*KRK NGNW*N*FFF*CS CENKYRSLFYLL QRFRKLL*NRSSRNC*SFYGR**TDR F*TAKSCHTFSFYMSRK*GNGFVKF KNWKKKRRAPYLSGRTL NQKKLIK *I*QDNRKSRKILKGFKKHSRWHNK RSKIVYASCFFRADYLCTLSHN*GT SRD TESKFYRTWSRISV*ISFV*TSDF GKIFKQFSSFR TSILSSFCYKK*KNET LDYYRQTNQSLCSTF*N*IAFSQS*T VC*EY*LGGKQTKAKH*WTWL**** |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | K*D**Q*DSSV*QKQLQSSSSCNFHK V*RRTRFRFNYKSSECCQRYTGYAN*E ETKATRLSTARQSVSCKNIHSASNL SESSRRPSSSLCVFS*TAVYVWRF*T LHKN*QKCRVFSVSH*RLFW*GKF MDWKRNTVG*WWMAHTLQ*WKG WKRRL*GSV*HSRCGSKAYF*NLG L*SL*MDHMETGSYGMCLS*GIC** MPKPRKGASSTKIQI*YGN**KQKIG YKKDNGKG*HSCKNCTSLCF*HNFI ERKYI*NF*Q*N**CRYPKSGHY*TY RWVCC*GPVRSSPLSCLKEWQTD SWSEDYSSWSRTGGLS*CLYTS*SP RISYVKDFC*QYSACSLVYQTWILS* P*TFSSALIIAFQ*WRKCWLC*CNYS KSIPYTVDGEDIWIIHISQ*KRGRKG SSKICGGPTKETRSLIH*NSGGI*RT* RKHNKTIFTITCTNKTASSCFARWC RAL*SSEECRPSLP*GLFQ*RAVKS LE*SQANVE**ETSSDPVGN*EGHGI C*TKGTRFIKGCHNRVEVAYCKLKF KRKRFSYTEYLAHIFSVNRRKEI QNLSSCNFKI*K*I*KS*HTVSSDKK NSVSTTTGFR*NFISDLPATGAPSLQ QIFRSRLSAILF*GGPNRICRFCCEKN RTCPFRLFVRRMLQFTGNKVLDRP* *GHY*ASYVNCKQPPVATRIQIRPS YFICWRFFCVFC*SKRGPLSRDIQON EKYC*EY*HTLQ*SRKQAYAYTAC K*SQVVHPN*RLYFRAVHCSNHSW YRKQASDVFS*L*DILSKSFITLYGQ KEVCFHTCLSPDDFKVL*RGERD*M PIGSKERPTFFEIFKTRCNKADLGPI LNWFEELSSEAPPYNSEPAEESSEHK NNNYEPNLFKTPQRKPSYNQLASTP IIFKEQGLTLPLYQSPVKELDKFKLD LGRNVPSNRHKSRLTVKTKMDQAD DVSCPLLNSCLSESPVVLQCTHVTP QRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLLHISCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF R |
| 3046 | 8543 | A | 3305 | 1 | 5771 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKS YFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEET LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NKNSVKQHIKMTLGQDLKSDISLNI DKIEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRD/C/S/YLMIRKLIEAEDRL*KR *WKGMTQLQKHLFSVFLT*FH*AQI YLKLLAIKLVVQIPKKWPLLNLQM GGMLLRPS*ILPS*LS*RMAD*QLVR RLFFMEQNWWALLMPVHLLKPQN LLC*RFLTTLVGLLAGIPNLDSTLTL DLFLCPYHRFSVMEEMLVVLM*LF KEHTLYSGWRRHHLDYTYFAMKE RKKRKQQNMWRPNKRD*KPYSLK FRRNLKNMKKTQQNHYYHHVH*QD SKFVLCKMVQSFMKQ*RMQQTQLT LRVISVKSS*EP*IITGKC*MIRNKLR SSWKLGRPWNLLNKRNVYQGM QPWGSCVL*AIQKKKKIQLY*VFGV HHQIYILC*QKERDTEFIILQLQNLK VNLKELTYS*QRQKKLSINNYRFQM KFYFRFTSHGSPFTSANF*IQTFSHL VLRWT**DLSFLL*KKQDLPLSSICQ TNVTIYWQ*SFG*TLMRTLSSLIC*L LQATSSGDQNPNAFLLYLLEIFLCF LLVQKRATFKRHSTK*KILLRILTYF AMKQKTSLCIYCMQMIPSGPPQLKT VLQGRITLLKSFLVQETSF*CLLLIVR YIIKVLVYHFVWPKGSLFPHLSQPR*L QSLVKGRKRLMTKRTAKREEPWIS* VDCLYLHLLVPFVHLFLRLHRRHFS HQGVVAPNTKHP*RKKN*ILLR*LH LKNMFKFLFWKVIQ*LTKNLH**IP KLFCLVQQEKNNLYLSVNPLGLLPP VQKIISD*NDVVLHL*SKNRRVPRP VRKNVRKISRTQLQLKNIS |
| 3047 | 8544 | B | 3306 | 16 | 10899 | MPNVLEDEVYETVVDTSEEDSFSLC FSKCRTKNLQKVRTSKTRKKIFHEA NADECEKSKNQVKEKYSFVSEVEP NDTDPLDSNVANQKPFESGSDKISK EVVPSLACEWSQLTSLGLNGAQME KIPLHHISSCDQNISEKDLLDTENKR KKDFLTSENSLPRISSLPKSEKPLNE ETVVNKRDEEQHLESHTDCILAVK QAISGTSPVASSFQGIKKSIFRIRES KETFNASFSGHMTDPNFKKETEASE SGLEIHTVCSQKEDSLCPNLIDNGS WPATTTQNSVALKNAGLISTLKKK TNKFIYAIHDETSYKGKKIPKDQKS ELINCSAQFEANAFEAPLTFANADS GLLHSSVKRSCSQNDSEPTLSLTSS FGITLRKCSRNETCSNNTVISQDLDY KEAKCNKEKLQLFITPEADSLSCLQ EGQCENDPKSKKVSDIKEEVLA CHPVQHSKVEYSDTDFQSQKSLLY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DHENASTLILTPTSKDVLSNLVMISR GKESYKMSDKLKGNNYESDVELTK NIPMEKNQDVCALNENYKNVELLP PEKYMVRVASPSRKVQFNQNTNLRV IQKNQEETTSISKITVNPDSSEELFSDN ENNFVFQVANERNNLALGNTKELH ETDLTCVNEPIFKNSTMVLYGDTGD KQATQVSIKKDLVYVLAEEKNSV KQHIKMTLGQDLKSDISLNIDKIPEK NNDYMNKWAGLLGPISNHSFGGSF RTASNKEIKLSEHNIKKSKMFFKDIE EQYPTSLACVEIVNTLALDNQKKLS KPQSINTVSAHLQSSVVVSDCKNSH ITPQMLFSKQDFNSNHNLTSPQKEQI TELSTILEDGSGQFEFTQFRKPSYILQ KSTFEVPENQMTILKTTSEECRADAD LHVIMNAPSIGQVDSSKQFEGTVEI KRKFAGLLKNDCKNSASGYLTDEN EVGFRGFYSAHGTKLNVSTEALQK AVKLFSDIENISEETSAEVHPISLSSS KCHDSVVSMMFKIENHNDKTVSEKN NKCQLILQNNIEMTTGTFVEEITENY KRNTENEDNKYTAASRNSHNLEFD GSDSSKNDTVCIHKDETDLFTDQH NICLKLSGQFMKEGNTQIKEDLSDL TFLEVAKAQEAHGNTSNKEQLTA TKTEQNIKDFETSDTFFQTASGKNIS VAKESFNKIVNFFDQKPEELHNFSL NSELHSDIRKNKMDILSYEETDIVK HKILKESVPVGTGNQLVTFQGQPER DEKIKEPTLLGFHTASGKKVKIAKE SLDKVKNLFDERARTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFTYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEET LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSSE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKEQITELSTILEDSSGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCNKSASG YLTDENEVGFRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVSMMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDLL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEAHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDERASHQWAK TLKYREACKDLELACETIEITAAPK CKEMQNSLNNDKNLVSIE TVVPPKL LSDNLCRQTENLKTSSIFLKVKVH ENVEKETAKSPATCYTNQSPYSVIE NSALAFYTSCSRKTSVSQTSLEAK KWLREGIFDGQPERINTADYVGNV LYENNSNSTIAENDKNHLSEKQDTY LSNSSMSNSYSYHSDEVYNDSGYLS KNKLDSGIEPVLKNVEDQKNTSFSK VISNVKDANAYPQTVNEDICVEELV TSSSPCKNKNAAIKLSISNSNNFEVG PPAFRIASGKIVCVSHETIKKVKDIF TDSFSKVIKENNENKSKICQTKIMA GCYEALDDSEDILHNSLDNDECSTH SHKVFADIQSEEILQHNQNMGLEK VSKISPCDVSLSDICKCSIGKLHK SVSSANTCGIFSTASGKSVQVSDAS LQNAARQVFSEIEDSTKQVFSKVLFK SNEHSDQLTREENTAIRTPEHLISQK GFSYNVVNSSAFSGFSTASGKQVSI LESSLHKVKGVL EFDLIRTEHSLH YSPTSRQNVSKILPRVDKRNPEHCV NSEMEKTCSEFKLSNNLNVEGGSS ENNHSIKVSPYLSQFQQDKQQLVLG TKVSLVENIHVLGKEQASPKNVKM EIGKTETFS DVPVKTNIEVCSTYSKD SENYFETEA VEIAKAFMEDDEL TDS KLPSHATHSLFTCPENEEMVLSNSRI GKRRGEPLILVGEP SIKRNLLNEFDR IENQEKSLKASKSTPDGTIKDRRLF VHHVSLEPITCVPFRTTKERQEIQNP NFTAPGQEF LSKSHLYEHL TLEKSSS NLAVSGHPFYQVSGNKNGKMRKLI TTGRPTKVFPVPPFKTKSHFHRVEQC VRNINLEGNRQKQNIDGHGSDDSK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; v=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NKINDNEIHQFNKNNSNQAAA VTFT KCEEEPLDLITSLQNARDIQDMRIK KKQRQRFVPQPGSLYLAKTSTLPRI SLKAAVGGQVPSACSHKQLYTYGV SKHCIKINSKNAESFQFHTEDYFX* |
| 3048 | 8545 | A | 3307 | 1 | 12500 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSTVLIVRNEEASETVFPHDTTAN VKSIFYSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGSFKVN SCKDHIGKSMPHVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVP SLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNG/K/TVMS**MPHRLVR*TAA SNLKVQLKLNGSLLAC*KMTVTKV LLVI*QMKMKWGLGAFILLMAQN* MFLCLKCKKL*NCLVILRILVRKLL QRYIQ*VYLQVNVMMILLFQCLR*KII MIKL*VKKIINAN*YKILK*LLALL LKKLLKITREILKMKITNILLPVEILI T*NLMAVIQVKMILFVFIKMKRTCY LLISTTYVLNYLASL*RRETLRLKKI CQI*LFWKLRLKKHVMVILQIKNS *LLKRSKI*KILRLLIHFFRLQVGKI LVSPKSHLIK*ISLIRNQKNCITFP*I LNYILT*ERTKWTF*VMRKQT*LNT KY*KKVSQLVLEIN**PSRDNPVNM KRSKNLLCWVFIQLAGKKLKLQRN LWTK*KTFLMKKSKVLVKSPVLAI NGQRP*STERPVKTLN*HVRPLRSQ LPQSVKKCRILSIMIKTLFLLRLWCH LSS*VIIYVDKLIKISKHQKVSF*KLK YMKM*KKKQOKVLQLVTQISPLIQS LKIQP*LFTQVVVEKLL*VRLHYLK QKNGLEKEYLMVNQKE*ILQIM*EII CMKIIQTVL*LKMTKIISPKNKILI*V TVACLTAPIITLMRYIMIQDISQKINL ILVLSQY*RMLKIKKTLVFPK*YPM* KMQMHTHKL*MKIFALRNL*LALH PAKIKMQPLNCPYLIVILR*GHLHL G*PVVKSFVFHMKQLKK*KTYLQT VSVK*LRKTTRINQKFAKRKLWQV VTRHWMIQRIFFITL*IMMNVARIHI RFLLTFRVKKFYNITKICLDWRKFL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KYHLVMLVWKLQIYVNVV*GSFIS QSHLQILVGFLAQQVENLSRYQML HYKTQDKCFLK*KIVPSKSFPKYCL KVTNIQTSSQEKKILLYVLQNI*YPK KAFHIMW*IHLLSLDLVQQVESKFP F*KVPYTKLREC*RNLI*SELSIVFTI HLRLDKMYQKYFLVLIRETQSTV*T QKWKKPAVKNLNYQIT*MLKVVL QKIITLLKFLHISLNFNKTNNSWY*E PKSHLLRTFMFWEKNRLHLKT*KW KLVKLKFLMFL*KQI*KFVLLTPKI QKTTLKQKQ*KLLKLLWKMMN*QI LNCQVMPHILFLHVPKMRKWFCQI QELEKEEESPLS*WENPQSKETY*M NLTG**KIKKNP*RLQKALQMAQ*K IEDCLCIMFL*SRLPVYPFAQLRNVK RYRIQILPHLVKNFCLNLICMNI*LW KNLQAI*QFQDIHFIKFLQEMKK*D T*LLQADQPKSLFHLLKLNRIFTLN SVLGILTWRKTDKSKTLMMDALMI VKIRLMTMRFISLTKTTPIKQQL*LS QSVKKNL*I*LQVFRMPEIYRICELR RNKGNASFHSQAVCILPATTTQNSV ALKNAGLISTLKKKTNKFYAIHDE TSYKGKKIPKDQKSELINCSAQFEA NAFEAPLTFANADSGLLHSSVKRSC SQNDSEPTLSLTSSFGTILRKCSR ETCSNNTVISQDLDYKEAKCNKEKL QLFITPEADSLSCLQEGQCENDPKS KKVSDIKEEVLAACHPVQHSKVE YSDTDFQSQSLLYDHENASTLILT PTSKDVLNLVMISRGKESYKMSD KLKGNNYESDVELTKNIPMEKNQD VCALNENYKNVELLPPEKYMRRVAS PSRKVQFNQNTNLRVIQKNQEETTS ISKITVNPDSSEELFSDNENNFVFQVA NERNNLALGNTKELHETDLTCVNE PIFKNSTMVLYGDTGDKQATQVSIK KDLVYVLAENKNSVKQHIKMTLG QDLKSDISLNIDKIPEKNNDYMDKW AGLLGPISNHSFGGSFRTASNKEIKL SEHNIKKSKMFFKDIEEQYPTSLAC VEIVNTLALDNQKKLSKPQSINTVS AHLQSSVVVSDCKNSHITPQMLFSK QDFNSNHNLTSPQKAEITELSTILEE SGSQFEFTQFRKPSYILQKSTFEVPE NQMTILKTTSEECRDADLHVIMNAP SIGQVDSSKQFEGTVEIKRKFAGLL KNDCKNSASGYLTDENEVGFRGFY SAHGTKLNVSTEALQKAVKLFSKIE NISEETSAEVHPISLSSSKCHDSVVS MFKIENHNDKTVSEKNKNCQLILQ NNIEMTTGTTFVEEITENYKRNTENE DNKYTAASRNSHNLEFDGSDSSKN DTVCIHKDETDLLFTDQHNLCKLS GQFMKEGNTQIKEDLSDLTFLEVAK AQEACHGNTSNKEQLTATKTEQNI KDFETSDTFFQTASGKNISVAKESF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNNDKNLVSIVTVVPPKLLSD NLCRQTENLKTSKSIFLKVKVHENV EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDGKNIHSASN LSESSSRPSSLCVFS*TA VYVWRF* TLHKN*QQKCRVFSVS/TLKIILVRK VYGLEKEYSWLMVDGSYPMMER LEKKNFIGLCVTLQVWIQSLFLEFGF IITIDGSYGNWQLWNVPFLRNLLID A*AQKGCFFN*NTDMIRKLIEAEDR L*KR*WKGMTQLQKHLFSVFLT*FH *AQIYLKLLAIKL VVQIPKKWPLL LQMGGMLLRPS*ILPS*LS*RMAD* QLVRRLLFFMEQNWWALLMPVHLL KPQNLLC*RFLTTLVGLLAGIPNLDS FLTLDLFLCPYHRFSVMEEMLVVL M*LFKEHTLYSGWRRHLDYTYFA MKERKKRKQQNMWRPNKRD*KPY SLKFRRNLKNMKKTQQNHIYHHVH *QDSKFVLCKMVQSFMKQ*RMQQT QLTRVISVKSS*EP*IITGKC*MIRN KLRSSWKLGRPWNLLNKRNVYQ GMSQPWGSCVL*AIQKKKKIQLY*V FGVHHQIYILC*QKERDTEFIILQLQ NLKVNLIKELTYS*QRQKKLSINNYR FQMKFYFRFTSHGSPFTSANF*IQTF SHLVLRWT**DLSFLL*KKQDLPLSS ICQTNVTIYWQ*SFG*TLMRTL LSLI C*LLQATSSGDQNPNAFLLYLLEIF LCFLLVOKRATFKRHSTK*KILLRIL TYFAMKQKTSLCIYCMQMIPSGPPQ LKTVLQGRITLLKSFLVQETSF*CLLL IVRYIHKVLYHFVWPKGSLFPHLSQP R*LQSLVKGRKRLMTKRTAKREEP WIS*VDCLYLHLLVPFVHLFLRLHR RHFSHQGVVAPNTKHP*RKKN*ILL R*LHLKNSMKFLFWKVIQ*LTKNLH **IPKLFCLVQQEKNLYLSVNPLGL LPPVQKIISD*NDVVLHL*SKNRRVP RPVRKNVRKISRTOQLQLKNIS |
| 3049 | 8546 | A | 3308 | 1 | 9344 | |
| 3050 | 8547 | A | 3309 | 1 | 18345 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESHE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMNPVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDTDLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSOK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSSE LFSNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEGFRGFYSAHGTLKNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVSFMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFVE EITDACRKDSVKMIQKAKKFQI*KK RSWLQHVTQYNIQKWNTVILTFNP RKVFYMMKMPALLF*LLLPRMFC QT*S*FLEAKNHTKCQTSSKVTIMN LMLN*PKIFPWKRIKMYVL*MKIHK TLSCCHLKNT*E*HHLQERYNSTKT QI*E*SKKIKKKLLQFQK*LSIQTLL NFSQTMRIILSSK*LMKGILL*EILR |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | NFMKQT*LV*TNPFSRTLPPWFYMET QVINKQPKCQLKKIWMFLQRRTKI V*SSI*K*L*VKI*NRTSP*I*IKYQKK IMIT*TNGQDS*VQFQITVLEVASEQ LQIRKSSSLNITLRRACSSKILKNNI LLV*LVLKL*IPWH*IKRN*ASLSQL ILYLHIYRVV*LFLIVKIVI*PLRCYFP SRILIQTH*HLAKRQKLQNFLLY*KN QEVSLNLLSLENQATYCRRVHLKC LKTR*LS*RPLLRNAEMLIFMS**MP HRLVR*TAASNLKVQLKLNGSLLA C*KMTVTKVLLVI*QMKMKWGLG AFILLMAQN*MFLCLKCKKL*NCLV ILRILVRKLLQRYIQ*VYLQVNVML LFQCLR*KIIMIKL*VKKIINAN*YYK IILK*LLALLLKKLLKITREILKMKIT NILLPVEILIT*NLMAVIQVKMILFVF IKMKRTCYLLISTTYVLNYLASL*R RETLRLKKICQI*LFWKLRKLKKHV MVILQIKNS*LLKRSKI*KILRLLIH FFRLQVGKILVSPKSHLIK*ISLIRN QKNCITFP*ILNYILT*ERTKWTF*V MRKQT*LNTKY*KKVSQVLVEIN** PSRDNPVMKRSKNLLCWVFIQLA GKKLKLQRNLWTK*KTFMLMKSKV LVKSPVLAINGQRP*STERPVKTLN* HVRPLRSQLPQSVKKCRILSIMIKTL FLLRLWCHLSS*VIYVDKLIKSKHQ KVSF*KLKYMKM*KKKQQKVLQL VTQISPLIQSLKIQP*LFTQVVVEKLL *VRLHYLKQKNGLEKEYLMVNQKE *ILQIM*EIIICMKIIQTVL*LKMTKIIS PKNKILI*VTVACLTAPIILMRYIMI QDISQKINLILVLSQY*RMLKIKKTL VFPK*YPM*KMQMHTKL*MKIFA LRNL*LALHPAKIKMQPLNCPYLIVI ILR*GHLHLG*PVVKSFFVHMKQLK K*KTYLQTVSVK*LRKTTRINQKFA KRKLWQVVTRHWMIQRIFFITL*IM MNVARIHIFLLTFRVKKFYNTTKIC LDWRKFLKYHLVMLVWKLQIYVN VV*GSFISQSHLQILVGFLAQQVENL SRYQMLHYKTQDKCFLK*KIVPSKS FPKYCLKVTNIQTSSQEKKILLYVL QNI*YPKKAFFHIMW*IHLSDLKL QEKY*K*R*QIYCCQ*KFS*LRI*WQ *FK*K*YCLYS*R*NGLAIFY*SAQHM S*IIWPVYEGGKHS*RRFVRFNFFG SCSSRSMSW*YFK*RTVNCY*NGA KYKRF*DF*YIFSDCKWEKY*CRQR VI**NCKFL*SETRRIA*LFLKF*ITF* HKKEQNGHSL*GNRHS*TQNLKE SVPVGTGNQLVTFQGQPERDEKIKE PTLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNNDKNLVSIVTVPPKLLSD NLCRQTENLKTSSIFLVKVHENV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFEVGPAPF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMGLEKVSKIS PCDVSLETSDICKCSIGKLHKSVS NTCGIFSTASGKSVQVSDASLQAR QVFSEIEDSTKQVFSKVLFSNEHS DQLTREENTAIRTPEHLISQKGF SYNVVNSSAFSGFSTASGKQVSILE SLHKVKGVLEEFDLIRTEHSLHYSPT SRQNVSKILPRVDKRNPEHCVNSEME KTCSKEFKLSNNLNVEGGSENHNH SIKVSPYLSQFQQDKQQLVLGTVSL LVENIHVLGKEQASPKNVKMEIGKTE ETFS DVPVKTNIEVCSTYSKDS ENYFETEAVEIAKAFMEDDELTD SKLPSHATHSLFTCPENEEMVLS NSRIGKRRGEPLILVGEP SIKRNLLNEFDRIENQEKSL KASKSTPDGTIKDRRLFMH HVVSLEPITCVPFRTTKERQ EIQNPNTAPGQEF LSKSHLYEHLTLEKSS SNLAVSGHPFYQVSAT RNEKMRHLITTPTKV FVPPFKTKSHFHRVEQ CVRNINLEENRQKQ NIDGHGSDDSKNKIN DNEIHQFNKNNSNQ AAAVTFTKCEEPLDLIT SLQNARDIQDMRIKKK QRORVFPQPGSLYLAK TSTLPRISLKA AVGGQVPSACSHKQ LYTYGVSKHC IKINSKNAESFQFHT EDYFGKESLW TGKGIQLADGGW LIPSNKGAGKE EFYRALCDTPGVD PKLISRIWVYNH YRWIWKLAAMECA FPKEFANRCL SPERVLLQLKYRST ASGKQVSILESS LHKVKGVLEEFDL IRTEHSLHYSPT SRQNVSKILPRVD KRNPEHCVNSEME KTCSKEFKLSNNL NVEGGSENHNH SIKVSPYLSQFQQD KQQLVLGTVSL LVENIHVLGKEQAS PKNVKMEIGKTE ETFS DVPVKTNIEVCST YSKDS ENYFETEAVEIAKAF MEDDELTD SKLPSHATHSLFTCP ENEEMVLSNSRIG KRRGEPLILVGEP SIKRNLLNEFDRI ENQEKSLKASKST PDGTIKDRRLFMH HVVSLEPITCVPF RTTKERQ EIQNPNTAPGQEF LSKSHLYEHLTLE KSSSNLAVSGHPFY QVSAT RNEKMRHLITTP TKV FVPPFKTKSHFHR VEQCVRNINLEEN RQKQ NIDGHGSDDSKNK INDNEIHQFNKNNS NQAAAVTFTKCEE EPLDLITSLQNARD IQDMRIKKK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QRQRFVPQPGSLYLAKTSTLPRISLK AAVGGQVPSACSHKQLYTYGVSKH CIKINSKNAESFQFHTEDYFGKESL WTGKGIQLADGGWLIPSNDGKAGK EEFYRALCDTPGVDPKLISRIWVYN HYRWIIWKLAAMECAFPKEFANRC LSPERVLLQLKYRYDTEIDRSRRSAI KKIMERDDTAAKTLVLCVSDIISLS ANISETSSNKTSSADTQKVAIETD GWYAVKAQLDPPLAVLKNGRLT VGQKIILHGAELVGSPDACTPLEAP ESLMLKISANSTRPARWYTKLGFFP DPRPFPLPLSSLFSDGGNVGCVDVII QRAYPIQWMEKTSSGLYIFRNEREE EKEAAKYVEAQQRLEALFTKIQEE FEEHEENTTKPYLPSRALTRQQVRA LQDGAELYEAVKNAADPAYLEGYF SEEQLRALNNHRQMLNDKKQAQIQ LEIRKAMESAEQKEQGLSRDVTTV WKLRIVSYSKKEKDSVILSIWRPSSD LYSLLTEGKRYRIYHLATSKSKSKS ERANIQLAATKKTQYQQLPVSDEIL FQIYQPREPLHFSKFLDPDFQPSCE VDLIGFVVS VVKKTGLAPFVYLSDE CYNLLAIKFWIDLNEDIKPHMLIAA SNLQWRPESKSGLLTLFAGDFS VFS ASPKEGHFQETFNKMKNVTENIDIL CNEAENKLMHILHANDPKWSTPTK DCTSGPYTAQIIPGTGNKLLMSSPN CEIYYQSPLSLCMAKRKSVSTPVSA QMTSKSCKGEKEIDDQKNCKKRRRA LDFLSRLPLPPPVSPICTFVSPAAQK AFQPPRSCGTYETPIKKKELNSPQ MTPFKKFNEISLLESNSIADEELALI NTQALLSGSTGEKQFISVSESTRTAP TSEEDYLRLKRRCTTSLIKEQESSQA STEECEKNKQDTITTKKYI |
| 3051 | 8548 | A | 3310 | 1 | 7988 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESLH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETFYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFS DNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRK FAGLLKND CNKSASG YLT DENEVGFRGFYSAHG TKLNVS TEALQKAVKLFSDIENISEETS AEVH PISLSSSKCHDSVVS MFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDLL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEA CHGNTSNK EQLTATKTEQNIKDFETS DTFQTAS GKNISVAKELFNKIVNFFDQKPEEL HNFSLSNELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNLVSI ETVVPKLLSDNLCRQTENLKTSKSI FLKVKVHENVEKETAKSPATCYTN QSPYSVIENSALAFYTSCS*KSQNIK KYL FES*ST*KCRKRNSKKSCNLLH KSVPLFSH*KFSLSFLHKL*WKTSVS QTSLL EAKKWLREGIFDGQPERINT ADYVGNYLYENNSNSTIAENDKNH LSEKQD TYLSNSSMSNSYSYHSDEV YNDSGYLSKNKLD SGIEPVLKNVED QKNTSFSKVISNVKDANAYPQTVN EDICVEELVTSSSPCKKNKNAAIKLSI SNSNNFEVGPFAFRIASGKIVCVSHE TIKKVKDIFTDSFSKVIKENNENKSK ICQTKIMAGCYEALDDSEDILHNSL DNDECSTHSHKVFADIQSEEILQHN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QNMSGLEKVSISKISPCDVSLETSIDC KCSIGKLHKS SVSSANTCGIFSTASGK SVQVSDASLQNA RQVFSEIEDSTKQ VFSKVLFSNEHSDQLTREENTAIR TPEHLISQKGF SYN VVNSSAFSGFST ASGKQVSILESSLHKVKG VLEEFDLI RTEHSLHYSPTS RQNVSKILPRVDK RNPEHC VNSEMEKTCSKEFKLSNNL NVEGGSSENNHSIKVSPYLSQFQQD KQQLVLG TKVSLVENIHVLGKEQA SPKNVKMEIGKTETFS DVPVKTNIE VCSTYSK DSENYFETEAVEIAKAFM EDELTD SKLPSHATHSLFTCPENE EMVLSNSRIGKRRGEPLILVGEPSIK RNLLNEFDRIENQE KSLKASKSTPD GTIKDRRLFVHHVSLEPITCVPFRTT KERQEIQNP NFTA PGQEFLSKSHLY EHLTLEKSSSNLAVSGHPFYQVSGN KNGKMRKLITTGRPTKVFPVPPFKTK SHFHRVEQCVRNINLEGNRQKQNI GHGSDDSKNKINDNEIHQFNKNS NQAAAVTFTKCEEEPLDLITSLQNA RDIQDMRIKKKQRQRVFPQPGSLYL AKTSTLPRISLKA AVGGQVPSACSH KQLYTYGVSKHC IKINSKNAESFQF HTEDYFGKESLWTGKGIQLADGGW LIPSNDGKAGKEEFYRALCDVKAT |
| 3052 | 8549 | A | 3311 | 1 | 14305 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPYQSPVKELDKFKL DLGRNV PNSRHKSLRTVTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGA EVD PDM SWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTS GNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCR TKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPN DTDPLDSNVAHQKP FESGSDKISKEV VPSLACEWSQLTLS GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSEN SLPRISL PKSEKPLNEETV VNKRD EEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETFYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCS QNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | <p> MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDS LFSDNENN FVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRK FAGLLKND CNKSASG YLT DENEVGFRGFYSAHG TKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVS MFKIENHNDKT VSEKNNKCQLILQNNIEMTTGT FVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDLL FTDQHNI CLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNLVSI ETVVPKLLSDNLCRQTENLKT SKSI FLKVKVHENV EKETA KSPATCYTN QSPYSVIENSALAFYTCSRKTSVSQ TSLLEAKKW LREGIFDGQPERINTA DYVGNYLYENNSNSTIAENDKNHL SEKQDTYLSNSSMSNSYSYHSDEVY NDSGYLSKNKLD SGIEPVLKNVEDQ KNTSFSKVISNVKDANAYPQTVNE DICVEELVTSSSPCKNKNAAIKLSIS NSNNFEVGPPAFRIASGKIVCVSHET IKKVKDIFTDSFSKVIKENNENKSKI CQTKIMAGCYEALDDSEDILHNSLD NDECSTHSHKVFADIQSEEILQHNQ NMSGLEKVSKISPCDVSLETS DICKC SIGKLHKS VSSANTCGIFSTASGKSV QVSDASLQNA RQVFSEIEDSTKQVF SKVL FKSNEHSDQLTREENTAIRTPE HLISQKGFSYNVVNSSAFSGFSTAS GKQVSILESSLHKVKG VLEEDLIRT EHS LHYSPTS RQNVSKILPRVDKRN PEHCVNSEMEKTC SKEFKLSNNLN VEGGSEN NHSIKVSPYLSQFQQDK QQLVLGTVSLVENIHVLGKEQASP KNVKMEIGKTETFS DVPVKTNIEVC STYSK DSENYFETEAVEIAKAFMED </p> |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DELTDSKLPSHATHSLFTCPENEEM VLSNSRIGKRRGEPLILVGEPSIKRN LLNEFDRIENQEKSLKASKSTPDGT IKDRRLFMHHVSLEPITCVPFRTTKE RQEIQNPNTAPGQEFLSKSHLYEH LTLEKSSSNLAVSGHPFYQVSATRN EKMRHLITTGRPTKVFVPPFKTKSH FHRVEQCVRNINLEENRQKQNIIDGH GSDDSKNKINDNEIHQFNKNNSNQ AAAVTFTKCEEEPLDLITSLQNARDI QDMRIKKKQRQRFVPPQPSLYLAK TSTLPRISLKAAVGGQVPSACSHKQ LYTYGVSKHCIKNSKNAESFQFH/T *RLFW*GKFMDWKRNTVG*WWM AHTLQ*WKGWKRRIL*GSV*HSRC GSKAYF*NLGL*SL*MDHMETGSY GMCLS*GIC**MPKPRKGASSTKIQI *YGN**KQKITNILLPVEILIT*NLMA VIQVKMILFVFIKMKRTCYLLISTTY VLNYLASL*RRETLRLKKICQI*LFW KLRKLKKHVMVILQIKNS*LLLKRS KJ*KILRLLIHFFRLQVGKILVSPKSH LIKL*ISLIRNQKNCITFP*ILNYILT*E RTKWTF*VMRKQT*LNTKY*KKVS QLVLEIN**PSRDNPVMKRSKNLL CWVFIQLAGKKLKLQRNLWTK*KT FLMKKS KVLVKSPVLAINGQRP*ST ERPVKTLN*HVRPLRSQLPQSVKKC RILSIMIKTLFLLRLWCHLSS*VIYV DKLKISKHQKVSF*KLKYMKM*KK KQQKVLQLVTQISPLIQSLKIQP*LF TQVVVEKLL*VRLHYLKQKNGLEK EYLMVNQKE*ILQIM*EIIICMKIIQT VL*LKMTKIISPKNKILI*VTVACLT AIPTILMRYIMIQDISQKINLILVLSQ Y*RMLKIKKTLVFPK*YPM*KMQM HTHKL*MKIFALRNL*LALHPAKIK MQPLNCPYLIVILR*GHLHLG*PVV KSFVFMKQLKK*KTYLQTVSVK* LRKTTRINQKFAKRKLWQVVTRHW MIQRIFITL*IMMNVARIHIFLLTF RVKKFYNTKICLDWRKFLKYHLV MLVWKLQIYVNVV*GSFISQSHLQI LVGFLAQQVENLSRYQMLHYKTQD KCFLK*KIVPSKSFPKYCLKVTNIQT SSQEKKILLYVLQNI*YPKKAFFHM W*IHLISLDLVQQVESKFPF*KVPY TKLREC*RNLI*FRTEHSLHYSPTF*T KMYQKYFLVLIRETQSTV*TPEMEK TCSKEFKLSNNLNVEGGSSENNHSI KVSPYLSQFQQDKQQLVLGTKVSL VENIHVLGKEQASPKNVKMEIGKTE TFSVDPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDELTDKSLPSH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPSIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNPNTA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVFPFPFKTKSHFHRVEQCVRNI NLEENRQKQNIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEYFGKESLW TGKGIQLADGGWLIPSNDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRAIK KIMERDDTAAKTLVLCVSDIISLSA NISETSSNKTSSADTQKVAIHELTDG WYAVKAQLDPPLLA VLKNGRLTV GQKIILHGAELVGSPDACTPLEAPES LMLKISANSTRPARWYTKLGFFPD RPFPLPLSSLFSDGGNVGCVDVIIQR AYPIQWMEKTSSGLYIFRNEREEEEK EAAKYVEAQQRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRA LQDGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSDEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFS VFSASP KEGHFQETFNKMKNNTVENIDILCNE AENKLMHILHANDPKWSTPTKDCT SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKKRRALDF LSRLPLPPPVSPICTFVSPAAQKAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSSE DYRLRLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTTKKYI |
| 3053 | 8550 | A | 3312 | 11089 | 17637 | NHCHRFHLEWMPWCGCRSPSGPRH VNQKPEELHNFSLNSELHSDIRKNK MDILSYEETDIVKHKILKESVPVGT GNQLVTFQGQPERDEKIKEPTLLGF HTASGKKVKIAKESLDKVKNLDFE KEQGTSEITSFSHQWAKTLKYREAC KDLELACETIEITAAPKCKEMQNSL NNDKNLVS IETVVPKLLSDNLCRQ TENLKTSSIFLKVKVHENVEKETA KSPATCYTNQSPYSVIENSALAFYTS CSRKTSVSQTSLEAKKWLREGIFD GOPERINTADYVGNYLYENNSNSTI AENDKNHLSEKQD TYLSNSSMSNS YSYHSDEVYNDSGYLSKNKLD SGIE PVLKNVEDQKNTSFSKVISNVKDA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; Δ=possible nucleotide deletion; ∇=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVSDEILFQIY QPREPLHFSKFLDPDFQSPCSEVDLI GFVVSVVKKTVRNEEASETVFPHD TTANVKSYSNHNDESLLKKNDRFIAS VTDSSENTNQREAASHGFGKTSNGSF KVNSCKDHIGKSMNVLEDEVYET VVDTSSEDSFSLCFSKCRTKNLQKV RTSKTRKKIFHEANADECEKSKNQV KEKYSFVSEVEPNDDPLDSNVAH QKPFESGSDKISKEVVP SLACEWSQ LTL SGLNGAQMEKIPLLHSSCDQNI SEKDLLDTENKRKKDFLTSENSLPRI \SSLPNPEEPLNEETVVNKRDEEQHL DSHTDCILQ*KQAISGTFPVASSFQG IKKSIFRIRESPKETFNASFSGHMTDP NFKKETEASESGLEIHTVCSQKEDS LCPNLIDNGSWPATTTQNSVALKN AGLISTLKKKTNKFIYAIHDETSYKG KKIPKDQKSELINCSAQFEANAFEA PLTFANADSGLLHSSVKRSCSQNDS EEPTLSLTSSFGTILRKCSRNETCSN NTVISQDL DYKEAKCNKEKLQLFIT PEADSLSCLQEGQCENDPKSKKVSD IKEEVLAACHPVQHSHKVEYSDDTF QSQKSLLYDHENASTLILTPTSKDV LSNLVMISRGKESYKMSDKLKGNN YESDVELTKNIPMEKNQDVCALNE NYKNVELLPPEKYM RVASPSRKVQ FNQNTNLRVIQKNQEETTSISKITVN PDSEELFSDNENNFFVFQVANERNNL ALGNTKELHETDLTCVNEPIFKNST MVLYGDTGDKQATQVSIKKDLVY VLAENKNSVKQHIKMTLGQDLKS DISLNIDKIEKNNDYMNKWAGLL GPISNHSFGGSFRTASNKEIKLSEHN IKKSKMFFKDIEEQYPTSLACVEIVN TLALDNQKKLSKPQSINTVSAHLQS SVVVSDCKNSHITPQMLFSKQDFNS NHNLTPSQKAEITELSTILEESGSQF EFTQFRKPSYILQKSTFEVPENQMTI LKTTSEECRDADLHVIMNAPSIGQV DSSKQFEGTVEIKRKFAGLLKNDCN KSASGYLTDENEVGFRGFYSAHGT KLVNSTEALQKAVKLFSDIENISEET SAEVHPISLSSSKCHDSVVSMFKIEN HNDKTVSEKNNKCQLILQNNIEMTT GTFVEEITENYKRNTENEDNKYTAA SRNSHNLEFDGSDSSKNDTVCIHKD ETDLLFTDQHNICLKLSGQFMKEGN TQIKEDLSDLTFLEVAKAQEAHGN TSNKEQLTATKTEQNIKDFETSDTFF QTASGKNISVAKESFNKIVNFFDQK PEELHNFSLNSELHSDIRKNKMDILS YEETDIVKHILKESVPVGTGNQLV TFQGGQPERDEKIKEPTLLGFHTASG KKVKIAKESLDKVKNLFDEKEQGT SEITSFSHQWAKTLKYREACKDLEL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | ACETIEITAAPKCKEMQNSLNNDKN LVSIE TVVPPKLLSDNLCRQTENLK TSKSIFLKVKVHENVEKETAKSPAT CYTNQSPYSVIENSALAFYTSCSRK TSVSQTSLLLEAKKWLREGIFDGQPE RINTADYVGNYLYENNSNSTIAEND KNHLSEKQDTYLSNSSMSNSYSYHS DEVYND SGYLSKNKLD SGIEPVLKN VEDQKNTSFSKVISNVKDANAYPQ TVNEDICVEELVTSSSPCKNKNAAI KLSISNSNNFEVGPPAFRIASGKIVC VSHETIKKVKDIFTDSFSKVIKENNE NKSKICQTKIMAGCYEALDDSEDIL HNSLDNDECSTHSHKVFADIQSEEIL QHNQNM SGLKVKISPCDVSLETS DICKCSIGKLHKS SVSSANTCGIFSTA SGKSVQVSDASLQNA RQVFSEIEDS TKQVFSKVLFSNEHSDQLTREENT AIRTPHEHLISQKGF SYN VNSSAFSG FSTASGKQVSILESSLHKVKG VLEEF DLIRTEHSLHYSPTS RQNVSKILPRV DKRNPEHCVNSEMEKTC SKEFKLS NNLNVEGGSSENNHSIKVSPYLSQF QQDKQQLVLGTVSLVENIHVLGK EQASPKNVKMEIGKTETFS DVPVKT NIEVCSTYSKDS ENYFETEAVEIAK AFMEDDEL TDSKLPSHATHSLFTCP ENEEMVLSNSRIGKRRGEPLILVGEP SIKRNLLNEFDRIENQE KSLKASKS TPDGTIKDRRLFMHHSLEPITCVPF RTTKERQEIQNP NFTA PGQEFLSKS HLYEHLTLEKSSSNLA VSGHPFYQV SATRNEKMRHLITTGRPTKVFPVPF KTKSHFHRVEQCVRNINLEENRQK QNIDGHGSDDSKNKINDNEIHQFNK NNSNQAAA VTFTKCEEEPLDLITSL QNARDIQDMRIKKKQRQRF PQPG SLYLAKTSTLPRISLKA AVGGQVPS ACSHKQLYTYGVSKHC IKINSKNAE SFQFHTEDYFGKESLWTGKGIQLAD GGWLIPSNDGKAGKEEFYRALCDT PGVDPKLISRIWVYNHYRWIIWKLA AMECAFPKEFANRCLSPERVLLQLK YRYDTEIDRSRRSAIKKIMERDDTA AKTLVLCVSDIISLSAN ISETSSNKTS SADTQKVAIELTDGWYAVKAQLD PLAS |
| 3054 | 8551 | A | 3313 | 1 | 207 | CNLC LPSDSSPASASQVAGKTGLC HHTGVVFVFLVEMGFHHAGQAGLE LLT*VICVPQPPKALGLQV |
| 3055 | 8552 | A | 3314 | 279 | 625 | SLYVCMHVCMYVFILRRSFALVAQ ARVQWCGLGSLQPPPPGFKRFISCL SLPTS*DYRRAPPHTNFFVFS AEME FHRVSQDGLYLLTSGDLHPRLASQS AGITGVSHRTRPFL |
| 3056 | 8553 | A | 3315 | 1 | 418 | GSIPPPGVYCVPYPLKHAPAPALP* TRQRGSPQSPGALRAK*HVLLET PQ PPGPAPPGARTRTRPESE*SQPGRSP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VSRQSLTGADALEGPCLGLATKQPS WPHRCGTSGSSPGWLLARGFQETQ QDCIVPLNAQDIG |
| 3057 | 8554 | A | 3316 | 1 | 354 | GFIPPPGV\YCVPYPLKHAPAPALP* TRQRGSPQSPGALRAK*HVLLETPQ PPGPAPPGARTRTRPESGAWRWVR AGSSPPPPSPHPTPPCFFQVHQGLRS GSANEASLEDPQSRDRA |
| 3058 | 8555 | C | 3317 | 299 | 365 | MSCPECNLTGISSKTNNKLNQ* |
| 3059 | 8556 | A | 3318 | 33 | 302 | PSSWDYRHAPPRLTNF*FLVEMGF HYVG/QAGLELLSSGDPPALASQSA RITGMSR\RAWPK*HNVLRKFTNLS LGHIQNHGPRVQAKP |
| 3060 | 8557 | A | 3319 | 3 | 409 | SNFRSNFGYNIPLKHLADRVAMYV HAYTLYSAVRPFGC/SGYWGCAIGK ARQAAKTEIEKLQMKEMTCRDIVK EVAKIIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREEAKEYAKE SLKEEDESDDDNM |
| 3061 | 8558 | A | 3320 | 1 | 255 | |
| 3062 | 8559 | A | 3321 | 1 | 395 | FGYNIPLNHLPDRVAMYVHAYTLY SAVRPFGCSFMLGSYSVNDGAQLY MIDPSGVSYGYWGCAIGKARQAAK TEIEKLQMKEMTCRDIVKEVAKIIV VHDEVKDKAFELELSWVGE\ESLKE EDESDDDNM |
| 3063 | 8560 | A | 3322 | 515 | 560 | |
| 3064 | 8561 | A | 3323 | 3 | 661 | KDGVVLGVRKISPS*TYEEGFQTKR LF*CLIGNVEMA\VAG\LLADARSLA DIAREEASNFRSNFG\YTIPLKHLAD RVAMYVHAYTLYSAVRPFGCSFML GSYSVNDGAQLYMIDPSGVSYGY WG\CAMRQAR\QLAKT\ELERLQLK KLPSGDIVKEVAKIIVHDEVKDK AFELELSW\VGDLTK*RHEILPK\DI LRDEAEKYAKESLKEEDESDDDNV |
| 3065 | 8562 | A | 3324 | 3 | 634 | |
| 3066 | 8563 | A | 3325 | 2 | 487 | HIFGKAKEYANSQVVTKDQYAVIC LGGDAVPSASLHVSETMEKT*KK/H RMSHFVTCLTEGRRKCIKPVHYD RVKKITQRKKEIPVFLNRVPEALG KCTHADPEAAEGK/LSRAMHFILQS APDIRRELQKILEARPQTPAVDFGR RLLRFSITDRTQMGR |
| 3067 | 8564 | C | 3326 | 373 | 727 | MKPRLWEFSLHREGNTGTTGLDSL LWPPARTTKWAHLTKRNQAQPGY AGPASPTSHVLCPAQPAYLTHDVNS QVSLIKTSLQASSGSXXXXXXXXXX XXXXXXXXXXGAQAFFFLGGGFF* |
| 3068 | 8565 | A | 3327 | 2 | 536 | VHLVPRQNACAIRLTEPCPPRLK*FS CLSLPSS/WDSQ/HAPPH/PGS/FCIFR RDGGSPMLS\GWFQTPDLRRSTRLSI PKCWDYRREPPHPVKIFLKLSSFFSY WVFPVCALNLSLSLFVYTFLSNSLS LLYSSHTGSKLQCYEMLHVETHIPK GEGVLSRVERRKVRLSSHTKPCQFS HESA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3069 | 8566 | A | 3328 | 3 | 334 | FLRQGL/NSVTQAGVQWGDLSLQ PPPPKLKGSSHPSPSSCRHYRHTPP/ RSG*FFVFL*RWGFAMLPRLV*TS G\PSDMPALASQGAGTTSMHTWR PYLNFGKFPRKKN |
| 3070 | 8567 | A | 3329 | 1 | 148 | PKLKGLCLSFHEGKKRLSYF/CIMA* P*YPLDFGEQWPLHGSHAYSTIL*L DLFCKKEEE*DEIPYV*CFMLLWKS TTM*KKRLSYFLSWNLNTHWISEN SGHCMVLMLTVRSCS |
| 3071 | 8568 | A | 3330 | 3 | 267 | FFFFLRDRFSLCGPGWSAV/VQS*LT VNS/TFLGPSNPPLSLWSSY/DVR/R MPANLS*FFRS*/SLAMLP RPVLKSW PQAIFLRHAPKVLGVEV |
| 3072 | 8569 | A | 3331 | 3 | 269 | FETESHVTRLECSG/TILAH CNTCL PGSSNSHASASQVAGIAGEHHHAQI IFIFLVETGFHHVGQAGLELLT*VIC LPRPPIVLGLQA |
| 3073 | 8570 | A | 3332 | 1 | 299 | FSLIKISMMLLMKMEK*NLQFIW/KP RRLQIAKARLNASSSSSSSSSSSSSS SSSVVWYWHKKRHIDHWNRLNS NINRHICSQILTKVPGANTKDHP |
| 3074 | 8571 | A | 3333 | 3 | 261 | RQDLSLCHPGWSAVVQS*LIALTS* \VKQSTYLRHPTSWG*RCVPPCPAN FCFFCRDRIL/TISPRLVSWAQVIELP QPPKVLGLQV |
| 3075 | 8572 | A | 3334 | 3 | 290 | VDFFFFSRRSNVLSHRLECSGTISS HGNLCLLGSSDSPASVASQVARITGV HHHTQLIFLIETGFRHVDQAGLDL LT*VILPPQPPKMLGLQA |
| 3076 | 8573 | A | 3335 | 3 | 358 | |
| 3077 | 8574 | A | 3336 | 76 | 386 | VLPPPSSPALHSPAPPSTCPYLPGA/P PPLLPPCAGRSPAAAAPHCPAPCA PRH*GSR*LESPAPQG PQSRAARMP AWPLPPAPPTDPTAPPAPRSHWPAA PPT |
| 3078 | 8575 | A | 3337 | 66 | 381 | VLPPPSSPALHSPAPPSTCPYLP GAL PPLE/GPPSRRPPRTFIGNPGGQGPGE VSPIVLRSPSQPH*PGNQGPCPSSQP PGSPRSEHGC*HRCWALYGQQEK APS |
| 3079 | 8576 | A | 3338 | 1 | 303 | KDRFSFCGPG*SAVTQLNLTADP*T PALK*SFHRSLLSRWDYRRAPPYLA N*KKFL*SRGLAMLPRLVFHSW/PQ VILSPLSRARATAPSFPLFSSKDEPI |
| 3080 | 8577 | A | 3339 | 2 | 212 | RFSCLSLPSSWDMHHASPG*FFIFLVE TGFAHVGQAGLELPASNDPPASTS QSVVITAMSHRRLALVPIF |
| 3081 | 8578 | A | 3340 | 2 | 273 | RRSSTQPPRLQCSGTIPAH CNLHPPS PSDYAPASRVAGTTGARYHHAQPI SAFSSAETGFHHAGQDGLKLLT*AI HPPRPPKVP GPQA |
| 3082 | 8579 | A | 3341 | 135 | 494 | IKHRGMGLDFAVLPLQVKWPPDPG FLECIHFLQLKGTIPDLKERAPVTSR VEPGHAGHC/TSYGQVCHL*GRC/V EKRKGIACDCAFSMYDGLFCSNSNS RADWSHCTVSGTYQHTENSIMS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3083 | 8580 | C | 3342 | 71 | 217 | MPQPNFFVLLVDRGFHHVDQAGLD LLTSSDSPALASQSARITGVSHHA* |
| 3084 | 8581 | A | 3343 | 1 | 106 | |
| 3085 | 8582 | A | 3344 | 2 | 1926 | MAAAAVDSAMEVVPALAEAAPE VAGLSCLVNLPGEVLEYILCCGSLT AADIGRVSSTCRRLRELCQSSGKVW KEQFRVRWPSLMKHYSPTDYVNW LEEYKVRQKAGLEARKIVASFSCR FSEHVPCNGFSDIENLEGPEIFFEDEL VCILNMEGRKALTWKYYAKKILYY LRQQKILNNLKAFLQQPDDYESYLE GAVYIDQYCNPLSDISLKDIQAQIDS IVELVCKTLRGINSRHPSLAFKAGES SMIMEIELQSQVLDAMNYVLYDQL KFKGNRMDYYNALNLYMHQVLIR RTGIPISMSLLYLTARQLGVPLEPV NFP SHFLLRWCQGAEGATLDIFDYI YIDAFGKGKQLTVKECEYLIGQHVT AALYGVVNVKKVLQRMVGNLLSL GKREGIDQSYQLLRDSL DLYLA\MY PDQVQLLLLQARVYFHLG\ILPEKS FCLVLKVL DILQHIQTLDPGQHGA VG\YL\VOHTLEHIL\ERKKEEVGVE VKLARSDEK\HRD\VCY\SFGFIMKA* RGMG\Y*LC*FYGWDPTWHGSGHE LDSRNMNV\HSLPHGHHQPFYNVL VEDGSCRYA\AQEN\LEYNAEP\QEI SH\PDVGRVYSQRFT\RTHYIP\NAEL VEIRYPEDLEFV\YETVQ\NIYKCKRK ENIE |
| 3086 | 8583 | A | 3345 | 59 | 339 | |
| 3087 | 8584 | A | 3346 | 1 | 342 | FCSCQPQAGVQRRDLSSLQPLPP\GF K*FSCLSLPSSWD\YRRPPP/RPGYFL YYLVEIGFCHICQAGLKLLRSGDPP AWASQSAGITGMSHHAQPHLLL N CLLPFLGIPLHSPL |
| 3088 | 8585 | A | 3347 | 1 | 294 | ETESHVTRLECSGTILAHCNLHLP GSSNSPASASQIAGTIGARHHTWLIF VFFVEMGFHHVGQTLELPGLK*SAC LKPLKVLG*QAGVQRHNLGSLQPPP PRFKQFSCLSLPNSWDHRCTPPHLA NFCIFCRDGFPPCWPDSRTPWPQVI CLPQASQSAGITGVEPLQPQRSYP |
| 3089 | 8586 | A | 3348 | 2 | 268 | EAESHVA\RLCSDAISAHCNLRLP GLSNSPASASRVAGIIGACHHDWLI FVFLVETGFCHVGQAGL/DNS*PQVI HPPRPPKVLGLQA |
| 3090 | 8587 | A | 3349 | 3 | 444 | FFFEIWSGSVA\RLCGGTIFAHCNL RLLGSSHPPTSAS*VAGTKGTCHHV QLIFAFFVDTGFHHVARLV LNS*TQ AICPPRPPKVLGSYASITAPGPTFFFL TIILGVQVDKRFYGNLTRKDIQKLG NYVWEGLELLSPQKFMLKP |
| 3091 | 8588 | A | 3350 | 1 | 318 | FFFFFLRQSFALAQAGM/QWHDLGS LQPPPPGFK*FSYLSLPSSWDYRYVP PRPASFEFLVEMGFHHVGQAGFELL TSSDPPASASQSAGIIGVS*RTQPGT NDFL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3092 | 8589 | A | 3351 | 16 | 848 | VGSGLVSAQQTGCGPGNPSPPGSVS GAMELRVEPAARGQGS LGDPPA\VL LPGALELPIPGSFFASQSCSPWVML QLTFPHF*LLLAPLPPVSPAPTGWDL VSQLOPVSSPRGRCPRSGPDLLPLH GQPFHSSSFSSSMQASGEPVQPCPS RSSGS/VKGGGLQTVEPESGPGALKC EALAWLRG*GLLGHS GFAGSVPEV TPGSPHVLNPA GRGLPCAGYCLHPA AL*GMVFGLPPLPGSSLV*PTIWLLT LKSPTS*GIP*HRKPWFVSVMHKVG WKV |
| 3093 | 8590 | A | 3352 | 1 | 293 | VL RQGLSLSTQDRMQWHYDSSLQP *TPGLK*SSASQVAATTGTCHHTWL TFLFVF/DFWRWSL/NCIAQAGLE/PP GFK*/CPKHWDYRHEPGMPGWVFLI S |
| 3094 | 8591 | C | 3353 | 127 | 345 | MFD FELEL FXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXLI AQGECLYVWKINSQHSVFKLLKKL CF* |
| 3095 | 8592 | A | 3354 | 2 | 215 | AHCNLCLPGSSDSPASASRV TGITG VHHRTQLIFVFLEEMGFCHIGQAGL ELLT*VICLPRPPKVLVLRT |
| 3096 | 8593 | A | 3355 | 164 | 311 | QRSQGIWVWRFIRRF*II |
| 3097 | 8594 | A | 3356 | 1 | 381 | YINVIIHFVHINCWRECQKVQLT*K\ SF*QFLKNLNIHLSYDLAIPVLGICPR EMKAYVHIKTCK*MLIAAFIIAQN WNQ/P/RCPSTGEWYKQTVIFYTMQ HYS AIKNNE*LIHKTTWKNLKEARA SGV |
| 3098 | 8595 | A | 3357 | 2 | 764 | RTLHLFAGGCGGTVGAIFTCPLEVI ETRLQSSRLALRTDYYPHVHLGTIS GAGMARPTSATPGLFHGLKSILEKE GPKSLFRGSRPNLVGVAPSRAVYFA CYSKAKEQFNGIFAPNSNIVHIFSAG SA/GVRGSKQMNTLQCARYVYQTE/ GIRGFYRGLTASYAGISETIICFAIYE SLKKYLKEAPLASSANGTEKNSTSF FGLMAAA/GSF*GLSSCIAY/PHEVIR TRLREETSTSF CQTARLVFREESYL PL |
| 3099 | 8596 | A | 3358 | 155 | 875 | DQHPVTPGLFQVLKAVYFACYSKA KEQFNGIFVPNSNIGHIFPAGSAAFIP NPLMD\PIWMVKTRMQLEQKVRGS KQMNTLQCARYVY/HDRKAFFGGFY RGLTASYAGISETIICFA\YESLKKY LKEGPLAFFGKWD*GKIPQVFLDL WPAAALSKGL\ASCMAYSHTEVH* GRRL\REKGHPSTKSFCPERRALGVP GEEGYPCLFIEGLFAPS FIRQIP\NTA\ IVLGYLWRLIVYLLGRP |
| 3100 | 8597 | A | 3359 | 1 | 281 | FFFAPETESYSVARLECSGTILVHCT LCLPGSSDSPASASQVAGTTGACHH TWLILVILVEIGFHHV GQAGLG/IS*L QVIRPPWAPKVLGIIG |
| 3101 | 8598 | A | 3360 | 135 | 218 | TLQFTSLISYSFCQSWGSKVPLSLPP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | P*/PANF/*FLVETGFLQVGQVGLKL LISSDPPTSASQSAGITDVSHCAGPE F |
| 3102 | 8599 | A | 3361 | 198 | 390 | |
| 3103 | 8600 | C | 3362 | 5 | 316 | MPAKLFLMVEFSGVACSSAKXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX YYRLLFSPCHSF* |
| 3104 | 8601 | C | 3363 | 186 | 323 | MPWLEHTAHFPDKAWITRMALLRN GIVPYDSLPWITLGRWPNGGT* |
| 3105 | 8602 | A | 3364 | 2 | 3096 | TPRLQSNTRALYQYCPPIINYPQLE NELFCNIYYLKQLCDTLRFPDWPIK DPVKLLKDTLDAWKKEVEKKPPM MSIDDAYEVLNLPQGQGPHEDESKIR KAYFRLAQKYHPDKNPEGRDMFEK VNKAYEFLCTKSAKIVDGPDPENIL ILKTQSILFNRHKEDLQPYKYAGYP MLIRTITMETSDDLFSKESPLLPAA TELAFTVNCALNAEELRRENGLE VLQEAFSRCVAVLTRSSKPSDMSVQ VCGYISKCYSVAAQFECEKITEM PSIHKDLCRVLYFGKSIPRVAALGVE CVSSFAVDFWLQTHLFQAGILWYL LGFLFNYDYTLEESGIQKSEETNQQ EVANSLAKLSVHALSRLGGYLAEE QATPENPTIRKSLAGMLTPYVARKL AVASVTEILKMLNSNTESPYLIWNN STRAEGLEFLESQQENMIKKGDCDK TYGSEFVYSDHAK*LIVR*IFVRVYN EVPTFQLEDPKAFAASLLDYIGSQA QYLHTFMAITHAAKVESEHQGDRL PRVEMAFEALRNVIKYNPGSESECI GHCRCIFSLLRVHGAGQVQV/AL* EVVNIVTSNQDCVNNIAESMVLSSL LALLHSLPSSRSAWFWETLYALDIR VQKLIKEAMAKGALNHLDMFCNS THPQVRAQTAELFAKMTADKLIGP KVRITLMKFLPSVFMADAMRDNPE AAVHIFEGTHENPELIWNDNSRDK VSTTVREMMLEHFKNQDNPEAN WKLPEDFAVVFGEAEGELAVGGVF LRIFIAQPAWVLRKPREFLIALLEKL TELLEKNPHGETLETLTMATVCLF SAQPQLADQVPPLGHLPKVIQAMN HRNNAIPKSAIRVIHALSENELCVRA MASLETIGPLMNGMKKRADTVGLA CEAINRMFQKEQSELVAQALKADL VPYLLKLEIGIGLENLADSPAAT*GS ELVKALQGG*LEVLQYGENRVNEIL C/RFLSVWECLSKIQEHDLFIS*/ESH TAGYLTGPGVAGYLTAGTSTSVMS NLPPVDHEAGDLGYQT |
| 3106 | 8603 | A | 3365 | 1 | 358 | NRLNATPIKIPTAFFAEMDKLNPCKFL KLNS*NLARNARDST*PKQY**RKR TWINKNNAGGLILPYCILLQRNNNQ DIG*KNVLKIM**WHRDRHDQ*NR NQSPEINP*TYGKLFSTVL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3107 | 8604 | A | 3366 | 2 | 40 | LPRLKQFS\CLSLPSSWDYKR\RPPC PANF/SVFLVETEFYHVGQAGLELFT SSDLPTLASQIAGITGVSHCAWPE*S AS |
| 3108 | 8605 | A | 3367 | 1 | 223 | IIVKKWKQPKCPPTDEWINKMWDI QAIEYNLAI*/DKVVIHATTCKMLN IMLSERSQLQRATYCNDAYIKNPE |
| 3109 | 8606 | A | 3368 | 307 | 332 | TTYHFFF*TESHSAAQAGAHWRDLS SLRPPPPGFKPFSCLSWDYRRTPPH PANFLAFLADTGLHHAGQAGLKL TSNDPPTPASQSAGTTGVSHRAQPF FSELPTIFFSL |
| 3110 | 8607 | A | 3369 | 3 | 411 | QTLPSATVSPEQAGAFPLALHSAQE SLGPAQTVPGSTGPPQPAPSGPGPPG EPG*ERLCASHKAFISHKQSH*SPQ* PFQGRFDAFPQYKQTRPGHT/GQK GLRGPRTQTLSTLTSQPTACSENSQG SQSPSKRTLS |
| 3111 | 8608 | A | 3370 | 3 | 166 | EESCSVVQGGVQWCDLS*LQTLPP GSSNFCASASRVAGITGAHHHAQL KKKMLF |
| 3112 | 8609 | A | 3371 | 4 | 312 | FLR*SFTLIVQAGVQWRYLGSLQPP PPGFKRLSCLSLPSSWDYRHVPP/*P GYFFVFLVKMGCLHVGQAGPKLLT SGDPAASASQSAGITGPSHRTWLRS FLI |
| 3113 | 8610 | A | 3372 | 3 | 282 | FFFETGSNSVAQAGVQWCNHSSLR PRPSGSSDPPNSSSQVAWTTGVHH TQLLFKFFCKDEVSLCFPDWSQTV* RVEHIRDEYETTQHCLYPSN |
| 3114 | 8611 | A | 3373 | 1 | 164 | ETEFRSVAQAGVQWRDLGSLQPPPS GFK*SSCV/SLPSTWDYRYMPPCA TLLNT |
| 3115 | 8612 | A | 3374 | 1 | 114 | ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS |
| 3116 | 8613 | A | 3375 | 363 | 1246 | DTEQIYCIQEPEYGGKKYCTKQSR YVSWTTHFSSSFIDQSLLSESMA*KS TAPHSSDF*DFLT*KT*NLFFLRSL ALSPQAGVQWRDLGSLQAPPPGFTP FSCPASPSWDYRHLPPCPANFFVF FLVETVSIFVFTVLAGMVSI*PQ/CD PPTLASQSAGITRLSHRAR\LCFVF* KKRNAREGGRLLTIKADFLIFFSFF FEMESCSVSKAGVEWHGLSSL*ALP HRFTPFSCLSLLSSWDYRRPPQLA NFCIFSRDEVSPC*PGWSGSPDLVIH LPWPPKVLGLHA |
| 3117 | 8614 | A | 3376 | 3 | 324 | DRISLCCPGWSAIV\QSQLTAA\SPLG LKQSFYISLPSS*GHRLAPLHPANIF GFPL*KWGLPMLPMLVLNSWAQVI LPKCWGLQASATVPGLFINFYDYIM DQSSFN |
| 3118 | 8615 | A | 3377 | 3 | 673 | RWSHSVTVQAGVQWRDLSSRQPPAP GSRDSPASAS*VAGTTGTTHHAQFF FFFFFLRRS/LSSV/SQDGVQWHDH SLQPVPPGFKQFSCLSLPSSWDYRC AAPRPANFFVF**RRVFSTLARLVSI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | S*PCDLPTLASQTAGITGVSHCTQLA KFCIFS*DGVCHVGQAGAVLILCLF LHSHKINMFSPLHCTPASTVYSHLPQ RPTKRRLYIRWRWERTWPANAEL |
| 3119 | 8616 | A | 3378 | 2 | 323 | RRSFTLVAQAGVRWHILGSLQPLPP GFKRFSCSLSPSGWDYRLMPPCPAN F*FLVEMRFHHVGQAGPERLTSGD LPA*ASQSAGITGVTATPSQYKLCSL IIMKLN |
| 3120 | 8617 | A | 3379 | 1 | 311 | DFFF*ETASHSVTQAGVQWCDPSSL QPPPPVFKQSSCLSLPSSWDYRHVP PCSVDT/CISILLIPFLRSGE*SPLLLS WSSCDLGQGTAPLGFWFPMGKARP V |
| 3121 | 8618 | A | 3380 | 3 | 404 | PCLANFF/VFFVETGTHYAA*CGLRL LGSSALPV*TS*SAGIIGMSHCTC/LQ ITLLKTESHS\VAQAEVQWHDLGSL QPLTPRFKRFSCSLSPSRWDYRCAS PRLANFCTFKFLYFLVETGVSPCWP GWSGTPDLR |
| 3122 | 8619 | A | 3381 | 739 | 1003 | NLYLNY/CFF*IETGSHSVTQSGMQ WHNLASLQRLPLRLKQTSHLSLLSS WDCRHMPNLA/NF/CVLRDKISPF CPGWSQTPGLKQCIFF |
| 3123 | 8620 | A | 3383 | 1 | 299 | ETESGS\LPRLCSGTISAHCNLRLL GSSNSPVSAS*VAGTGACSHAQLIF VFSVESGFRHVGQAG\NF*PQVIHP PRPRKVLGLLPVSHHTRPISFFL |
| 3124 | 8621 | A | 3384 | 12 | 336 | SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTSPADAHT/AGLSKTPPHWAA RARLDDVFSRLTFSSHSLNMELVQD LTASAPMYSSTSRDPP/CLGLPKCW DYKREPPRAH |
| 3125 | 8622 | A | 3385 | 2 | 318 | FLSSHLFLTQSL/DSVAQAGVQWHN LGSLQAPPPGFTPFSCSLSPSSWDYR RPPPRPANFF\VFLVKTGFTVLARM VSL*PHDPPASASQSAGITGVSHW CPANN |
| 3126 | 8623 | A | 3386 | 1 | 325 | ASTAQAGVQWPAAQLQTPPPGFTP FSCSLSPSSWDYRRPPPSANFLYF* *RRGFTMLARMVVIS*PCDPPASSSQ SAGITGLSHRAPVIRILRRAGRNT IGGLD |
| 3127 | 8624 | A | 3387 | 3 | 530 | RQSL/DSVAQAGVQWRNLGSLQVL PPGFMPFSCSLSPSSWDYRRPPRPA /NFFVFLVETGFTRGSI*PRDPPAS ASQSAGITGVSHRTRPKDCYS*RCS YCKVLTRLCFRKLLTGEEAPMP/PF* RQS*CLTSVTLSSAWRSICYDRLVDI QFKILFMKTKLPLFFSQNELYFIIL |
| 3128 | 8625 | A | 3388 | 3732 | 4979 | NFVFLYLRELSSQAKSLTSHPLSNFF FKRQGLAMLPRLECS/GLFTGAVIA HYSLQLLGSSNPASANQVAGTTGA CYHAQSIF*S*NFFIFLSSVS*NLCLN QNAGFYLLFFYF*Y*MCRYASSTFLT NELCGKKK*TLSIEIKSIFKHHVLY WFLGLVFLNLLLILPVLYNEHRKIL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | E*GRKVYQDILPGFGCKF*RMVFLIF VHIL*APRYPSQ*GKLIPCI*LLYL*W LSPSPSTVSLAFHDKFVNLHFYIDMS LFHGQACSIKMIFLKDVNCA*LIGYI LFCFFFFFFFLRCGVS\SVAQAGVQ WRNLGSL\QAPPPRFMPFS\CLSLPS SWDYRRLPPRPANFFFFFFLDF**RPL VFL/SFTVLARMGL\IS*PRDLPTSAS QSAGITGVSHHVQLPYFVLNKFTV LGSNSGF |
| 3129 | 8626 | A | 3389 | 1 | 585 | AFFFFLRQGLALV/THAGVQGQDYS SLQPLPPGLKAILLPQPPECWDYRC MSPCLA/N/FFVFFVAMGFRMLPTL/ VLELLGSSDPPTLAS*SAGITGVSHC TWPLFI*VWSFGKV*ELS*HRFCISSF IHI*KFWKRWG\SLCSPGWS*TAGL KRSS*LGLPKYRDYRHEPPCPAFFTF LLECYDLHILLICSHFYLR |
| 3130 | 8627 | A | 3390 | 3 | 459 | QPGVQWHDLSMQPPPPRFKCFSC SLL/SS*DYRCAPMPQPNFCIFI*RY GFT\MLASLVLDS*L*VIRPPWVSQS AGITGVSHHTWARDRADF*MGVW ASPIARVPRGQQVRSCQPL*GS/WDP ET*HNGHFHFWIKQSEPPIFKGRR*N P |
| 3131 | 8628 | A | 3391 | 1 | 258 | FFFKTDSCSVARLEYSGAISAHCNL RLPGSSDSPALAPQITGTTGMC/RS* FFIFLVETGFHHIGQAGLKLLTLWIH CPPKMLGLQA |
| 3132 | 8629 | A | 3392 | 3 | 316 | VAQAGVQWWYLSSLQPPPPGFTSC LSPQCSWDYRHAPPCSANF*FLVET GFHHDGQAGLELLTSSDPALASQS AGITGVHHPAPNSSCLHTDKRVHT WHKPS |
| 3133 | 8630 | B | 3393 | 49 | 279 | SSSDSDDEEKKHEKLKKALNAEEA RLLHVKETMQIDERKRPYNSMYET REPTTEEMEAYRMKRQRPDDPMAS FLGQ* |
| 3134 | 8631 | A | 3394 | 2 | 357 | |
| 3135 | 8632 | A | 3395 | 1 | 1765 | MSATVVDAVNAAPLSGSKEMSLEE PKKMTREDWRKKKELEEQRKLGN APAEVDEEGKDINPHIPQYISSVPW YIDPSKRPTLKHQRQPQEKQKQFSSS GEWYKRGVKENSIITKYRKGACEN CGAMTHKKKDCFERPRRVGAKFTG TNIAPDEHVQPQLMFDYDGKRDRW NGYNPEEHMKIVEEYAKVDLAKRT LKAQKLQEELASGKLVEQANS PKH QWGEEEPNSQTEKDHNSEDEDEDK YADDIDMPGQNFDSKRRITVRNLRI REDIAKYLRNLDPNsAYYDPKTRA MRENPYANAGKNPDEVSYAGDNF VRYTGD TISMAQTQLFAWEAYDKG SEVHLQADPTKLELLYKSFKVKKE DFKEQKESILEKYGGQEHLDAPPA ELLLAQTEDYVEYSRHGTVIKGQER AVACSKYEEDVKIHNHTHIWGSYW KEGRRGN\KCCHSFSKYSYCTGEAG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KEIVNSEECIINEITGEESVKKPQTL MELHQEKLKEEKKRRKMKKKKHR KSSSDSDDEEKKHEKLKKALNA*E A\RLLVKET\MQ\NDERKRPYN Smy *TSRPIEEEMEA YRMKRQRPDDPM ASFLGQ |
| 3136 | 8633 | C | 3396 | 106 | 426 | MFLKEPVXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXRLXXXXG* |
| 3137 | 8634 | A | 3397 | 25 | 435 | TKYWLLFFLILILPFFFWRRRSRV QAGGQWHDLGSLQPPPPGFKQFSC LSLPSSWDYRRAPLHLANFYIFSRD/ MDFTMLARLVSNRSQ/CDPLASAS QSAGISGKSQHTRPVLVLLKTYTNS H/SF*VKGLGWEFIL |
| 3138 | 8635 | A | 3398 | 3 | 320 | KTESHSVTQAGAQQDLSSVQSPP PGFKRFSCSLPSNWDYRRVPLHPA NFL*/FLVETGFHHAG*VGLELLTSG DPPTLASQNAGITGVSHCARPIVIFL YLITSR |
| 3139 | 8636 | B | 3399 | 70 | 199 | XMQVTGFGRGQNHNVQGSTPTDAS PRRRDVCTAQTQDSKLVNS* |
| 3140 | 8637 | A | 3400 | 198 | 397 | TKNRNTLSRFLLEAPRVFGPPSP/RP PKP/ASGP*PIACPAGTHIPCGPYPC CHVGGGWPAQPLAALG |
| 3141 | 8638 | C | 3401 | 164 | 313 | MTLHFQELKSLKFYLNXXXXXXX XGGRFKGSLGGPKFTRACNVKAFS L* |
| 3142 | 8639 | C | 3402 | 165 | 361 | MVKFCANNQGKTKLIFMFFHKESHI IIGRPRAQREKKEKEEGNPNECLLD VSLRTGFSGHLPGRV* |
| 3143 | 8640 | C | 3403 | 146 | 389 | MTPISLKGRCRQLGDGKRCSEDLA LIEGCPHAGRPPPRKSTLEPAFGSPR CQDPVSAMCMTRSPPANLDSAERQ APGLGR* |
| 3144 | 8641 | C | 3404 | 157 | 404 | MLSLTSSPLNQKGVVSFVHAILKY QGCKPHFIKKLSRXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXP PAPSFLWGEG* |
| 3145 | 8642 | C | 3405 | 73 | 252 | MHTPLLA WPGMAWCYRQPLSTPRL ILNYVKPRKMIFRTFAYIRLYLCTYF AVFHRRKWP* |
| 3146 | 8643 | A | 3406 | 2 | 617 | IYIFLKALNFCREVVPISPPPKVRVLF KDSQVTSFPVPAL*KGGQGLGYKT APYKEKTNSLQARVNLGPSRGPLK RPPSSSSSPNPALLFIQTRVKLVNG KRPEATCLGRKASYSVRFSAA WDP PAGCAQPPTVSPDPTTKQVSR TKAR N*TKNRNTLSRFPS*KLPRVSGPTQV PNPPKPRSRGD*QRTFPFPVPDGNPV LN |
| 3147 | 8644 | C | 3407 | 129 | 281 | MSSHARVNLGPSKDPLKRPPXXXX XTQRQLFKTFINRCLQFVDFFEKIKL * |
| 3148 | 8645 | A | 3408 | 1 | 303 | QAGVHWRNLG\SLQPPPPPTLRRFS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | CLSLPSSWDYRHPPSHPANFFFFLL LVEARFHHVGQGGLELLTSSDPSTS ALQIAGITGVSHRAEPAPFFK*CFG |
| 3149 | 8646 | A | 3409 | 3 | 1039 | QQPFVNPALPPGYSTGLPYTGMF SAFQYGPTMFVPPASAK*HGVNLST PTPPFQQPVGYGQHGYSTGYDDL QGTAAGDYSKGGYAGSSQGTKQV CRFWGLGKGVSVSSSTTGLPDMTG SVYNKTQTFDKQGFHAGTPPPFSLP SVLGSTGPLASGAGPWLCTPTIPTH LASPPAAPLTAAAPPSAGCTEWLG SAQPAQLPAAQVSSLQTCLRQLSIL GQLNPGERGGAGAKAYPGQERTTR ARIWEPKCPFSKNSPTCVSHALCGE SASPDWATVCNVFMYVFVNVIEVW GGVGGWRQMLARSAPPHSKPPSPN CSKISTPNPHLPFRSFLHSLATAQWA H |
| 3150 | 8647 | A | 3410 | 2 | 344 | LRQSVSLLPRTQAGVQWPNLGSLQ PPPPRFQRFSCLSLLSSWDYRHAPPC PTKFVFLVET\GFTMLARLVSI*PH DLPALASQS/AGITGVSHCAQHGV YIRCFRELA\SYSIL*SLQWPHV*SL AYSIL |
| 3151 | 8648 | A | 3411 | 52 | 174 | |
| 3152 | 8649 | A | 3412 | 2 | 692 | RPP/QADPPRCWPR/PLGLGGCVPW GAGRLRRGHGPEPDSPFRRSPRGP ASPQR*PPRPDPWPPRQASPRCPT D*SRTAGRTTDPQEEAVGGQGPSR GG*APSNSSEPPLYGSGPLDSAFSLG TAFRKTLRIDLTQSQRPPHRSLSLYS GKGLAPGELADALNFLIYPTDFGL HCTIGDVATGPWRCNQIKRRKHCQ LGKSKLIYFFFPPTPSPAKNFFSRY RHHS |
| 3153 | 8650 | A | 3413 | 3 | 367 | MLNYPLDFHPSFFVGFFFFEMESRS\ VARLEVPVGVISSHCH\LCLPGS\SDS PASASQVAGTT\GVCH*AQLIFVFLV ETGFHHFDQDGLDLLTS*SVHLCPS KCWDYVIHPPQPPKVLGLQA |
| 3154 | 8651 | A | 3414 | 1 | 595 | MGIHHVGQASLELLTSGDLPASASQ GRGVRLYYTEGRSSQSASVTALFLS SLPTVTSAMAGTRPPSARSHQTLQA CRAQKTKTRMSSI*GTGAKHQASSP GKAPLSTSPYFWKPSLQTSPCSGSR SLWASLPSPLAALFLCFWQDAT*RS STTRSSLPSWPSRSTRALRLSTS*PE CAPSA*ASSKAGERSTGDRL |
| 3155 | 8652 | A | 3415 | 259 | 941 | PVSWSLNSCRFFFF*DQSLPSVV/Q AGSGQ*RNLDL\QPLASRFK*FSSS RL\SSWDYRHMATMARLIFLVE MGFTMLARLVNFLTSSDPPTSAPF KWLGLQGVKPNTRAVGFN**LGYY SIILYHSNSPGTDLVFILFTYLYFL RQEQNSAAQARVQ*WHNLGSLQSP PPGVH*FLCLSLPSSWDYRCAPPHQ ANFFIFSRDGVSPCWPGWS*TPDLR |
| 3156 | 8653 | A | 3416 | 165 | 289 | ISGLSGLYHIDRLILVCNCKQKPTYS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | *NPGLSW*TDFKCLI |
| 3157 | 8654 | A | 3417 | 3 | 796 | PGPRAPPIRCSPLRSAPRRPST*SAA AWPASAAAGFCPCFYSA PPSSTSSR WPAAAGCSLATTAKTSSRVVEMLP RAAAAAGSYEGRAVRA/VM EYAW GRAAA/DHALSVASSILVILFHPLLL RPLCWTPECLSS*EVIGLLALAAV FQIISLGNLPREVHPDLHPSCQAPLS LTSITGAYGFGVGQPRIILTRLCLLL LAASPTTEDGPSGAMPSPGTSTHLP NLGMKCGRKSLPAEMGLPEGRKLF LPGGLWNPIFWPVFHHY |
| 3158 | 8655 | A | 3418 | 2 | 603 | GFFFFKIVLIQDLFPSTPLPSSVHSGD YGD SGQDPSGTRNTFRRFCSPSFPPS COLPRPEAHTHANTRNPPSPHLLSF PHQSSEP*EGVKS LFEEA*KWGEMA ITP*PTPLWR*LWRTPNSFPLSGQPF STP RPSVPSPIQPKTKHVQQHPPAS T*KTGSVPTSLTPSTGVLGEWPPEDP AKGLMPEGKEEQKAFGP |
| 3159 | 8656 | B | 3419 | 34 | 375 | MLLGRLTSQLLRAVPWASLPRKGA QLELEMLVPRKMSVSPLESWLTA RCFLPRLDTGTAGTVAPPQSYQCPP SQIGEGAEQGDEGVADAPQIQCKN VLKIRRRKMNH HKYRKL* |
| 3160 | 8657 | A | 3420 | 2 | 361 | YSTSPAGQVGR LSPSQGGPAGAGG DAG/TPGRCP SAPWRAGSRPAASCP DWIPG/PAGHVAPPQSYQCPPSQIGE GPGGTPETQADQVRERPEAH LAEG GAKGSPRRAGRPPRSTCGANESG |
| 3161 | 8658 | A | 3421 | 1 | 417 | RITAATGGKGGARLICPAGR/CLGV CQPSGASFSPAFSQMPSSPCSAPSPI WLGGHW*DCGGAT/CPCGPGIQSG QEAAGREP/GSPGG*RTSSWGPASPP APAGPPCEGERPPYLGRPAMCCKG ARRPGCPALQRRAKAGGR |
| 3162 | 8659 | A | 3422 | 31 | 756 | GRRALRQAGPGSSREGPGARQRDS RGGEPGEGAGLPVLGPFGASERDTA RVGGLGASGRELCWKQSPPCGLGW RREKGSEGRGGTRRPSGPPATTEG AAA*PE/PGTCVPAPLGP GPPPTDH APGAPDFPAVEGRSLGRRPPALAQ S /P/GSAGQPGLRSPFTH/OPAGPGRR GLSPSQGGPAGAGGDAGPQEDVRQ PPGELGSRPARFLPQTGLPGPAGTC GLHRNPTQCPPSPDRGKGPKQGG |
| 3163 | 8660 | A | 3423 | 69 | 258 | PRTNRCATNHTPANF*FFVETGFLH VAQAGLELLGSSSSPALAPKQLVTG ASHHTRPQ*NFLQ |
| 3164 | 8661 | A | 3424 | 8 | 292 | QSFLFLKTRYLLRHPGWNTVAQ*Q LTVVTSRLN*SFHLSLPSS\WAI AVR MPPCPANFLFF/TRDRVSLC*PRLVS NTWVQMILLPQPPEMLGLQA |
| 3165 | 8662 | A | 3425 | 123 | 357 | WGKRPGQGGRNPWGPPLPGGK/PP KKGFLGPFTGRFQGSSPGL*KGPFL KGGP/QF*KPKPGSQNRVFKPPKIWE TPLGN |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3166 | 8663 | A | 3426 | 2 | 311 | FHSCYPGWSAMVRSQLTATSASQF K*FSCLS/LPSSWDYKCAPHPANFL FLVEMRFHHVLVRLVLNS*TQVIHL PRPPKVLGITGVRLGAQPCTFFFFYC SSV |
| 3167 | 8664 | A | 3427 | 7 | 534 | TSDFIYKALKKLQQEVPKAKSHLVQN YRFFFFFFLRWSLAPVAQTGVQWH DLSSLQPPPPGFKRFFCLSLPSSWDY RCPPPRPANF*FLVETGFHHVDQAG LKHLTSDDPASASPSAGITGVHPRP GQENQDLPGLCVDQLYTENSRRFFSK NYYQTPNFTSRKRDLSVFFFA |
| 3168 | 8665 | A | 3428 | 368 | 688 | LTVEFLNLLNILSLVCFIHQTN*IICY FNT/SSSHQNAIY*EPHVPS*GQRGK ASRQRG*TPPRSGTAASWPRVEK*R EARPQNPAQQTTYVRESPTDASPSS PKMAA |
| 3169 | 8666 | A | 3429 | 1 | 90 | FFFVLSHQRNLCLRRYSRDMAAIK SKFFL\WPGRVAYAYNPSTLGGRGG QIT*AQEFKCS*AAIKSKFFL |
| 3170 | 8667 | A | 3430 | 259 | 331 | RNE*LLTRFSPLSLSH*VLGVSMF |
| 3171 | 8668 | A | 3431 | 1 | 639 | LGKFHTFQMSPGGGVGLLSL*SYRN SCLAG/GGCDHMSVHVCIRARGVK VRSKNSNHPTETRK\VLGGMRLSLT RESSISDSMWLARKQTLHTPVMMQ TPHLTPTI*EEPQRI\RPEDTFMSV/Y YPMQTEHHQTPLDYNRRGTSLLD DEEPIVEDVMMMSSEG\RIEDLNEGM DFDTMDIDLPPSKNR\RETE\LKAD FFDPASIMDESVLG\VSMF |
| 3172 | 8669 | A | 3432 | 1 | 354 | LETSPLMFTMLDRDMSG/TMGFNEF KELWAVLNGWRQHLSSFDTRSGT VDPQELQKALTMTMGFRLSPQAVNSI AKRYSTNGKITFDDYIACCVKLRL TDSFRRRDTAQQ\FIQCVMSV |
| 3173 | 8670 | A | 3433 | 1 | 788 | MAYPGHPGAGGGYYPGGPSVVKEE NLIRQNDVYVFPVSQYGGAPGGPA FPGQTQESL\YGYFAAVAGQDGQID ADELQRCLTQSG\IAG\GYKPFNL\ET CRLMVSM\DRDMSGTMGFSIEFK ELLGLLLEWAGR\QHFIS\STDREW EQ*DPQELPEGP*QTMGF*V*VPPGC *ISFAKRYSTNGK\TFDDYIACCVQ T*GVFTDSFSKTGILAQCGCLLNFI WIDFHFCVHGVFKSLGSCMNVIN DSNWSSPLLVLFAFG |
| 3174 | 8671 | A | 3434 | 6222 | 7046 | RTVTTFLSKDSHGVCYCAQGGKIPDH QNPQCNRKQHPVSTILMLDKASFC QLRKRKHNLVNCINRNPMSLKN TSWHSSLSVTQRHQQQSKLHFQGS LLH*PSQNIL/SNI*KCINYC*HCSSV LLSYLFIETESYSVAQAGVQWHDLG LLQLPLRFKQFSCFSLPSSWDYRS APSCPANFCILVEMGFCHVGQAGL KLLASSDPPALASQSAGITGVSHYT QPCSPFLKSTGLFSCKVLSNPYHKG RIYLGRCFLNSTWHLVKSTLFCPL FI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3175 | 8672 | A | 3435 | 3 | 287 | SRSVAQAGVRWRDLSSLQPPPPRFK QFSCLNFPSSWDYRCAPPRPANF*I LAEMRFRHVGVGLELLTSGDPPA SASQSAGITDTSCHAWPFTF |
| 3176 | 8673 | C | 3436 | 88 | 303 | MTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPEVLECLSTQQVKSL QTLGGAAVSHKTNICLPFTKLW* |
| 3177 | 8674 | C | 3437 | 354 | 416 | MKESPGGELPQTGKKPVFLF* |
| 3178 | 8675 | A | 3438 | 274 | 460 | TLKNLRSAASTLGNPASPAHSSILS CPMRGHCRTL*KCHDWSFRAKMPS PFPQVGIYPPPN |
| 3179 | 8676 | A | 3439 | 480 | 613 | LSFRAKMPSFPQVGIYPPPN*GPIC LLCFSLCECVFYRNHLD |
| 3180 | 8677 | A | 3440 | 1 | 864 | YPTTPYQHHPISPPPIPTHNHQKP PTPSHRPQPTQRYTYHHNHTALPI APTRQSNPPHNTHHHTPS/TPRTNSS PPH\HHTLPQRIPPYPPT*HTPQAHS HPAG*RASSQPRRAPSPASRPSPTDP ALRANPLSRSYGSLPTFPYLHCSN MPKACSPWRPAADMCTAR\PRFRPF KPDFQGPAAHRTTPETRRFPRHGPI SRGEP\PGQPCPSQRKENSTPEFPPA SSGIGRVTDGTGLAAAPSPPLRIRGS EPDSPFESAEGHRRSPRPFRTALAQ SLRNE |
| 3181 | 8678 | A | 3441 | 23 | 266 | EMESHVTRLECSGAISAHCTLRP GSSDSPASAS*EAGITGMCTT/ARLIF GFHHVGVQAGLKLL/NIVILLPRPPKV LGLQA |
| 3182 | 8679 | A | 3442 | 840 | 887 | |
| 3183 | 8680 | A | 3443 | 127 | 593 | DKATKLTFRSYAAVILKIHVLTW VILFRRKIIRDETLKLLDLISLSVGKG QCYRVVFFWFFFFFEMKSHSVTR LECSGAISAHCNLCPLGSSDSPASAS LVAGVTGM*HHTQPIFVFLVATGFH HVGQWSRTPDIRVIRPPWPPKVLG LQA |
| 3184 | 8681 | A | 3444 | 2 | 514 | FFFFLQRSL/DSVAHTGGQ/WGGS/ LQPPPPRFEGFLGLKLLGS*HYK/PP RMANFIFSRDGVFAMLARLVLNSS ASSDLPGLASHSAGITG\VSHHARPI FSYKEHQSY\GLRACPAPV*PHLSYL QPQPQYFQIRSHTEAPGST/WNFG DTIQPSTFSFYLT*KIIPILYRVKK |
| 3185 | 8682 | A | 3445 | 2 | 147 | FFFCRD/RSLTMLPRLVLYSWAQVIL PSWPPKMLG*QAQATVPSPPKSIN |
| 3186 | 8683 | A | 3446 | 2 | 328 | TITYRGAKIRITSDSSSETMQAREE* SEIF*VLK/ESSSPH*PKILYSGKLSFK SKGEIK/YF*GKQN/LKEFVSSRPVL QGMLKVVLQREGKLYRSETQTYKK KEKASEKE |
| 3187 | 8684 | A | 3447 | 1 | 357 | GDRVLLCCPG*SADHSSLQS*PSGL KRYFCLGLLSNWKHRCMPPCPANF FNFYFCRDK/SLPMLPRLVSNSWAQ GIFLSQPPVSVGDYRCGAYHALTLFI YGRMGVFAMLAQAGPQTPGL |
| 3188 | 8685 | A | 3448 | 2 | 84 | GLTLLPRLVSNSWPQEILLPW/PPKV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LKL* <u>AQAGLKLLASGNPPALAPKVL</u> KL |
| 3189 | 8686 | A | 3449 | 1 | 439 | |
| 3190 | 8687 | A | 3450 | 1 | 552 | GNEFSILKSPGSSVFRNGNWPPIGER IPDVAALSMGFSVKEDLSWPGLAV GNLFHRPRGYPSWVMVKSGGTKL ALTPQAVVISYPLENRVYVMVGKAN SVFEDLSVTLRQLRNRLFQENSVLS SLPLNSLSRNNEVDLLFLSELQVLH DISSLRHKHLAKDHSPDLYSLEL AGLDEIGKRY |
| 3191 | 8688 | A | 3451 | 3 | 1111 | ILKSPGSSVFRNGNWPPIREARDPP DVAALSHGLPL*KKDLSWPGLAVG NLFHRPRATVMVNVNGVNKLDLP PGSGISYPLENAVPSLDSVANSIH SLFSEETPVVLQLAPSEERVYM/VK GRANSVFEDLSVTLRHSRNRLVFK KTLFLSFTPPQILLSRNNEVDLLFLS ELQVLHDISSLPSRPKHLARDHSPD LYFTGSWAGLDEIGKALLGEDSEQ FRDASKILVDALQKFADHDHVPVFM VGNPVVELVHCPSHLNTSPPLGKTR DLPLRPKQAQEPQQVPYNLA/YKYN FEYSVVFNMVLWIMIALALA/VIIT SYNIWNMDPGYDSIIYRMTNQKISE WIECYLWPRIRKRGFGNWLFC |
| 3192 | 8689 | A | 3452 | 3 | 371 | MLPLARCSSSCLAPLSTYQTQVKTO VHTETCI*MFIAALFIIVRR*KQPKCP SENK/WNKIWHIHTMK*YSATKKN KVLTYATI*MNTENMLSQRSY*QKT T*YLFLLMYMKIQNREMYRYKVD |
| 3193 | 8690 | A | 3453 | 2 | 318 | ETESRSVAQAGVQ*RNLSLQ/PLPP GFK*FFSLSLRSSWDYRCMHDA*LI FLFLVETGFCHASQAGLELLTSSDPP ASASQSAKITSMSHHALPLFSNKVT FWDSW |
| 3194 | 8691 | A | 3454 | 33 | 504 | GLHNFLTYKATIISAVWYAVRVEN RSTEQNRVQK*TYMYVVKDAR*VN GNRILF*YC/WNN*IITWRKMNLNL DLTLHRKVYLKWVIDLNVKAKTVS PLGQNITESLHNFGVGKYFLDT*SI/ MPHKFFFNKLDIIRIKIFCS*KDAINK MKKWPGVVAH |
| 3195 | 8692 | A | 3455 | 16 | 1011 | WPVRAQAGQRPVLHTQVASLFAGV PCVLSHPKKGLLVPPFPSPKKGHLG KPHCPLPSAGRGAAGLGPLAQQPVS PAPASPMAPCKPKGLPPLPMGVEPE ILATMPVLTSHPP/SPEPMQSGNMPP S/PPSLCAFVPRWSHPPVPGWARWS CP/ALPAAPPSL*HWTRMQPPFCVPL RVPWVPSSGARGMKESGLDGQGFL GPTPSASPWGPWFDIRLPGCKQGIL AFKVTGPPTGFPDFEGKRFKKENKP PG*LESKAPDTVK*NPPSTNPPPA FLTWDCGAYRGPAFLVCQPSLLS LILKNIDDTLKCVERFEKLTASKQP KATVVLARRS |
| 3196 | 8693 | A | 3456 | 1 | 348 | PQQLRCFSFWRKDTKVDWLLNLRG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | ARWLEKKTRLHRGPWARPRLMRA QREEALRREGGNPPPRGPGGEEAPL LRSSSGRPAR/HQT*QKSGASPSDPR SASR*ALRREGGNPPPRGPGGEEAP LLRSSSGRPARLRPSRSPERHPPTLA PPPARPSCPALPRLSMSAG |
| 3197 | 8694 | A | 3457 | 2 | 247 | PGCTILAHCNLCLSGSSDSPASAS*V TGNNRHAQPCPLI*RTGFCHVG/R MNMLVFNSLTSSDPLEVST*GPQPP KVLGLQA |
| 3198 | 8695 | A | 3458 | 1 | 515 | GLGSLGPPAAVPTCPPRSPPP/GSPE GALQCGTLPAGTATPDGHVGVAVP FPPTVAPTRRSRSPQSC*WGLQH QLCPGSMEEMHTPHGLALPGASHIV PPTLCAPGGSEGARGI*PPA*AGYAL SLPTQFQTLILHPSCCRPGVP/PINLA AQLPPQVPHAPHAWQLPSAPK |
| 3199 | 8696 | A | 3459 | 2 | 223 | IYISPKALKFCREVGPICPPK\KGSF PKIPR*QIFPFRK*KTGKGQGIKRP IRGKVLRCCKPGLNLGPPRVL |
| 3200 | 8697 | A | 3460 | 2362 | 2696 | |
| 3201 | 8698 | A | 3461 | 1586 | 2325 | SPQRSGAARARPAPHRALLGRVPA RDAGSGRRTRSSRTRCGGCARRWS SISRRRSSETSAGSWRRLSKPSGPG RWRHCARNTGRRCRPWWQISVVP RPSSRP/WLAALAEALKDSGEKPGK GASRPEDLQLIGRLQTRLKEREDIK QLTKKKVEDVPSRVVSVPNLASA KNFLSGDLSSRINAPPITSPSLDPSP SCGRITYKPNQSTDAKTATRTPDGET AQAKEVQQKQGSPPHQEWFTKYFSF |
| 3202 | 8699 | A | 3462 | 125 | 489 | YYLFFFFFFLRLQSLTLVAQAGGQW RNLSSLQPLPPGFKRFPCLSLSSWD YKCPPP/RPG*FFVFLVETGFHHVAQ AGLELLTLGDPPTSISQSAGITGVSH QARPD*ETLEFQGDVRNLEE |
| 3203 | 8700 | A | 3463 | 1503 | 1511 | LFPVPFACPSLNCPSPPPIGVHLP IG*IQRLETPP*EEGRWIPRRTCGPARPGP PPGAPSVTLPPRTVHFGHPAKGIHFR KP/RHPG*CVFILTLD\CVHLH*KIND FIDTNFAMKSGYPNRIVRISFCLHT |
| 3204 | 8701 | A | 3464 | 54 | 593 | RTALPAQHVASTWPGRPSRLLLRG GPGAPRSMQTGDSVGRGASKEPN\ PHSGLPKHPLARSPPQRPSHRAMGQ GSPMPAGPT*TCAQALPPPSQDGLD LGNRAGWGCSPECLSKAPGGEGPA QAHPGPNPHTYRKQWCWKLSPGH ALAPSPPRREVALNLVSFIVPRDSP RPCIISL |
| 3205 | 8702 | A | 3465 | 2 | 324 | FFFFFLKWSLA/SFAQAGVQWCDLG SLQALPPGFTPFSCSLSSWDYRRP PPHLA/NFFVFLVDMGF\TVLARMV SIS*PHDPPALASQSAGITGVSHACP AYNVFKDDG |
| 3206 | 8703 | A | 3466 | 142 | 413 | AQEFKTS LGNMAKPCLYK KYKKM SWDYRRPSR PANFSCFLVETGFCH VAPAGLELLGSSNSPT*ASQSAGITG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VSHHTRPQIFLLPLSN |
| 3207 | 8704 | A | 3467 | 241 | 523 | NISGSFCMPILTAPLFTVAKRWKQY VPISG*MINKMWYIHTVEYYASAKR KIR*/PCAA TWMNLEDMMLEVSQS LEDKYSMLPFM*SIYVKYLEQSNA |
| 3208 | 8705 | A | 3468 | 137 | 382 | NSAVHQKFISIPNTSLPHSLAILKPQI NSLEEET*PFWCKKSSPVPKMRGER NDDNFHKVLLNVTNVDKPQGLRSP KWFCWG |
| 3209 | 8706 | A | 3469 | 2 | 363 | FFFDTESYSVAQAGVQWHDLC SLQ PPPAGFKQFFCLSLPSSQDYRHALP WLANF*FLVETGFHHVGQAGLKL TSSDLPASGSQSAGITGMSQRTLQ LSLKTTELNRNRCVPYCINA |
| 3210 | 8707 | A | 3470 | 135 | 466 | GIDTILTLNQ*SLKTRQ*FTLIIF/IFF FFLRWSL/DSVAQAGVQWRDLGSL QAPPRGFTPFCLSLPSSWDYRRPLP RPANFFYF**RRGFTMLARMVSIS*P RDLPAEFL |
| 3211 | 8708 | B | 3471 | 27 | 21189 | MKVSAARLAVILIATLALCAPASASP YSSDTTPCCFAYIARPLPRAHIKEYF YTSGKCSNPAVVFVTRKNRQVCAN PEKKWVREYINSLEMSMICSGHHV YPNLPTDSFPGLDQFRGNYLHSRDY KNPEAFKKGKRVLVIGLGNSGSDIAV ELSRLATQVHDVKVLGNKPKVIIST RSASWVMSRVWDDGYPWDMMYV TRFASFLRNVLP SFISDWLYVQKMN TWFKHENYGLMPLNGSLRKEPVFN DELPSRILCGTSLIKPSVKEFTETSAV FEDGTMFEAIDSVIFATGYDYSYPFL DETIMKSRNNEVTLFKGIFPPLMEK PTLAVIGLVQSLGAAIPTADLQAW WAAKVFANSCTLPTTNEMMDDTD EKMGGKCLKCPYQFRLMGPGKWDG ARNAILTQWNRTVKPTRTRVVSEV QRPHPFYNLLKMLSFP LLLAVTLT FY* |
| 3212 | 8709 | A | 3472 | 9 | 339 | ITLSLLSFFNLRPSFALLAQAGVHW RDLDSLQPPPLRFK*FSYLKSPRSW DYGHAPPRPANSVLLVETGSLHVSQ GGLILPTSGDPPASASQSAGITGVN CARPPSLFS |
| 3213 | 8710 | A | 3473 | 1 | 50 | |
| 3214 | 8711 | A | 3474 | 1 | 1256 | MAAAAAQGGGGGGEPRRTEGVGPG VPGEVEMVKGQPFDVGPRTQLQY IGEGAYGMVSSAYDHVRKTRVAIK KISPFHQTYCQRTLRENQILLRFRH ENVIGIRDILRASTLEAMRDVYVVQ DLMETDLCKLREKPSKLSNDHILLT FLLPDSL AGPSSYIHSANVLHLRS* SPPTWLIQHHLADLKVCGFGLAGIC RSWRHDHTGFLTEYVATRWRAP EIMLNSKGYTKSIDIWSVG CILGE MLSTRAIFPGKHYLDQLNHILGILG SPSQEDLNCIINMKARNYLQSLPSK TKVAWAKLFPKSDFKALDLLDRM LATFNPKNRITVEEALAHPAYLEQYY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DPTDEPVGEGSPSPFGMEL\DDLPE RLKELIFQETVARFQPGSAGRPPSPR QTSLHPGGWTCPPARPLSRRDC |
| 3215 | 8712 | A | 3475 | 877 | 1463 | LPFTAWP*E/QLQQA VHAGLPQQAK ILFDGGSEIGKILPAFQSGNLSCQLH **IGQRAGRGGRLRIGRQGGFSFHQ* DGQQLIALH/QPGPERVAASGPRWF APAGENPV*WWFRNRQNPLIALRSL PAFQSGNLSCQLH**IGQRAGRGG RIGRQGGFSFHQ*DGQQLIALHRLA LRELQQA VHAGLPQQAKILFDGGSE IGKIPV*GLLRWPPLPRDVQWDSAP LLRARWGL*GER*PREVPAALQGE* PQALLPGGGEPGWQPAEPHPAGGV HRAGPPGGGCWARAGGHQKHL RPAAGVPPDRGCLLQLGQIPH*AGE QVQAGPGTGQPAGEQAQRGLSGNA GPHQVPAEGDTGHLCD |
| 3216 | 8713 | A | 3476 | 29 | 1076 | EQRDPQDIFSQRKSSAFPPSPEIEILS GGKSLSLQLHTPSPG/QQGETPRGG QQSQH/PCQGGGGVPRYACAGGV PVTERGAQGWVHPALRRARYPDA GVQSHMKPAGDWGPGSNKPAGTD ADAVSGRR*LPKTLPSLGLGKKSP GVPGHPEYPE/HGGSEALLHEFLLP VSRL\HGPLYPQMSNGTLHHYFVP DGDYEENDDEKCCQL/PLQGE*PQA LLPGGGEPGWKPAEPHPAGGSSPC WAARWEDAGRVLGGHQQKHLRP RRGRELWQVPAAGVPPDRGCLLQL GQIPH*AGEQVQAGPGTGQPAGEQ AQRGLSGNAGPHQGPAGDTGHLC GAQGLIRAAGPHH |
| 3217 | 8714 | A | 3477 | 3 | 591 | ERNYLFFLRWSLTLSSRLRGQWRN LG*MQPPPPGFKAFSCLSLPSSWD YRRMPPCPANFCILVEIGFHCLAKL VLNSRPHDPPTSASQSAGITGVSHR AQT*KGIHLNELCTALAKEGRAWS GR*RAGAATPAP/PAPFTL*PGCIPES WSPMPPPHLPLTALCKATHAGTK HPLHTKTVSSCGAVLQPTPQRKD |
| 3218 | 8715 | A | 3478 | 1 | 235 | RDHPGQH/GETPSLRKIELAGHGVR HL*SQLGRLRQENCLNSGGRGCSE PRSCHPTLAWAIEQGSVSRKEGHF RLA |
| 3219 | 8716 | A | 3479 | 2 | 928 | RPPRPGTERALPSRLRSRPRVRTETP SPSSSGPPPSRSNTGMAPLRR*RV*R GTVPRSG*KGR*PCSRRRRSVPSGR TPALRGTRAPSDQGKGKARPPEP APSRPCPGSRFCRASRSRTSPRPPTP ARESGNPGRSPDGGEKAAAQGS*K ESAACSNRAWS*WAA\SPPWITVTR QKRRGTLDQPPNQEDKPGARTLKS EPGKQAKVPERGQEPVKQADFVRS KSFLITPVKPAVDRKQGAKNFKEG LQRGISLSHQNLAAQSALMMEKEL HQLKRASYASTDQPSWMELARKKS QAWSDMPQIHK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3220 | 8717 | A | 3480 | 1 | 435 | EKINKIRWLPQQNAAHFLLGTNDK AIKLWKISERDKKAEGYNLKDEDG RLRDPFRITALRVPIKPMMDLMVEA SPRRIFANAHTYHINSISVNSDHETP NIVDIKPANMEELTEVITAAEFHPH QCNVVFYSSSKGTIRLCDMR |
| 3221 | 8718 | A | 3481 | 204 | 397 | VPILKPMGSYG*EASPRRIFANAHT YHINSISVNSDHETYLSADDLRINL WHLEITDRSFNIV |
| 3222 | 8719 | A | 3482 | 1 | 1462 | PLRSWLPRLPDSQADIISTVEFNYS GDLAT/GDKGGRVVIFQREQEVLAQ PRRPALP*SVSSFLSTSCREVVWQCE FSLPFRERIK/GRPHSRGEYNVYS/TA FQSHGTGGFDYLSLEIEEKINKIRW LPQQNAAHFLLSTNDKTIKLWKISE RDKRAEGYNLKDEDGRLRDPFRIT ALRVPIKPMMDLMVEASPRRIFANA HTYHINSISVNSDHETYLSAR*PGGI NLWHLGNHR*EAFNIVDIKPANME ELTEVITAAEFHPHQC�VVFYSSS KGTIRLCDMR\SSALCDRHS/KSFFE EPEDPK/SSRSFFS\EIISIS\DVKF\SH SG\RYM\MTRGLPVRWKVWGPSTW EEAGPVGGPTRVHEYL\RTKL\CSL YENDCIFDKF\ECCWNG\SDSAIMT GSYNNFFRMFDRDTRRDVTL\EASR ESSKPRASLKPRKVCTGGKRRKDEI SVDSLDFNKKILHTAWHPVGQCYL PWLATN\NLYIFQDKIN |
| 3223 | 8720 | A | 3483 | 603 | 659 | MCGFFVFFFWRRL/DSVTQAGVQ WRDLGSLQPLPPGFKRFSCSLPSS WDYRRPPCLANFLFLVEMGF/TTV LARLVSNS*PRDLPTSASPSAGITGV S*HASSRL |
| 3224 | 8721 | A | 3484 | 84 | 202 | |
| 3225 | 8722 | A | 3485 | 3 | 577 | ILGFPPFVRWGSHTVAQAGVQWCD HGSLQPRSPGVK*SSHLSLLGSWNH RHATTTPG*FCFFSRIRSHCVAQAGL *LLTSNHPPALASQTIVGITGVSHWT WPNTGFSVLTATNKNLKKFFHYAISK CLVRAKLSSRLLKIEERNKALSAPV VSVSIFDRVLRLLGYSASDWQPEFV ETAVSNFVIYGIFRGQ |
| 3226 | 8723 | A | 3486 | 3 | 248 | SLYIEIPGGALPEGSKDSFAVLLEFA EEQLRADHVFICFHKNFSFLGFEIV RPGHPLVPKRPDACFMAYTFERESS GEEEE |
| 3227 | 8724 | C | 3487 | 185 | 340 | MDNFCSSLCDFCHQNKNLRLVXXX XXXGGRFKGPLEGPKFTRACNELV FSL* |
| 3228 | 8725 | A | 3488 | 1 | 546 | NDRLN*TRELTSHERRRFRPSSRLT DAQ\RNWRQVLSAGS\LYNEIPGRR AAEGGARNFAVLLEFAEG\QLRAD HVL\ICFHKNREGQKPPLLARTFSFG LEDGEDRGNPLVPKETPDACFHGLT TFEREASSG\EEEEVGARLRGLGQFP RPGAHLVPKPGWGKEPVDSPHLAL GLSPML |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3229 | 8726 | A | 3489 | 1 | 526 | FFFLERDPCSVTQAGMQWHDLGSL QPPPPGFKWFSCLSFSSWDYRCPPP HPANFCIFSRD/MGFTILARLVSNS*P HDPPTSASQSAGTTGVSHSAWPVC/ LFEIEFHSAQAGVQWRDLGSLQP LPPEFK*FSCLSLPSSRDHRHLPSLPA KFHIFSRDRVSPCWPGWS*TPDLR |
| 3230 | 8727 | A | 3490 | 276 | 735 | FFFFFFLRQSFSLVSQAGVQWHNLG SLQPPPPGFRQFSCLSLPSSWDYRHP PPCPANFCIFNRELIIVYLIKTF/IHV GQAGLELLTSGDPPALASQSAGIPG MSHCAQSTH*FLLAQQLFCSIYPSFH AQGVIPRIVTHKRETGSQTLYSIV |
| 3231 | 8728 | A | 3491 | 2 | 344 | FIFIF/NFLRWSL/DSVAQAGAQRD LGSLOPPPGFTPVSCSLPSSWDY RCLPPRANFFAFLVETGFTVLARM VSIS*PRDPPASAYQSAGITGVTTAP GLLF*INICLAAFYFV |
| 3232 | 8729 | A | 3492 | 109 | 559 | QFLHRLVHDSGEVWMKLVE**NTL LAKMVSISWPRDLPASASQSAGITG LIGALVLSVGIYAEVER/HEI*NP*KC LPGSSHHPHPPGRRHVHGLLHWCA GVPP*QPGKH |
| 3233 | 8730 | A | 3493 | 1 | 593 | ETESRSIVQAGVQGRELGSLQTLPP GFTPFSCPSL/SWDYRHPPQHSANFL AFLVETGFTVLARIVSIS*PHDPPAS ASQSAGITGVSHHARPQTGRFLLFL FFFETESCSVTQIGVCSGHDLGSL/ QLRPPGITPFSCSLPSSWDYRRPRL RPANFFFFVFFSRDGVSLC*PGWSRS PDLVICPPRPPKVLGLQA |
| 3234 | 8731 | A | 3494 | 3 | 484 | RFFFFFFLRRSFT/SVAQAGV*WHDL GSLQPPPPWFR*YLCLGPLNSWDYR RGPPRLVNLICIF/M*R*SFTVLARLV SNSWPQ/CDLPP/SASQGAGNTGVS HCARPDEIFYQC*Y*ETEMVRRST TQDRAGSTTVLKLGLQRLPEREIVN LALGALVYRNITPN |
| 3235 | 8732 | A | 3495 | 104 | 288 | GEVICGRRRSEVSRCNLVDLEPKGP WGHWQGG*GDRRAGGTP*GE/GHL RKKAI*GLQVQPRPRTEGPLGA/PG KGDP*TPTEGPRGDARNCDACPRPR ARPVLVW |
| 3236 | 8733 | A | 3496 | 3 | 641 | RPPFFFFFFFRRSL/NSVTQAR LQWHYLGSLQAPPPGFTLFSCSLP SSWDHRRPP/RMPG*LFFAFLVETGF QRVSQGWVSIS*PQ/CDPPASGLSKC WGLQGVSHLRPSHLSFLAFSFFSFET GSFSAQAGLQWANHSSLQAPSP GFTPFCHSLPSSWDCRHPPRPANF /CCIFSRDGVSPC*SGWSRSPVLVIRP PRPPTVLGSQG |
| 3237 | 8734 | A | 3497 | 1 | 296 | VSRRFKQSIPP*AS*GWDHRCVPPAS LANFFLLEMGFPMPLPRLVLNSWA QVILPSQPSQSAVITGMSHCACLYW LLKTKQIKIKQTGMSKVIKLFPL |
| 3238 | 8735 | A | 3498 | 1 | 347 | KKTGRRKRNMIDYEKKKNKEQEER |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RKKRKKRKSSSSSSSPEEKKEEKKK KREEEENRKKEEEEE*DK/KEED RRKHESRRRLRAVGDEVNKVCQE LKRTIPVGRDYRPLDPSS |
| 3239 | 8736 | A | 3499 | 2 | 286 | PQPCSLAPNPPRMPPGSF/TPCSPPR SNITL*KQRPPSPPPSPEPPR\AQQRV AQNLTSRPAAAKPPGWLSTNLSK ALPETPTVAQSPVLFTHF |
| 3240 | 8737 | A | 3500 | 3 | 954 | RPRAGAAGGGGGGSRPSGAHPSRS AC/GCPAGTRPGRAPPAASARPSRS KRGGEERVLEKEEEEDDR*R*R*RR SMCQRSEVAPSSDRPGRCAPP SLTASGDLRVPRRGSRSPPAGTAPGPG *RAGASPGQRHPPGCSPWQP*TRKG EQVFFSFPASVATGPDSPSPVPLPPG KPALPGADGTPFGCPPGRKEKPFDP RSSWNVMGFRSNILLEA*FPEQATA FPRAGN*WQIFAAHAAHRCASPAC SPRASPENLRAPHQGASARPL*GM MDPDGFL/ALSAQPHPCPKPIPAPISP KIPQSPGSWTGDTLSPH |
| 3241 | 8738 | C | 3501 | 68 | 199 | MPIIPALWEAQAGGLLRPGVCDQPG QYSKTSSLINKLKNPPSL* |
| 3242 | 8739 | A | 3502 | 11 | 520 | IRVDDFVAAHSRCCVAFPSSTPRSR RRPKRRRRRRRENDPAASSLP PAHLPCSVSQAAGARLVLRPRACGAQAQ RP*LASGLRTSALRRRGHPRAELRS GPQRRQASE/PSPRGVAGARWWR EDG/RPSKRSRMAQREAQRTSPQR GNRPKTSEKCPPEEKAVCRTPG |
| 3243 | 8740 | A | 3504 | 78 | 595 | NQNRLKEAGWRLKLADETSSSSHQ QVCGTHHVSACYS\GSPYS*KHPD SPSPATSRKQNLSTQSCISPMWPCSQ RSICQFGHGGTESGQGILLGLLRKAI GSPGKRSAPVQPNWEGGNG*EAAW ASSSSPCKVTAPLAPSELFPSKFL LNKKAQRKISHLLEVTVGHL |
| 3244 | 8741 | A | 3505 | 2 | 267 | ADLSAEAL*TRREWDDIFKVLKTSS/ LGQPKILYPSKLSLINEASSSSSSSS SS/REFTTRLVL*EMLKGILHMEAQG QYLPS*KHTKV |
| 3245 | 8742 | A | 3506 | 1 | 323 | IAGEVNTPRSVTDRSS*Q/IIQEGIVQ LNSAIH/QTGCTNINRILPLTTAEYTF FSLYRTFT/KIAHILGHMTHLNKG KRIEIIQSMLSDHNGIQPEISNRKIAG KSPNT |
| 3246 | 8743 | A | 3507 | 3 | 814 | SSGLAGTPPPFSEGAVCRSQPG*GSG \SPPLPVGPACWYLPCGP*DQRCPPG SLGPSAEPGS*NLSCPGRPMCSPAGT SCPAPV/PDSVTPVLRARGTACLSP TFPAWSVPRFQPGAAPSSADLVH FHAASGPSASLSSSLSTKAPSLPLGAC LPAGGVT*LFGPPSG/RLWRPP*GLTG GGLVWAAGVHWACLWPGQASGG SIRHVCVAVGVQGAPAQKEGGAGL GKGLGSFACGRPHLPPAYFACGRPH LPPAYFVLDLPPFAKVLRNINI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3247 | 8744 | C | 3508 | 112 | 252 | MFRSMYNXXXXXXXXXXXXXXXXXXXX XXXXLGMSEXXXXXXXXXXXXXXXXXX LF* |
| 3248 | 8745 | A | 3509 | 448 | 715 | FFIISIKIIEFFFFETESCSSVTQTRVQ WFDLGS\LQPPPPGFKQFSCLSLSIS WHYTHVPPHLANYRIFSRDGV*PC WPGWSQTHDLE |
| 3249 | 8746 | A | 3510 | 55 | 295 | SQYAYTKEMESIVNNLPKKKTPGL HSFTGEFYQTFKNEMIL/YIL*FLPEI* SRG/TYPSSSSSSSL*LPKLDKDIIRK EN |
| 3250 | 8747 | A | 3511 | 2 | 853 | DLMCKKMKHLWLFLLLVAAPRCV LSQLSSSSSSSSSSSSSSSSSSSSSS DSVRHNSYYWGWVRQPSGKELEW IGSLYFTGTTHYSPSLKSRVTISADT SENQFSLTLTSVTAADTAVYYCARP RNIVGSSSSSSSSSSSSSSSPSTKGPS GFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPA/V LQSSGLYSLSSVGTVPSSSFQHPRT YACNGKSQSPATTKVDKGELSPKIS\ CDKNSTHAPPGPQHLETPWGGPVS LFFFPKKT |
| 3251 | 8748 | A | 3512 | 3 | 2310 | QLLTMDWTWNILFLVAAATGAHSQ VQLVQSGAEVKKPGASVKVSCKAS GYTFTNGLAWVRQAPGQGLEWM GWTIASNGKTNYAQKFQGRVTMTT DTSTNTAYMELRSLRSDDTAVYYC AREKDNYATGAWFAYWGQGTLV VSSGES*AWYPGIQCISMLEL*ISAF WGRPGLTLAGGREGAKVTQVAPA RCTPNAHEPRHWTLHGPRIDKNR GASAPWAQLCPTPRSHGTTSLAAS KGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGK TYTCNVDHKPSNTKVDKR/VW*EA STGREGVCWKPGSALLPGRTPAVQ PQPRAARHAPSVSSPGGL*PPHSCSG RGSSGFFHQAPGRHRLDAPTPGPAH KGAGAGLRPAKSHIREDPAPDLSP QRPNSPLPQLGHLLSSQIPVTPNLLS AEPKSCDKTHTCPPCPGKPAQASPS SSRRDRCPRVACIQGQAPAGC*HVV LHLFLAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGGTRGV RGPFGQRPARPTLCPESDRCTNLCP YR\QPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMEALHNHY TQKSLSLGK |
| 3252 | 8749 | A | 3513 | 1 | 1677 | AEVQLVESGGGLVQPGGSLRLSCA ASGFSFSKAYMNWVRQAPGKGLE WVGRIKTKKDAAGTTDYAAPVKGRF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TISRDN SKNTLYLQLNSLRAEDTAV YYCAKDEFSSSTRKNFLTGQSKTFAA YYGMDVWGQGT LVT VSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDY FPEPVT VSWNSGALTSGVHTFPAVL QYSGLYSLSSV VTPSSSLGTQ\TYT CNVNHKPSNTKVDKTVELKTPLGD TTHTCPPCPTP*L\LGGPSVFLFPPKP KDTLMISRTPR\ VTCV VVDVDPRKT PEGQVPTWYV\ DGLAEVHKCQDKSR GKEQYNSY\YR VV\SVLT VV\HQDW \LNGK\ EYK\CRVSHKSPPQAPIETH LPKPKGSPQNPQVYTLPPSRDELTK N\QVSLTCLVKGFY\SDIAVELESN GQPGNNFK\TTPVLDSDGSFFLYSK LTVD\KSRWQQG\NVF\SCSVMHEA LHNPYTQKSLSLSPGKMIPTADKPP LPGSLAGRTKDAWHGTPVYILPRAP KHGNKAPTPWPWAKKKKKKKKKK KGGRSRVSLEGPKLTRTQLS |
| 3253 | 8750 | A | 3514 | 1 | 164 | TRVNENQIESKAAYALFYKRQDVA RRLSPAGS/SGAPASPACSSPPSSEF MDVN |
| 3254 | 8751 | A | 3515 | 1 | 712 | EILIIHLKRFSYTKFSREKLDTLVEFP IRSGARERMAGGRQGKEGVYQY*P SPHPQ\DLDFSEFVIQPNESNPELY KYDLIAVSNHYGGMRDGHCMCQA VGGACPGGSGQGGDQDLPSE*LGM *ASGEGSSVVGK*TRSEIWTLSEEA RKGRRG*LSFPFR\TTFACNKDSGQ WHYFDDNSVSPVNENQIESKAAYV LFYQRQDVARRLSPAGSSGAPASP ACSSPPSSEFMDVN |
| 3255 | 8752 | A | 3516 | 3 | 3090 | IPLLQLLLRRLWRRHGRWTEPREPQ HEELPGLDSQWRQIENGESGRERPL RAGESWFLVEKH WKQWEAYVQG GDQDSSTFPGCINNATLFQDEINWR LKEGLVEGEDYVLLPARAWHYLVS WYGLEHGQPPIERKVIPLNIQKVE VYPVELLLVRHNDLGKSHTVQFSH TDSIGLVLRTARERFLVEPQEDTRL WAKNSEGSLDRLYDTHITVLDAAL ETGQLIIMETRKKDGTWPSAQLHV MNNNMSEEDDFKGQPGICGLTNL GNTCFMNSALQCLSNVPQLTEYFL NNCYLEELNFRNPLGMKGEIAEAY ADLVKQAWSGHRSIVPHVFNKV GHFASQFLGYQQHDSQELLSFLLDG LHEDLNRVKKKEYVELCDAAGRPD QEVAQEA WQNHKRRNDSVIVDTFH GLFKSTLVCPDCGNVSVTFDPFCYL SVPLPISHKRVLEVFFIPMDPRRKPE QHRLVVPKKGKISDLCVALS KHTGI SPERMMVADVFSHRFYKLYQLEEP LSSILDRDDIFVYEVSGRIEAEIGSRE DIVVPVYLRERTPARDYNNSYYGL MLFGHPLLVS VPRDRFTWEGLYNV LMYRLSRYVTKPNSDDEDDGDEKE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DDEEDKDDVPGPSTGGSLRDPEPEQ AGPSSGV TNRCPFLLDNCLGTSQWP PRRRRKQLVQLQTVNSNGHNRLH HSPCTKSNAPVHCYSTWKPEMK K\RYDE*EGEGLREGNAFRRGYV* RKAPVRLQECIELFTTVEPPPFGGK\ EREKPW\YCPASCKQHQLATKKLD LWMLPEILIIHLKTFPPYTQVLPEKK LEHPSWKFPYPGTLDFFS*/EFVIAH QNEVEIRELYK\YDLIAVSNH\YGG MRDGTLTQHLACNKDSGQWHLLI DNSVFPLFN*GIQIRVPRAAYVL\FY QRQ/DTLARRLLSPCRAHLAPSVLP CLHAPSPQLVSSCDVILRALGPAPPE KKKKKALSALSLVSAPLLLFVLGA PARHCRLSRGYCSPVPLNRSPLPGKN RSCLLAVRAPPCVCPSSSDPPF |
| 3256 | 8753 | A | 3518 | 1 | 271 | PLPPGFK*FSYLRLPSSWDYRCPPPH PTNF*FLVAMWFCHVGQAGFELLT SGDPPTSASQSAGITGVSHRSRPVD FLNYLLRKSYPFT |
| 3257 | 8754 | A | 3519 | 3 | 633 | FFFI*DRVSLIAQAGVQWRNCGSLQ PPPTGFKQFSCSLWRSWHYRCRH HAQLIFVFLVKTGFTMSVKADLEL LTSGDPTASASQSAGITGVNHQCPA SKQF*FHCKSW/CLF*MQSLSFFLG GGQSRVSGQAGVQWHDLSLQPLS PGLKQFSSLSLPSSWDYRGVPLRLA NFCIFSRDGVSLCWPGWS*TPDLKA NPTRLGLPKGWGL |
| 3258 | 8755 | A | 3520 | 2 | 430 | CLKNMVGAGEVDEDELEVETKEECE KYGKVGKCVIFEIPGAPDDEAVRIF LEFERVESAIKG*WYS*ILKNKKVEF TALIFTSKAYCLIKVKPLSYRIPALF CLLFAFQRLTLNGRYFGGR\VVKA CFYNLDKFRVLDLAEQV |
| 3259 | 8756 | A | 3521 | 3 | 1076 | HEERQRQRELERQKEIEEREK\RRK DRHEASGFARRPDPSDEDEDYER\ ERRKRSMGGAAIAPPTSLVEKDDEL PRDFPYEEDSRPRSQSSK\AAIPPPVY VEQDRPARSPT\GPA\NSFLANMGGT VAHKIMQK\YGLPGGPRVLGKHEQ GLSTALSVEKTNKRGGKIIVGDATE KDASKKSDSNPLTEILKCPTKVLL RNMVGAGEVDEDELEVETREECEK\ YGKVGKCVIFEIPGCPLMMEASTG YFLEI*EELNSAIKAVVAL\NGRYFW CTGW*KAMFLQIWAKFRVLDLARN QVWIFKEPRARVISGDPLNELQAVE KKEKGPQPPWLFAYPRLLEGLLRY MLIDPFFYFVVF |
| 3260 | 8757 | A | 3522 | 1381 | 1787 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH |
| 3261 | 8758 | A | 3523 | 1147 | 1553 | LEYVAHPLHQLLILNNFYSVLNEKY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 3262 | 8759 | A | 3524 | 1456 | 1862 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 3263 | 8760 | A | 3525 | 889 | 1295 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 3264 | 8761 | A | 3526 | 743 | 1149 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 3265 | 8762 | A | 3527 | 2583 | 3580 | DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTSDSPT LASQSAGITGVNHHAWLFFFC/SD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR/YPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGF/TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLFYFHRDEGSLCCPGWS* TPELK |
| 3266 | 8763 | A | 3528 | 1966 | 2372 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 3267 | 8764 | A | 3529 | 10304 | 11097 | FAFSPK*HSCLRPCCI*FSSGLLHEVL *LLPLCWP*THGWDPGSREANKSPK LHAIRCWVWLEENLWLSSNSQSLQ TVKN*ESHIN*SCRSNLI/HH*FWNQ VK*K*LLNISGNCFFFLRWSL/DSVA QAGVYWRDLGSLQPPPPGFKRFSCSL SLPSSWDYWHLPCLAKFCIFSRDG/ GFTIWARLVLNS*SCDLPASGSQSA GITGVSHHTWLQVTYFLKEMRSCY FSQVGWPQTPGLKQCSHLKLLSSW DYRHMSPHLAISGS |
| 3268 | 8765 | A | 3530 | 87 | 411 | ARLVQNTVAQLKEVQYKLFFGFLF FE*/QSHSVAQAGYSAVIAHCNLSL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LGSSDPFFSAS*VAGTTGMCQHAW LIFDR*WR*GLAMLPRLM*IFLISH LRLIWSAWS |
| 3269 | 8766 | A | 3531 | 31 | 403 | THLNLQIRGSPLFFF/FELESSVA\ RLQCSGVISSHCNLRPGSSNSPASA S*IAGITGAHHNPG*FF\VFFSRGRFH HVGQAGLELLTSSDPPRPSTLPQSG WGFRHGAIA PQWGQVPFHRS |
| 3270 | 8767 | A | 3532 | 7 | 1047 | |
| 3271 | 8768 | A | 3533 | 3 | 53 | |
| 3272 | 8769 | A | 3534 | 7 | 960 | |
| 3273 | 8770 | A | 3535 | 1538 | 2287 | WWSSSKLRLIYYYSLFFFFFFFFFG M*SYSVTQARVQWHHLGSLQPLPP GFKQFSCSLPSSWDYRHPHPLANF LYF**RWGFTMLARLISNS*PQ/CDL PASASQSAGTTGLSHCAQ/LLFAFLT DNSVLIETALT*LQSCAS*KLN*IPL ESSDFYTFEFETESHV/TQAGVQCR NLGSLQPPPPRFKQFSCSLPSSWDY KCTLRPANFCIFTRQGFTMLARIVS PGSLGLMISLPRPPKVLGLQV |
| 3274 | 8771 | A | 3536 | 3 | 263 | LGVGDRVSLCHPVWSASSL*SQT PG LK*SSHLSPSRWDNRHAPCLA/SL KNFCRDRGLTMLPRLVSNSWAQAI LPPQLPEVLGLQV |
| 3275 | 8772 | A | 3537 | 33 | 295 | AGMQWCSLGS LQPPPPVLRRSSHLS LPSSWEYSHTC\NFCIFCRDGFVLP RLLG*SNRPASSS*NTGITGVSHRAQ PSLFLSYSFFF |
| 3276 | 8773 | A | 3538 | 3 | 33 | |
| 3277 | 8774 | A | 3539 | 1 | 375 | |
| 3278 | 8775 | A | 3540 | 3 | 340 | HEVVAA*YY\G*PSIAQEVAGTLAE LDVTLQLEDKFLQNKVFLTGP HIS LADLVAITELMHPAGAGCHVF*GLP TLATWRQLVEASPGEDLFQEVHEVI LKATDFPPADHTI |
| 3279 | 8776 | A | 3541 | 30 | 284 | YSVSTPLRDSNPNNHLSLGHCPASS QTEPQAPQALGQPATKLLPHPP QPP /MPQPSSKP*VSATSLCTSPPLPPLCP AGGSSGTT |
| 3280 | 8777 | C | 3542 | 127 | 435 | MAASXNPEVLDITEETLHSRFL EGV RNVASVCLQIGYPTXASVPHS IINGY KRVLALSVETDYTFPLAEKV KAFLA DPSAFVAAAXLGCHHSCSXCCC SP S* |
| 3281 | 8778 | A | 3543 | 3 | 417 | |
| 3282 | 8779 | A | 3544 | 2 | 881 | RGKLCAYGRPPMMRRSIEGN/LENN PASEELLPH*RGHLGFCFTRED\LT E\NRDMLLANKVPTAARCWCQLPP CEVTVP\A\QNTGLG\PEKTSFFPGL* VSPTKNLPGGTH*KS*SYVQL\IKTIG DKMGSQTKAKAAEKMLKNLPPSPF GAGQPKQGV\RKNGKHPTNPESA*I STRGKLCHSRFLGGCPANVAKCLS CKIGYP\TVASSTPIPI\NGYKRVPGP CLWTPDYTFPLAEKVKAFLADPSC LCVLLPPVGAATTACFALLQPPA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KVEAKEESESEDEDMGFGULFD |
| 3283 | 8780 | A | 3545 | 2 | 311 | DGVSLLLSPRLQWHNLGLLQPPPP* FKGFSCSLPGSWDYRHV/PPCLAN FVFLVETGFRHVGQTGLELLTSGDP PASASQRAGITGVSHRTWQKMYFL SQKYF |
| 3284 | 8781 | A | 3546 | 1 | 290 | KTFFFF*DRVLFCCPG*SAVAQSW LTAALTSWAQGSS*DHRLKP/HMLS FFYFCRQGLTMLPKVVLNSWAQAI LPPQPPM*PGLQACTYAWSLRAL |
| 3285 | 8782 | A | 3547 | 229 | 486 | IKIKINQAWVCACLSLPSSWDYRHG PPHPANFVFFLVETGFTMRARLA SNS*PCDPPTSASQSAGITGVSHRAG CSEAFRSQV |
| 3286 | 8783 | A | 3548 | 2 | 431 | ARGSIYQNDTTI*NMVLDNRASECT VRELVKQK/R*MEKPTIIFGDFNNPV SLIEGSSK*KISGTMENLKNANTFT* LFIKCSAQHQNAHSFPV/PHRTF/S KIDHFLWCKRGLNKCKMIQIQNVV CDHTALNKKPMPERSLEK |
| 3287 | 8784 | A | 3549 | 2 | 194 | VDFFFFFLRWSI/NSVTQAGVQWRN LGSLQALPLGFMPFSCSLPSSWDY RCPPPAHPANFFLHF**RRGFTVLAR MVSIS*SHDPPASDSQSAGITGLSHR AR/LKGHYDF*EMAC/HCLICKRGRQ VP*LFFFFFEMEYHSVTQAGVQWR NLGSLQALPLGFMPFSCSLPSSWD YRCPPPAHPANFFLHF |
| 3288 | 8785 | A | 3550 | 2 | 489 | ARGTQALMMMT/GTACHASPH*GG RLTS*PGAICFTHGDMAA*WREESC LLVT/WDLVMSEGLGMRYAFIGPLE TMHLNAEGML\SYCDRYSEGIKHV VQTFGPIPEFSRA\TAEKVNQDMCM KVP**PGSTLAAR\RHWRDE\CLMR LAQV*RSSSCSPQLNFLC |
| 3289 | 8786 | B | 3551 | 13 | 441 | MEGVEEKKKEVPAVPETLKKKRRN FAELKIKRLRKKFAQKMLRKARRK LIYEKAKHYHKEYRQMYRTEIRMA RMARKAGNFYVPAEPKLAFFVIRXR GINGVSPKVRKVLQLLRLRQIFNGT FVKLNKASINMLRDCRAIYCMG* |
| 3290 | 8787 | A | 3552 | 1 | 775 | RRVPA\VPETLKKKRRNFAELKIKR LARKKFAQQML\RKAR\RKLIYEKAK H\YHKEYRQMYRT*NFEWARMGK KKLANFYVPAEPQIWRVFVIRIRGIN GVSPKGSERFFQLRLRQ\FNGNLL *KLNQGFRFNMAEDF*SPYIAMGGT PNLKVSKMN*SYKRGLWAKSNKK RUALTDNAL\IARSLGKIRHILawe DLIHEIYTV\GKRKF\EAANNFLWPFK LSFSTKVEMKKKTTHF\VEGGDAGN REDQINRLIRRMN |
| 3291 | 8788 | A | 3553 | 1 | 356 | SHHVQLLEFFVEMGSPCVSQA\VL* LLGSSDPPVLASENVGIK/GPPHPA* S*F*IIACVFVYIYFLEMGSCSFAQA GVLWYNHSSLQR*TPGL*QISLLSPL SSWDYRHVPPCLVIYF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3292 | 8789 | A | 3554 | 3 | 352 | HEGFTMLVRLVSNS*HRDPQASASQ SAGITGVSHHANP/CFFLTESNWVA QAGVQWRVLS*LQPPA*FKGFSC SILSSLS/WGYRCLPP/HPANFFFF*K GFFWFPSWNAMGKKWFN |
| 3293 | 8790 | C | 3555 | 55 | 201 | MPKNYPRLWWQHVCNPQPTWEAE VGELLEPQAEVAVSQDHATALQP G* |
| 3294 | 8791 | A | 3556 | 3 | 212 | QEFFFFFEM*SRCVTRLEGSGAISA HCKLCLPGSCHSPASASQDSIFNTQ HLNVGRNSTSKSKPIDYF |
| 3295 | 8792 | A | 3557 | 2 | 265 | EKESRSVTRLECRGAISAH*NLHLP GSSHSPPSASHVAGTTGACTT/AQLI FFVFLVETGIHHVGQDGLNHL/NLVI RLPQPPKVLGLQA |
| 3296 | 8793 | A | 3558 | 354 | 675 | HFISYFPDGAELTSSIRVPFFYSNVLF FF/CRQESRCHQAGVQWHDLGSLQP PPPGFKRFSCLSL*SS*DYRQAPPRP ANFCIFNRGPVSPCWPGWSQSPDFV LVPNS |
| 3297 | 8794 | A | 3559 | 1 | 1203 | |
| 3298 | 8795 | A | 3560 | 2 | 634 | VNTEKLTAFVNTLNGKNGTGSHLV TVPPGPS*ADALISSPILAGESGAML GLGASDFEFGVDPSADPELALALRV SMEYQRQRQEEYARRAAAASAAE AGIATTGTEGERDSDDALLKMTTSQ QE\FGRT\GLPDL\SSMTEEEQIAYA MQMSLQG\AEFGQAESADIDASSA MDTS*PAKEEDDYDVMQDPEFLQS VLENLPGVDPNNEAI |
| 3299 | 8796 | A | 3561 | 506 | 930 | IRTTQIGLCLSQVYFIVFDLHAQYEII KATNITTPTLSKIISIRPRRFIPVT*L LNMFAFSSPMVPVSLSQRIGTI*FLF RFFNT*IFSDGLTNRLTCSRANCKV NPVIGSISKYVLCSSSFGFNPSIGSET SGLAYRK |
| 3300 | 8797 | A | 3563 | 3 | 271 | FFLET*SCSVG\RECSGVILAHCKL RFPGSSDSPASASGVVGTGAAHHT RLFCIFSRDGFHHVGQDGLDLL/NL VIHPPWPPKVLRLQA |
| 3301 | 8798 | A | 3564 | 1 | 218 | ETGSPSVTRLECSSIQ\SAHCNLDLP GSSDPPVS\APQVAGTTGTCHNTQLI FVFFVEMGFCHLSQAVLQLLG*TIH PLWPPKVLGL*AQVILLSQTPQVAG TTGTCHNTQLIFVFFVEMGFCHLSQ AVLQLLG |
| 3302 | 8799 | A | 3565 | 1 | 294 | ASTFFFFGDRVSLFLPRLEYNGAIS AHRNLC/LPGFSSDSPAS\AS*VAQD YRHAPPHLANFVFLVETGFLHVGQ AGLKLPELSVIHPPWPPKVLGLQA |
| 3303 | 8800 | A | 3566 | 3 | 292 | FFETKFSSVTQAGVQWHNLGSLQPP PPAFKRFSCLSLPSSWDYRHLPPRPA NF*FLVEMGFHHVDHADLELPTSS DPPTLASQSAGIIGVSHRARP |
| 3304 | 8801 | A | 3567 | 3 | 389 | |
| 3305 | 8802 | A | 3568 | 1 | 672 | |
| 3306 | 8803 | A | 3569 | 1 | 2018 | MSDNGVRTGAPSTDQRTGMSVRAE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | WRRGEFLVTGRRPLVGGGAGEEGE LGGDARSSRDPELQSYAAFVAVVT RIWLPAPRCPALGGLASGPGKAEQF SRSLYLPDHLGEGNGLLGKSLEPY RSACMSAAGLKITGSKETKRRLLI SIDWSRDLMLNLCIYFRVYCQEKQEE RRELPRITGPPPEAAVVAFEWLKTS TLTGLHPQLPLSLPQPECALPYLVR AFSRGDYMGRIQEVGWVTAGLVIW AGTCYYIYKFTKGRAQSVRTLARN GSTVKMETVVGVSQTLAINEAEIK TKPQVEIGAETGARS GPRAEVETKA TAIAIHRANSQAKAMVGAEPETQSE SKVVAGTLVMTEAVTLTEVKAKAR EVAMKEAVTQTD AEAGKIVKKEAV TQTKAKAWALVAKTEAKREAMTQ TKAETHILAEKETEINRVMVTQSET LAVPREVAKMGATNKTGIVDETKT RALEETVSVAKTQSEARPGATVDA RGNPNGMSREVAGVDMKSCAQSQ AVTKIQGDDMPGTGVEDMGNCKT MSRAESGADTRASAQPQIFAKTQTE AIPGAKIDAGGNTNAMCKVGAGAD VRACIQPQTVAKKQAEVTSGARVD GRGNTNVISKAITGADMRAAAQPQ AVASTHAEAMSDAKVKNRGNPNA MTKAGAKANLRANSQVEALPDAR DKSRGNPNVMAKVGDGTDMLSCT QPQLVASVQADTLSDGKIKVRGNV NTMPKEGAGVDMKAQGMASQSGE ALPNTRGKARGKAKAKCKTGPGM DMKTCTQPQAGVKTPAEALLDSRV DGRGNPNATSKAGTKADQRCVCGQP LVVANPQGEALPGAKNKVKGNPHT VLKVGAGEGTTDSAQPEAVVSFQG EALLGTKNKVKGNPNVVLKAEVGE GAMGTAQLQIMASSKGEALLDSKN KVKGNSNAVSKAGAGTDTTGSVQP QIVANSQGEVLPGAKNKIRGNPTTV PNSGVGPYTTDSARLQAVANSQGE VLPGAKNKVKANLNAVSKAEAGM GATGSVQPQAVANSHCETLPGAKN KVRGNWNAVSKAGAGMDTRGSAQ PQAVANSQGEVLPGAKNKVKGNPN VVS KAGAREDTVGSTQPQVLASSQ RETLPGARNKVKGNSNVVSKAGAR EDTMGSAQPQVVANSQRETLPGAR NKVKGNSNAISKAEAGAGIMGSVQ VQVVASFQGEVLPGAKNKVRGNSN AVPKAEAGADTVGSAQPQAVANSQ SETLLGARNKVKGNTIAVPKAGTG AGTRHSAQPQIVAGSQGETLPGARD KSMSTSEAEATAEDEAYAKPEAEA MPTSESEGGSGTQACRKTQPNIH DY YWNGIGVEDWIAAERWIKFRFQTM DGDWENS VSWADDENEASIGSWSG ASDKAGIIRSWAVACDETSVKSWA GARAENVVGIGTWARAGEQASGGL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WAGGQTSEGTWAGDKASGGAWT GAENQASGGSWALAGNQAIGELW AAGQASDGSWPGGQASGVSWVGE EAIGGSWTGAENQASEGSWAGAGA GNMSSVSYWAGVVDQAGGGSWA GTSDQSGGGGSKPRFEDQASGEGSW AGAGGQASGGGMLGPEDQSSGRSW ADTADQASGG SRLGHVDQSSGGA WAGTLDQSGGGGSKPRFENQTTEEG SWAGAGGQAGGGGSKVGPEDQSSG RSWANS GDQISGGFLVGIVDQANG GSWTGAGHPASVGP KPIFEDQVSGR GSWADAREQVVGDSRLGLRDQSSG DSWAGTGDQASGWFCVCPGSQTN GGSWG GASGDVGGSRPGPTNQSS AGSWDSPGSQVSGSCWTGAGAVD QAGGCSKPGFEDQAIGGGFWPGAG DQTGGGSRPGSEDQSSGIGSWGVA GGQVLGGARPGPADQSSGGSWAGT GNQSSGRSWIGPDQAVDCSKPEFE DQACGGGSWAGAGSQASGESWAG SRPGNEAIGGSRMGSEDQATGGSW ARSEDQASGRFQVSFEVEANEGFW FGPGA EAVIGSWCWTEEKADIVSRP DDKDEATTASRSGAGEEAMICSRIE AENKAKSRLGAGEEAGVESWTLAR NVGEDELSRESSPDIEEISLRS LFWA ESENSNTFRSKSGKDASFESGAGDN TSIKDKFEAAGGVDIGSWFCAGNEN TSEDKSAPKAKAKKSSES RGIYPYM VPGAGMG SWDGAMIWSETKFAHQ SEASFPVEDES RKQTRTGEKTRPWS CRCKHEANMDPRDLEKLCMIEMT EDPSVHEIANNALYNSADYSYSHEV VRNVGGISVIESLLNNPYPSVRQKA LNALNNISVAAENHRKV KTYLNQV CEDTVTYPLNSNVQLAGLRLIRHLT ITSEYQHMTNYISEFLRL LTVGSGE TKDHVLG*EQRQSQCHD*SRGQ GK LEGQFPG |
| 3307 | 8804 | A | 3570 | 1 | 611 | YAALGADVTRVSLPTPRCPALGAL ASGPGESGPTLLQDCGAKCPG/GPQ PRGENREKEETTRIGPGVMESKEKR AVNSLSMENANQENEEKEQVANK GEPLALPLDAGEYCVPRGKS*GGSA FRAAHP EYRWDMMPHRPW RTHRPR DEEKRIMEKDWGGGETADGKKLE GEKPVGVISLRGESGTDPPSPMTHH D*VFALLPLNP |
| 3308 | 8805 | A | 3571 | 1 | 379 | EMESHVTRLECS/GTILVHCNLCL LGSSDSPASAFQVAGITGVHYNA*V IFVFLVETGFCYVGQAGLEFLTSTD PPASGFQNCWNYRDEKPHPAETVS KTTTTKNYICVSTINYKKKNLGLSNI L |
| 3309 | 8806 | A | 3572 | 6 | 222 | DRVSRSA AQAGV/QWC/NLSSLQPL PPRFK*FSCLSLPSTWDYRHTPPRPA NFCIFSRDRVSPCWAGWSQSLDLK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3310 | 8807 | A | 3573 | 1 | 445 | |
| 3311 | 8808 | A | 3574 | 1 | 3212 | DSINNLAELNKFALRKQLEQDVL SYQNLRKTL EEQISEIRREEESFSL YSDQTSYLSICLEENNR FQVEHFSQ EELKKKVSDLIQLVKELYTDNQHL KKTIFDLSCMGFQGN GFDRLASTE QTEIMKDLSKGGCKNGYLRHTESKI SDCDGAHAPGCLEEGAFINLLAPLF NEKATLLLESRPDLLKVVRELLLGQ LFLTEQEVSGEHL DGKTEKTPKQKG ELVHFVQTNSFSKPHDELKLSCEAQ LVKAGEVPKVGLKDASVQTVATEG DLLRFKHEATREAWEEKPINTALSA EHRPENLHGVPGWQAALLSLPGITN REAKKSRLPILIKPSRSLGNMYRLPA TQEVVTQLQSQILELQGELKEFKTC NKQLHQKLILAEAVMEGRPTPDKT LLNAQPPVGAA YQDSPGEQKGIKT SSVWRDKEMDS DQQRSYEIDSEICP PDDLASLP SCKENPEDVLSPTSVAT YLSSKSQPSAKVSVMGTDQSESINT SNETEYLKQKIHDLETELEGYQNFIF QLQKHSQCSEAITVLCGTEGAQDG LSKPKNGSDGEEMTFSSLHQVRYV KHV KILGLAPEMIDSRVLENLKQQ LEEQEYKLQKEQNLNMQLFSEIHNL QNKFRDLSPPRYDSL VQSQAARELSL QRQIKDGHGICVISRQH MNTMIKA FEELLQASDV DYCVAEGFQEQLNQ CAELLEKLEKLFLNGKSVGVMNT QNELMERIEEDNLTYQHLLPESPEPS ASHALSDYETSEKSFFSRDQKQDNE TEKTSVMVNSFSQDLLMEHIQEIRT LRKRLEESIKTNEKLRKQLERQGE FVQGSTSIFASGSELHSSLTSEIHFLR KQNQALNAMLIKGSRDKQKENDKL RESLSRKTVSLEHLQREYASVKEEN ERLQKECSEKERHNQQLIQEVRC GQELSRVQEELKLRQQLS QNDKL LQSLRVELKAYEKLDEEHRLREAS GEGWKGGQDPFRDLHSLLM EIQALR LQLERSIETSS TLQSR LKEQLARGA EKAQEGALTLAVQA VSIPEVPLQPD KHDGDKYPMESDNSFDLFDSSQAV TPKSVSETPPLSGNDTDSLSCDSGSS ATSTPCVSRLVTGHHLWASKNGRH VLGLIEDYEALLKQISQGQRLLAEM DIQTQEAPSSTSQELGVTKGHPAP LSKFVSSVSTAKLTAEAYR/RGLK LLWRVSLPEDGQLPLHCEQIWRNE RQRVPKLHKKLFEQEKKFAKTP*RF LQLSK\RQEKVIFDQLVVTHKILRK ARGNLELRPGGAHSRT\CSPSR\PGS ALATRKEHRNQQHS AEQASRNSWQ GGQRRHRKEPSLWLSKPCPSLRCPF SLTNTMVTNIPWKVIHLC LIPPRQ SGNIKVLERFLYIDTKFSQNR CQKA LPMASAYQSNLPHNYTMTVHNN |
| 3312 | 8809 | A | 3575 | 1 | 1362 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QLAQUALRVYSQHAIGAVLYKYSMQ VHEDCYKFWSNGWMLCEERSLTD QHCVHKFHSPLPKSGEKPEADRNPPV LYHNSRARSTGACNCGRKQAPRDD PFDIKAANYDFYQ\FWEEKCCGKIG SYSISQYLEPSTPGSWLLA*KWNP/ RPAPPDSADKLKEKEPQTQGESTS LSLALSLGQSTDLSLGTYPADPQ/DRR R*SRSSWSSRSEN/SRRDQTSIDRH/ LTVEYLPGLMLHSNCPKGLLPTFSSW VFVKLGPG*SYNFHTRFR/NQQGFIP GNKLSYALGTLSSRARSWR*RRLR HKLLACSK*SYSWKEKCGCNGKRR TAR*H\TRAFVGFYEDSRGRRFMC SGALTK**K*WGSQA/IRDSAFKSP*I VDMPLYIRHPLKVEGLKTLITLQL MRLFVVVPDASFAR |
| 3313 | 8810 | A | 3576 | 1 | 673 | EGGWMEDYDYVHLQKKEEFEMTH IELLDKGSITRQGMSQL*LEQLKLFV RLEQEVSRPIDHDLAIWTPAQPLAP GRSGG\LGPSDRQLLLFYLEQCEAN LTTLTNAVDAFFTAVAATNQPPKILV GASKVLL\SAHKL\FIGD\TLRQA KAA\DVRSQVTHYSNLL\CDLL\QGI VATTK\AAALQYPIAFPGPKDMV/E KRVKELGHSTQ\QFPPRS*GQLGSPP EGW |
| 3314 | 8811 | A | 3577 | 3 | 531 | FLLQSL/DSAGQARVQWCDLGSLO PLPPRFMRVSCSLSSWDYRHLPP RLAMIFVFLVEIQGFTVLARLFSNS* PQ/CDPPTSASQSAGITGMSHHA\RL FLFFETGSGSIAQGGVQ*CNLGSLOP LPPRLKPSSHLSS*DYRRVPTCP SNFCIFGRDGVSPCCPDWSGTPGLK |
| 3315 | 8812 | A | 3578 | 1 | 223 | GSGGIHRLPLSSRPEQPIVWLWAPG CFSHLSRLQVTV*/GEIKQRCRELHH SLAQHPRHQAGNHISHPILHLKIL |
| 3316 | 8813 | A | 3579 | 3 | 341 | FFETESCSVSQAGVQWRDLGSLQA LPPGFTPFSCSLPSSWDYRHLPPHP ANF/SVFLVETGFHRVSHDGLDLLT RDPPTSASQSAGITGVSHRARPVAI FMFCEYPLFSSH |
| 3317 | 8814 | C | 3580 | 168 | 347 | MTYGLLLFLGNNPHLNLYXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXSTIV* |
| 3318 | 8815 | A | 3581 | 852 | 1216 | GFLINGNTDFFFETESRSVAQGGV QWRDLGSLQPLPPGFKRFSCLSLPSS WDYRHLPPQYPS*IFVFLVETGCSSY STIL**RPHVGQAGLELLTPGDPPAS TSQNAGITGLSHRTWSAI |
| 3319 | 8816 | A | 3582 | 2 | 238 | |
| 3320 | 8817 | A | 3583 | 680 | 891 | |
| 3321 | 8818 | A | 3584 | 697 | 979 | IFGVSQGYKILWKMNSLPGVSFES KRSF*QK*LQILSS*FAKKIFYWHEN NRCKWRPNIPKCIYSITSQKLFYPS LLFFPLPTFLGVGGAR |
| 3322 | 8819 | A | 3585 | 2 | 518 | GRGYQNPGRQCTSDRLSEHVSEGES |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PPDSQEDSFQGRQKSKDKAATPRK DGPKRSLSKSVPGYKPKVIPNAIC GICLKGRESNKERKG*IHFIHCSQCE NSG\HPSCLDMTNGACFYD*DLTPW QCMECKTCHICG\NPHHEEEMMFC\ DMCDRGYHTFCGGPGSNPTRPLNL |
| 3323 | 8820 | A | 3586 | 1 | 165 | SLEDRVLLCHPGTAYCSLELLGSISP PALTLTSEASLPGRDYREIPGSPCQL FL |
| 3324 | 8821 | A | 3587 | 1 | 249 | LVDRVLLCHPGTA/VLQP*TPGINQS SCLSLPSS*DIYRYVPPCLVYCFIFLA EMGLTVLPRLISNSWPQAILPSQPPK VLGLQT |
| 3325 | 8822 | A | 3588 | 3 | 282 | NSWDYRHPLSCLANFCIFSRDGGFT ILTKLVLNS*PRDPAASASQSVGITG VSTHGLASWN\FNKLKNSYTQVD*L GSQEWPLKVCLAKPRTAS |
| 3326 | 8823 | A | 3589 | 1 | 714 | |
| 3327 | 8824 | A | 3590 | 1 | 726 | MAEGETESPGPKKCGPYISSVTSQS VNLMIRGVVLFFIGVFLALVLNLLQI QRNVTLFPPDVIAISIFSSAWVPPC CGTASAVIGLLYPCIDRHLGEPHKF K\REWSSVMRCVAVFVGINHASAK VDFDNNIQLSLTLAALSIGLWWTFD RSRSGFGLGVGMLFLATVVTHL*V YNGVYQYTSPDFLYVRSWLP\CIFF AGGITMGNIGRIQLAMEYCKVIAEK I/LIRNEEGKK\YLLYRKAR |
| 3328 | 8825 | A | 3591 | 469 | 537 | PGLARRAMASGRSHGWP*IPPLRST FQGGRTLDAAFTRINCHGKTYLFKG SQHWRFEDGVLDPDYPRNISDGF GIPDNVDAGLALPAHIYSGRERVYF FKGKQYWEYQFQHQP NLEEREGSS LSAVFEHFAMMQRDSWEDIFELLF WGKTSAGTRQPQFINLDWHGEPWQ ADAAMAGRIYISG |
| 3329 | 8826 | A | 3592 | 193 | 384 | |
| 3330 | 8827 | A | 3593 | 96 | 1635 | ARSPAMAPLRPLLILALLAWVALA DQESCKGRCTEGFNVDKKCQRDEL CS\YYQSCCTDYTAECKPQVTRGDV FTMPEDYTVYERLGEEKNNATVH EQVGGPSLTSDLQAQSKG\NPEQTP VLKPEEEAPAPEVGASKPEGIDSRPE TLHPG\RPQPPAEELCSGKPFDAFT DLKNGSLFAFRGQYCYELDEKAVR PG\YPKLNRDVWGIEGPNDAAFTRI NLFRGRPYLFKG*\QYW/RAFEDGV\ LGPWYPRNISWTAFDGHSPGQTW D\AALGLPCPLAYSGRERVYFFQRG KQYW/ESYQFPGTSPVQEECEGSS\A SAVFEHFAMMQRDSWEDIFELLF \WGAERSGWVTR\QPQFHLAGEWH GVPG\QVD\AAMG\GRILHLQGMAT RPLLWPKKK\RFRH\RNK\GYRS\Q R\AHSRGR*PETPRRPSRA\MWLSF VLPSEESNLGA\NNY\DDYRMD\WL VA\ATCEPIQECFFSFSGDKYYRVNL RTRRVDTVDPPYPARSIAQYWLGCP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | APGHL |
| 3331 | 8828 | A | 3594 | 44 | 166 | |
| 3332 | 8829 | A | 3595 | 3 | 1173 | SSAPEAAKKPTPCHRCRGLVDKFN QGMVDTAKKNFGGGNTA WEEKTL SKYESSEIRLLEILEGLCESSDFECNQ MLEAQEEHLEAWWLQLKSEYPDLF EWFCVKTLKVVCCV\PGTYGPDCLA CQGGSQRP\CSGNHCS\GDGSRQG DGSCRCHMGYQG\PLC\IDCMDRL QLRSRNETHS\ACTAVRTGLSDSYPP CCLSLGCWRGVGHA WIRGRNTHITQ PGYSSRVWIAAFSPACDESKTCSG LTNRDCGECEVGWV\RTAPCVDV EKCAAQT\PPCSAAQFCKNANGSYT CE\ECDS\CVGCTGEGPGNCKQCIS GYAREHGQ\CADVERVPH*PEKTL EEKTKTCYNTPG\SY\VCVCPDGFE T/RRCLCAAGRRLKPQKGESPTQLP LP |
| 3333 | 8830 | C | 3596 | 1 | 300 | MRSFGQLTLCPRNGTVTGKWRGSH VVGLLTTLNFGDGPDRNKTRTFQA TVLGSQMGLKGGAGSVWLQAAGL GLLPASLLWPSLLCHCYVLPPAPGV PLV* |
| 3334 | 8831 | A | 3597 | 359 | 1229 | MPQPPTLGQEMTGPSQPWTGKGG LPGP*QLRAKAEVDSHLGRKKIKQ QNRSKSC |
| 3335 | 8832 | A | 3598 | 2 | 311 | VRWNSAAPLVTSRGAPASARPRGQ ALPGGSAPSAPHGQLPGRAPAPVS GPPPTSGLCHFDPAAPWP\GLGLG MLPPHPQDWPAQP*HPPGLGLFFE IFSAS |
| 3336 | 8833 | A | 3599 | 1 | 426 | |
| 3337 | 8834 | A | 3600 | 18 | 738 | |
| 3338 | 8835 | A | 3601 | 65 | 425 | RLPQPPGAAVGGSTRPCPSWKAVR VDLVVAPVSQFPFALLGWTGSKLF QRELRRFSRKEKGLWLNSHGLFD/R GAGKQQWQDS*VTEVLLLLQKTFF QAASEEDIFRHLGLEYPPEQRNA |
| 3339 | 8836 | A | 3602 | 3 | 233 | FFFFFKTLQIPLLSPPPPGPCRVQSL LPNPFPEKGA\PPFQTDERGQDFRLD PPLGSPSPRV*SLNCYVPVPPKEK |
| 3340 | 8837 | A | 3603 | 7 | 510 | THAPASPRAQAP*PLFIHCP*APRV TPPPQPVKCVVPAEVI/SPPPGPCR VQSLIPLTRFPEKGAYLLSRQMKRG QDFKAGIQPLGLSLPQPGSTGRGRV TAGD |
| 3341 | 8838 | C | 3604 | 846 | 989 | MKSYNGMREMGDQASRRKLIKNW TDSKFLDMENGEQKKITPRPGVKI* |
| 3342 | 8839 | A | 3605 | 3 | 232 | KSLREGLESAMLVLKSLLPFSYFV SSMSSGNWSALHNHLGPEDTGTAS PYNRCS*RGRDHLGKRSSTRGTTLG PN |
| 3343 | 8840 | A | 3606 | 303 | 400 | |
| 3344 | 8841 | A | 3607 | 3 | 404 | LRQRLTVTQAGVQ*HRLSSLQPLPP RLKRFSCLSLPSSWDYRRVPPHMA NFLY/FLVETGFHHVGQAGLKLLISS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DLPALASQSAGTTGMRHRAQPKSF QLEQKWKTEPHKLIYVVTLNKRM YKLKTYHIPYYF |
| 3345 | 8842 | A | 3608 | 2838 | 3122 | FFFFFFETKSCSVARLECSGTISAHC NLHLPGSSDSPASAS*AAGITGACH HTRLVFLYF**RRGFHHVSQAGLEL LT*VIHPPQPPKVLGLQA |
| 3346 | 8843 | A | 3609 | 1 | 325 | RLFFFFFFETVSHSVTRLECT*AILAHC NLCFPRSSNSLASASQVAEITGACY YTQLIFVFSVETGFHHVQGAGLELL T*VIHPPPPPKVLGLQVSATVPGLII GTFSL |
| 3347 | 8844 | A | 3610 | 3 | 398 | GSLQPPPPRLK*FSCLSIPSSWDYKR LPPCPANFCIFTELGFHQVGQAGLE LLTSGDPPASTSQTVGITGISHHAWP PEILSKGTMGKQMVNMLLLASSCR EMGHSAPAHLGQCLPMILPKDLAVI IINPV |
| 3348 | 8845 | A | 3611 | 3 | 311 | AQTGMQWDLCSVKPPPPRFERFSC LSLLSC*DYKRTPTCPANFC/DFVVE TEFHHVGQAGLELLTSSDLPASASE NPQITGMNYCIWPEWYYYIHSLTNT IHK |
| 3349 | 8846 | A | 3612 | 310 | 415 | SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRSL/DSVAQAGVQWRDLGS LQRPPPGFTPFSCSLPSSWDYRRPP PRLANFFVFSVETGF\TVSARMVSIS *PRDPPASASQSAGDTGVSQAPV |
| 3350 | 8847 | A | 3613 | 1 | 114 | ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS |
| 3351 | 8848 | A | 3614 | 335 | 477 | TPASLKIPVE**NTLLAKMVSIS*PR DLPASASQSAGITGVSHRARC |
| 3352 | 8849 | A | 3615 | 135 | 804 | GIDTILTLNQN*SLKTRQ*FTLIIF/IFF FFLRWSLALSPRPDCGLQWRDLGSL QAPLPGFTPFSCSLPSSWDYRCPP RPANFFCNFFFSRDGGFTVLARMVS IS*PQ/CDPPTLASQRAGITGLSHCT RLFFF*WMESPSVTQAGIQWHDLS LQPMPPQFR*FSWLSLPSSQDYRCM PPCQANFCIFSRDEVSPC*PGWSGS PDLVIHLPWPPKVLGLHA |
| 3353 | 8850 | A | 3616 | 3 | 285 | HEIIVLRVRVSPCCPGWSA\TVD*SW FIAASYS\VKRLSCLSLRLIWGCRQ VPPWLSFKLFWRQGLAVLPKLVS SWPKMTLLPOPLRLLGLQE |
| 3354 | 8851 | A | 3617 | 3 | 575 | PSLRHASHEAGWQCPHLGQPLPGY TELRTLPQ*GDGYGRPGVSAASQR R/GLAGQCVEGRDWVEGKAG*CSG GHGGEKGPLD*GALLPGPQNRSIS GAGDPC*AVESVGCQ*PGECHFQR DPPGSGAAPGAPPAVP*LHRQPDA AAGGTAGPSLPHLPPPLPGLRVERS KPGGAAEEQGHPHLEHGGPD |
| 3355 | 8852 | A | 3618 | 3 | 379 | FFETESCSFTQAGVQWHDLTGTL*SP PPGFK*FSLSLLSSWDYRRPPRTA/ NYIYIVFLVETGFPYVGQAGQKLLT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SCNLPALVSQSARITGVSHCAQLCN FLLTVKHFKPLTLRLEARTPQSFL |
| 3356 | 8853 | A | 3622 | 1 | 214 | ETESRSV/SQAGVQWRDLGSL*PPPP PGFQRFSCLSLPSSWDYRRAPPLPH NFCIFSRDGVSPCWPGWSQIS |
| 3357 | 8854 | A | 3623 | 2 | 309 | WCVFFETETHSAAQAGVQWCNLSS LQPPPPGVKQFSCLSLPSSWDYRCA SPCLASFCIFSRA*GFTMLTCLELLT SGNPPTSASQSAGIQGVSHHTWPSI F |
| 3358 | 8855 | A | 3624 | 1 | 294 | FFFFFFLRQGLTSLARLECSGMISAH CSLDLPG\SGDPPTSAS*VAGTTGTC HHAWLIFLFLVETGFHHVAQAGTLS KHRNHIQPVQVRATCSKDGG |
| 3359 | 8856 | A | 3625 | 23 | 282 | ASTGKPLSPQVQSES/CLALQLP*RS WN*TRVMSTTPWPNFFGIFVEMGF RHIGQAGLELLTSSNPILASQSAGI TGLSHRVQPTSS |
| 3360 | 8857 | A | 3626 | 37 | 289 | QWHDLGSLQPLPPGFRRRLSCLSLTS SWDCR/QPALRPANFFCIFK*RWGF TVLAQDGLDLLTSSDLPASAS*SAGI TGVSHRAWA |
| 3361 | 8858 | A | 3627 | 70 | 362 | KLHFKAIEGISSLGEQMKPSMWML LCPQIKIKLTLPIQIKQAKTCRQIPKV QGSQ*KNVGPSSFPVPW/EHGSBMI EAPWALNPYLGLGPVQILETQK |
| 3362 | 8859 | A | 3628 | 60 | 303 | KLKNHHHHHQQQQQKQQQQQKK QMDPRVSFSFFKKKKSSTPKPSQ*FP *SSRNS/HPR*ISESDLRPTEAIPGL KMKLPL |
| 3363 | 8860 | C | 3629 | 193 | 285 | MLLVSYPRNSNRCQIQYHEAFCPIIF LRVL* |
| 3364 | 8861 | A | 3630 | 159 | 483 | DPTSFGHGYLVFPTPCFKGFYFF*DR VSFCCSGML/IGSLQAQPSGFKPKPS SHLRLSSEDCRHTPPRLANLFFYFF L*RWDLTMLPRLVSNS*AQVILPSW PPIMLG |
| 3365 | 8862 | A | 3631 | 6 | 244 | DRVLLVTQAGVQWHDLGSLKPPPP GFK*VSCLSLPSSWNYRRLPPRPAAN F*FLVETGFLHVCQAGLKLPTSGDP PASA |
| 3366 | 8863 | A | 3632 | 2 | 262 | NDLGSLK\PPPPGFK*VSCLSLP/RVS WNYRRLPPRPSLIFVFLVETGFLHV CQAGLKLPTSGDPPPSASQSTWITG VNHRRARPQIGF |
| 3367 | 8864 | A | 3633 | 1 | 1149 | |
| 3368 | 8865 | A | 3634 | 280 | 602 | TDFFFFFFLRWSFTLVAQAGV*LHD PE*LQPPPPGFKRFSCLSLPSSWDYR HPPWPANF*FLVETGFHHVGQAG LELLTSGDPPASASQSVGITGVSHR ARPELNF |
| 3369 | 8866 | A | 3635 | 3 | 679 | SLHQSGRSNPTCCFPSSKGTGTNGH PTPSQSPPGTRDGPLFFPHSASTPP PTGASQPLTGTRGPPSPVEPVSHAC ASL*FSEGLRSEHPAVACGKTLQSP TGSKPEACSGEQGNCVLAIEIVLGT QDPSAH*GGAGARGGGALWVTEG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VKGPGPVSGQCRKSQPHACGEIPCR APPTMGTSGLPLGLPKLCPHFHCSR ASPAPSNPFCFWSPSTSGGPNPFPC |
| 3370 | 8867 | A | 3636 | 1 | 334 | EMESRSVAQAGVQWHDLGSLQPLP PGFKRFSCSLPSSWDYMRAP/PRP G*FFVFLVEMGFHLVGQAGLKLLTS /S/DLPTSASQSAGITGMSHRTRPNSL LVIQSGRFNTKITR |
| 3371 | 8868 | A | 3637 | 2 | 309 | FFFFETRFRFVAQAGV*WHAYGSPQ PRPPGPKPSSQLSLPS*DYRHTLLCL ANFDFLVETGFYHVAQTGLELLSV RDPPALASQSAGIAGVSHRARPGCI F |
| 3372 | 8869 | A | 3640 | 19 | 458 | KHLFYSSNLYFRSTFRHTRRRSPCEP SLALR/WCVLEPGSSRV**RLHPNTV GFQDASAKPRERTTSFHAFANF*K QYIFQC*LPPLTWLEIFSPFSRETGST KRCRLQDPGPSHFWRVVLCGLLWG QDRAPSWAPLQMQLCHCLYL |
| 3373 | 8870 | A | 3641 | 1 | 322 | FLRRSLALVTQARVQWHDPGSLQP SPSGFKRFSCSLPSTRDYRHPPRL ANFF/VFFLYL**GFATLAWLVLSH L/CDPPASASQSARTTGASHHAQPP VSFFKTRI |
| 3374 | 8871 | A | 3642 | 333 | 438 | |
| 3375 | 8872 | A | 3643 | 391 | 492 | |
| 3376 | 8873 | A | 3644 | 598 | 699 | |
| 3377 | 8874 | C | 3645 | 176 | 319 | MCSAQPAFSVDIIKSRHLGILGFYK PRILCQKHMLRLLHSFQNFQR* |
| 3378 | 8875 | A | 3646 | 2 | 50 | QLLGTGMHHYA*LIF |
| 3379 | 8876 | A | 3647 | 3147 | 3308 | FFKKNLCASAHYY/TWCVPLPFFFF LRQGL/NSIGQAGVQWCNHSSLQPC PPQDLE |
| 3380 | 8877 | A | 3648 | 1554 | 3041 | GTRERRAPDPCAGKCRNHVAGGRL KLSLHLSLPSSWDHRHAPL/PHD*FF KYLRR/RSPCVTQAGLKLLGSSDPPI LASQSIGITDMSHCT/WPSSPTPCHF LRDSFAPSPRPGMQ*CDHSSL*PQTL GLKQFSHQPPFYFFVQMGFAMLPK LVLNSWPQ/DNPSALAPQSAGIVGM SCCAQPPCFNINSHS*IQE |
| 3381 | 8878 | A | 3649 | 280 | 444 | |
| 3382 | 8879 | C | 3650 | 135 | 377 | MAGSWGAGQVQWLMSVIPILWEA KMGGSLPRSLRPAAWVTQGDVSN RLFHSSASVLWLQATLGTPKSLEYI TLAFRAK* |
| 3383 | 8880 | A | 3651 | 1791 | 6596 | CPKDTQILIFQKNNFSIRRFTQHLAD FLKEFCLTFKKKGRSOLL*FCCFVYI IF*KKFVCFCSLLHWCVPLPFFFFLR Q/RSHSIGQAGVQWCNHSSLQPCPP RLK\HPCTSASQVAGTTGMHHYA*L IF*IFETGSPCVTQAGLK/PPGLK*SS HLGLPEYWDYRHEPLHLPSSPTPCH FLRDSFAPSPRPGMQ*CDHSSL*PQT LGLKQFSHQPPFYFFVQMGSCYVA QAGLK/PPGLKQSFCLGPPKCWDCG HELLCPASMF*YQHPHMYTLKTTV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TFSTQNYIRYSLNCRKIKTIPKSDCR VDFFLQNT |
| 3384 | 8881 | A | 3652 | 3 | 332 | ETESHVAQDGVQWRHLSSLQPPLL GFK*FSCLSLPSSWDYSCPSPT/P*LI CFFFFFLIEPGFHHFGLAGLELQTS DLPASAFQDAGITGMSH*TRPELLS LDHTPFT |
| 3385 | 8882 | A | 3653 | 3 | 272 | FETESH/VSPRLECSGVIFAHCSFCL PGSSDSPASAS*VSGMIGTRNHAQLI FVFLVEVRFHVGQAGLELLA*VI HPPQPPKVLGLHV |
| 3386 | 8883 | A | 3654 | 1 | 272 | ETGSRSTRLLECSGAITAHCSLDLPG RSNPPTSAS*/RIAGASGECRHTQL/I* KFIFFVNTGCRYVVQAGLKLLASGA KQSSCLGLSKCWD |
| 3387 | 8884 | A | 3655 | 249 | 906 | RIHFPRVSGPSQSNPKFAVASRGFFS LSLSSAQPDPLPPPLGEALALSLHPV PRRSTETVAGDSSELQLGLRSPQQP LAGLAFLARLFLFPPP*RCKSKPN* NDRRRSSVDSQIHLVGRESAHPLAG LRVCVSLPLLARCFGQVLQGVPG WIPSPGGS/AGVSGRRREERHMGVV VMRVRVEARVSS*ESKI/SRALR*ST HLGLPKCWDYRREPPCPAH |
| 3388 | 8885 | A | 3656 | 1 | 514 | FFFFSRSL/NSVIQAGAQRDLGSLQ P/LLPPGLKQFSCLSLLSSWDYRCP PRLANFYIF/M*RRGFTILARLVLS* TQ/CDPPTSASQSAGITGVSHPTQ/LL FSF/CLKESGSSLMVSATLRFHK*RH SGPSRAALSSSP*LEPRKLKFGTASL QNKWAMQQTRQHWAAQRGSKPM |
| 3389 | 8886 | A | 3657 | 2 | 307 | FFFFFFETESYSVTQAGVQWHDGL LQPLPPGLKQFSSLSLPE*L/DVTGSP PPCPVNFCTFGKGLGFTMVGQAGS GTSDLKVICPPGLPKVLGITGCEPR L |
| 3390 | 8887 | A | 3658 | 79 | 91 | NTFW*RRGFTVLARMVLIS*PHDLM TC/PASASQSARITGMSHCARLVLYF SRDGVSLCWPGWSQTADLR*STCL GLPKCWDYRYEPPCPASLHHFLIYA TSIIKYL |
| 3391 | 8888 | A | 3659 | 162 | 493 | DGSSPPVAQAGVQWRDLGSL/QAPP PGFTPFSCLSLSRSDYRRPPPRPA NF/SCIFIVETGFHRVSQDGLDLLTS* S/VPASASQSAGITGVSHRARPRSCIS FDSTVTLAQ |
| 3392 | 8889 | A | 3660 | 3 | 251 | GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLGSLQPPPPRFKRFSLI LPSSWDYRH |
| 3393 | 8890 | A | 3661 | 3 | 251 | GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLGSLQPPPPRFKRFSLI LPSSWDYRH |
| 3394 | 8891 | A | 3662 | 17 | 287 | KYHRIQCPNSG\CEAVYSSVSGLKA HLGCTLGNFVAGKYKCLLCQKEF VSESGVKYHINSVHAEVRLL*SCGP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DM*ATREVDVFPIVMD |
| 3395 | 8892 | A | 3663 | 3 | 567 | DRKLKYTRPGLPTFSQEV LHKWKT DIKKYHRIQCPNQGCEAVYSSVSGL KAHLGSCTLGNFVAGKYKCLLCQK EFVSESGVKYHINSVHAEDWFFVN PTTTKSFEKLMKIKQPAARRRKAEA AAQEQKVSKKGGSSLGIELPETEPS LRVGKDQRRNNEWDW*CQPPCKEP/ GAGASASTVPESKAPKD |
| 3396 | 8893 | A | 3664 | 1 | 184 | SSRDILLCTDIASRG LDSTGV ELVVN YDFPPTLQD\ELAARRRRSLPGLASS VKEPLQAT |
| 3397 | 8894 | A | 3665 | 2 | 1748 | HEARTKGNMALSAA RLRLLPFVN SVCFLAPRRGLTVRSPDEPLPVVR IPVASTSGKLEQRQSRRRNLP EGRC LVRPGPLLVSARRPELNRPARLT LG RWERAPLASQGWKSRRARRDHFSI ERAQQEAPAVRKLSSKGSFADLGA WKPRVLHALQE\AAPEVVQPTTVQ SSTIPSLLRGRHVVC AETGSGKTL S YLLPLLQRLLGQPSLDSLPIAPRGL VLVPSRELAQQVRAVAQPLGRSLG LLVRDLEGGHGMRRIRLQLSRQPSA DVLVATPGALWKALKSRLISLEQLS FLVLDEADTLLDESFL ELVDYILEK KDLAVFLYHLRLEAEVEVVEMLGP HGQPCPQHNSDISA YTYERTLMME QRSQMLRQMRLTKTERERE AQLVK DRHSALRLESLSDEEDES AVGAD KIQMTWTRDKYMTETWDP SHAPD NFRELVHIKPDQSNVRRMHTAVKL NEVIVTRSHDARLVLLNMPGPPRNS WCTTSSRTEKRQWNC PAVRTEKNA QTRQTHAETKTQKKDTEPRIPEADL AVQYDNHYTNTKYCLCQMLREQL ESPQGRLLHAAQSSREIW |
| 3398 | 8895 | A | 3666 | 1 | 1704 | MALTRPVRLFSLVTR LLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRRNLP RPVLVRPGPLLVSARRPE LNQPARLT LG RWERAPLASQGWKS RRARRDHFSIERAQQEAPAVRKLSS KGSFADLGLEPRVLHALQEAAPEV VQPTTVQSSTIPSLLRGRHVVC AAE TGSGKTL SYLLPLLQRLLGVHPSLDS LPIAPRGLVLVPSREFFQHLRAVA QPLGRSLG LLVRDL\EGGHGMRRIR LQLSRQPSADVLVATPGALWKAL KSRLISL\EELSFLVLDEG\DTLLG*K ASWELVDYIL\EKSH\AEGPADLED PFNPKAQLVLVGATFPE\GVGQLLN KVASPD AVTTITSSKLHCIMPHVKQ TFLRLKGADKVAEL\ VHIL\KHSR AEKGLGPSGTGFVFCNSSSTVNWL GYILDDHKIQHLRLQGQMPALMRV GIFQSFQKSSRDILL\CTDIASRG LD STGV\ELVVNY\DFPPTLARLTFHRA GESGPVWGAEGPG\TVISFVTHPW DVNPWFKKD*SLAARPKEEVL PGL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3399 | 8896 | A | 3667 | 2 | 222 | AIPR*KKPFAPQSNPDFEQNLIKMRWSLTLFQAGMQWPNLSSLQPPPPRFKQF*CLSLPSSWDYWYTPPRLANFCIFSRDGVSPCWSGWSRTPDLR |
| 3400 | 8897 | A | 3668 | 1 | 29 | |
| 3401 | 8898 | A | 3669 | 2 | 206 | VTQAGVQWLALSSLQPLPPG/LK*FYCLSLPSSWEYRHTPPHPTKFCIFFLVEGVSPYWPGWSQTPGLR |
| 3402 | 8899 | A | 3670 | 3 | 139 | TSHMWWCRHVVSATREAEVGEPL EPRQSRLQ*AMTAPCTPAWATK |
| 3403 | 8900 | A | 3671 | 86 | 384 | |
| 3404 | 8901 | A | 3672 | 3 | 746 | RQEEGLPPVVDAIDDASVEEDLAVAVAGGRLEEVSFQYPARRRRALLRASGVRRIDREEKRELQALROSREDCGCHCDRICDPETCSCSLAGIKCQMDHTAFPCGCCREGCENPMGRVEFNQARVQTHFIHTLTRLQLEQEAESF/QGAGGPCPGQPTQPW*GGPGPYFPTGQAPHEQ*AGRQQLQQRHD\YSSTASSSASGTSEAPDCPTHPLPGPGFQPGVDDDSLARILSFSDSDFGGEEED |
| 3405 | 8902 | A | 3673 | 72 | 332 | LPALETPRAQSKCSPQPSWVSRDYRCVP TH ALANF*IFGEMGS/LLCCPRLISNS\WPQGILPPPPKVLGLQGSYS AKITTGFFLK |
| 3406 | 8903 | A | 3674 | 33 | 396 | RVWYLHRVTGRPASCLREVGP GD SL LETASLREI W RSRRCRAT/ECSQ Q RL NHRLARQREHEARLRQ Q REQNSRY FTDV*HL\RSKQAEWSSKTY Y QRSM HAYHREKMKEEKRRSLWARLEKL M |
| 3407 | 8904 | A | 3675 | 217 | 935 | QRQREKEDQIRQQWEQNSRYFRMS DICSSKQAEWSSKTSYQ RS MHAYQ REKMKEEKRRSLEARREKLRQLMQ EEQDLLARELEELR/REHELAGKKN PGAAREAEISQRRAEETDC*TTFVR TLEKEQPETS RD GAGPSPEACRKL GNAE/MKKKKQ Q EASAEQGNKRYE NEYERARREALERMKAEEERRQLE DKLQAEALLQ Q MEELKLKEVEVGT SPSQP*PPPQLLVSMRWALERLP |
| 3408 | 8905 | A | 3676 | 1 | 382 | EMEPCFVS* T GV*W H DLSSLQ P PLP KFKRFSCLKIPE S WDYRRTP/PMP/V LTGFHHVDQAGFELLTSSDPPTSAS QSVGITGMGDHTWPTLHTLTKPCE VDENAVMRELKLTGQGPLRKWQF EHLNPA |
| 3409 | 8906 | A | 3677 | 1 | 2456 | MPTYPKLEKTDQSTSYTKFNDLSPD SSRERYTSLEIKSVCYTALPEQGQK QLQLWYNVCVKTQCKTTQECSLKIWI FTMNETSDREDGLPKGHHVTDSEN DEPLNLNASDSESEELHRQKDSSE SEERAEPASDSENEDEVNQHGSDSE SEETRKLPGSDSENEELLNGHASDS ENEDVGKHPASDSEIEELQKSPASD SETEDALKPQISDSESEEP PR HQASD SENEPPKPRMSDSESEELPKPQVSD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SESEPPRHQASDSENEELPKPRISD SESEDPPRHQASDSENEELPKPRISD SESEDPPRNQASDSENEELPKPRVS DSESEGPQKGPASDSETEDASRHKQ KPESDDDDSDRENGEDTEMQNSDF HSDSHMDRKKFHSSDSEEEHKKQ KMDSDEDEKEGEEKVAKRKA LSDSEDEEKASAKKSRVVSADADD DSDAVSDKSGK\KRRTIASDSEEEA GKELSDKKNEEKDLFGSDSESGNEE ENLIAD\NLENLVMKRK*NLQVLTK KIWEEKGETQVKEAEDSDSDDNK RGKHMDFLSDFEMMLQRKKSMSG KRRNRDGGTFISDADDVVSAMIV KMNEAAEDLKETFIDSGVMSAIKE WLSPLPDRSLPALKIREG\VLKILQE LPSVSQETLKHSGIGRAVMYLYKH PKESRSNKDMAGKLINEWSRPIFGL TSNYKGMTREEREQRDLEQMPQRR RMNS/DLVVRHPERDLEKVLTGEEK ALRPGDPGFVPRARVPMPSNKDYV VRPKWNVEMESSRPGILKKGLSRLE KHKRRFAEQRLSKVHRAVKFSIEG NRMPL |
| 3410 | 8907 | A | 3678 | 1 | 564 | TLKQVGLTEHVMYLYNDPKESRSN KDMAGKLINEWSRPIFGLTSNYKG MTREEREQRDLEQMPQRRNDST GGQTPRRDLEKVLTGKEKALRPGD SLNLV/PRARVPMPSNKDYGVPRK MKCGNGVIQVSGDPPQKGIQSDWI NQMRKFHRY*GKKADLAHAVENP AIEGNKMPIGDPCPGMCPPIILL |
| 3411 | 8908 | A | 3679 | 63 | 361 | |
| 3412 | 8909 | A | 3680 | 151 | 384 | |
| 3413 | 8910 | B | 3681 | 385 | 479 | MAGAFRRRFASEVRAQGLESLEH GLRCAGSLRGGQSLPTTMWSPVKV GFE* |
| 3414 | 8911 | A | 3682 | 3 | 698 | VFFFFSGCTRGPLFESDFHRAPHRC GQGLAAP*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGQAA\PPALVP GEGPSWDS DPRGHRC SQATLPRVL AGPLQP*LS*LSL*DPPELRSL*PPL* LRLL**SLEPP*PPLDLSNRFP*PRSP PPLENPRPRPRPRKKPRPPAEPPRY PTESVSDDLPAWSTRISVHLQTSHS WPSWASLASSMFFKVTKPNSRELW SS |
| 3415 | 8912 | A | 3683 | 138 | 550 | FCCCFTSSEHSLAYGSCSPRRTEVL CAQQNPSETQAAPLAS\YMWK*PC NSRLKGPGLGEGWPESRMTSGV TVPGGTSPGTRAGGSPCPGGLSPEA LRQ*GAGSGPRVSPGA/PGCGAPAA YGAASPCPQRCGAL |
| 3416 | 8913 | A | 3684 | 2 | 555 | FFFFFFLGAHVALYSNPTFTGLHIVV GKDWPPP*AAGAPQPRAPGETRGPE PAPHWRSASGDKPPGASGCLQLLF QGEVPPGDS*PQRSSLALRPPFPRVL GPGPFQPAKAKQRYRPPQGSQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | APP/GPPRKQPQPLRKVSG*SGGCDL RLRHRPACPGRVCTLAQLEPATRM GWSYVGQCGL |
| 3417 | 8914 | B | 3685 | 95 | 371 | MASDEGKLFVGGLSFDTNEQSLEQ VFSKYGQISEVVVKDRETQSRGFG GFVTFENIDDAKDAMMAMNGKSV DGRQIRVDQAGKSSDNPIPWX* |
| 3418 | 8915 | A | 3686 | 314 | 1055 | SKCFHLHQVWKQKGEEYRVGTGYG GWSWISKTHVYRFVPKLHGNTNVN YRKSLEGTKNNMDENMDESDKRK CSRSPKKIKIEPDSEKDEVKGSAA KGADQNEMDISKITEKKDQDVKEL LDSDSKPKERTNGSRR*HENRVT CKLSGEFSSRCGQC**GFSSKD*LQK ENKIIQTRWTS*KEN*TVYTGRKTA TRKNQVGGWN*GYRKDASTNSSKN LSESPVITKAKEGCQSDSDETRTEPK CK |
| 3419 | 8916 | A | 3687 | 11 | 345 | DSLTVASGVQWHNLISLQPLPPGV K*LFCLSLPSS*DYRRAPHPANFSV LVEMGFYHVGQAGLELLISSDLTSL ASQSAGITSVSHWAWPENVYLNQ QTEKSLMVSG |
| 3420 | 8917 | A | 3688 | 1 | 521 | NPTKSCMLEG*NPHVHCK\REGAQA ITGMPI*KATKYLKYFLLQKLCVPF QS/YESGVGRCTQDRHWGWTHHQ WPRKGTEICLQVQSYAELKGIDVDS LVIEHIQ/V/NKAPIMYHLTYRTHGQ MNP/YHKLPCHIQMMLSEKKHLVP KAEKEDARKKKIPQKKHKLKRQTN SAKRKCK |
| 3421 | 8918 | A | 3689 | 1 | 281 | ETGSHSDAQAGVQWHDLGPMQPLP PGFKRFSHLSLLSSWDYRHAP/PRPG LFL*RWGFHQVGQVDLELLNSSDPP ASTSQSAGITSASHRAWPN |
| 3422 | 8919 | A | 3690 | 3 | 314 | HAEHEITELTATFTKFDRDGNRILDE KEQEKMRQDLEEER\LTRRVLQLET VLERVVAQIDALSSKLEMLEKKG VLSLFTSFNIRAFKSLFSHYSSVTPIN YL |
| 3423 | 8920 | A | 3691 | 61 | 400 | LVTGIWSATCLWVLLLLLFEKGCP SVPRLQCS\NVITACCSNLARGSND PPTSASRVPGDHRCCHYTWANFLIF LWEMRSHCVGFRLGLGTPVLKLQT ILQPQPPKVLGLQA |
| 3424 | 8921 | A | 3692 | 33 | 436 | REQEL/CKGKQKDGTSFGGEYGGWY KACKVDSPTVTTTLKNLGALYRRQ GKFEAAETLEEAAMRSRKQGLDNV HKQRVAEVLNDPENMEKRRSRESL NVDVVKYESGPDGGEVSGRASFC GKRQQQQWPGRHR |
| 3425 | 8922 | A | 3693 | 37 | 355 | NSEYGGWYKACKVDSPTVTTTLK NLGALYRRQKGFEAAETLEEAAMR SRKQGLDNVHKQRVAEVLNDPEN MEKRRSRESLNVDVVKYESGPDGG EEDGTGSLKRS |
| 3426 | 8923 | A | 3694 | 229 | 2000 | QRERARPSGARRMYDTMSTMVYIK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | EDKLEKLTQDEIISKTKQVIQGLEAL KNEHNSILQSLLETCLKKKDDDES LVEEKSNMIRKSLEMLELGLSEAQV MMALSNHLNAVESEKQKLRAQVR RLCQENQWLRDELANTQOKLQKSE QSVAQLEEEKKHLEFMNQLKKYDD DISPEDKDTSTKEPLDDLFPNDED DPGQGIQQQHSSAAAAAQQGGYEI PARLRTLHNLVIQYASQGRYEVAVP LCKQALEDEKTSBGHDHPDVATML NILALVYRDQNKYKDAANLLNDAL AIREKTLGKDHPAVAATLNNLAVL YGKRGKYKEAEPLCKRALEIREKV LGKDHPDVAKQLNNLALLCQNQG KYEEVEYYYQ/RFLIFQTKLGPDDP NVGKTKNNLASCYLKQKFKQAET LYKEILTRAHEREFGSVDDENKPI WMHAEERECKGQKDGTSF/GEY GG/WYK/ACTVDSPTVTTTLNLGAL YRRQGFEEAETLEEAAMRSRKQG LDNVHKQ/RVAEVLN*PLRTLEKPQ EPVESL/NVDVVKYESGPDGGEV SMSVEWNGGVSGRASFCGKRQQQ QWPGRRHR |
| 3427 | 8924 | A | 3695 | 1 | 314 | KVDSPTVTTTLKNLGLYRRQKGF EAAETLEEAAMRSRKQGLDNFTKQ RLPEVLNDPENMEKRRSRESL/NVD VVKYESGPDGGEVSMVKWNGM RKMKLGA |
| 3428 | 8925 | A | 3696 | 2 | 450 | VNKAGGLIYQLDSYAP/RAEAEKTF SYPLDLLKLHDERVLVAFGQRDGI RVGHAVLAINGMDVNGRYTADGK EVLEYLGNPANYPVSIRFGRPRLTS NEKLMLASMFHSVKFVVLADPRQ AGIDSLLRKIYEIYSDFALKNPFYSL EMP |
| 3429 | 8926 | A | 3697 | 2 | 823 | FGTRGKAAMAFSVYVVKAGGLI YQLDSYAPRAEAEKTFSYPLDLLK LHDERVLVAFGQRDGI RVGHAVLA INGMDVNGRYTADGKEVLEYLGNP ANYPVSIRFGRPRLTSNEKLMLAS MFHSLFAIG/SQLSPE/QGSSGUGCLE TDPFQFH/CSRTLTKIKF/VVLADPR/ QAGIDSLLRKDFMEILLQTLPLKNPI PIPLEMP/IRCEPL*PQNPEA*SLEVA/ EKAG/TFGPRVHRLNPVMGPPQNPE SSLQOEYCLLTLPEIPAALVSAP |
| 3430 | 8927 | A | 3698 | 165 | 354 | ENFGGKITNFAKLFGYILPYSHYFW CLEKNRNR/SLTLLPRLVSNSWAQA FLLLWPPKVLRLQA |
| 3431 | 8928 | A | 3699 | 3 | 166 | SETGFCHVAQAGLELLVSRSPASV SQSTGISHQARPSISYFYDHSAPITH TDH |
| 3432 | 8929 | A | 3700 | 1 | 421 | ETKSHSVTKTEVEWRDPSSLQPLSP GFKQFSCRSLPN/SWDYR/PSPANFV FLVETGFYLVGQAGLELLTSNDPPA SASQSAGITGVSHCAQPRITNSLTTA SFIQPRKHSEFPVMTCPSSNATESK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VGGRGPHGAIARLM |
| 3433 | 8930 | A | 3701 | 2 | 205 | APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQHLP RPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ |
| 3434 | 8931 | A | 3702 | 2 | 205 | APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQHLP RPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ |
| 3435 | 8932 | C | 3703 | 282 | 445 | MISAHCNLLPPEAGELLEPGGRRFS EPLHSSLMTEQDSVSKINKNNKTSIS NPE* |
| 3436 | 8933 | A | 3704 | 170 | 607 | WPSG*FQR*SMRLLYKIHLNVSRR PQLAPGKELYFSF*LLFYFYFYFIHIII FEMESHVTRLECSGTISAHCNHL PGSSDSPASAPVAGTLIDACHHTW LIFYNF*VEMGFHHVGQAGLKLLT *VTHPPRPSKVLGLQA |
| 3437 | 8934 | A | 3705 | 3 | 231 | FETESLFPRLECSGTISAHCNLRSLG SSNFWLIFCNLVEMGFHHVGQTSLE LLTSSHPPTSAFQSARITGVSHRTW |
| 3438 | 8935 | A | 3706 | 4 | 144 | |
| 3439 | 8936 | A | 3707 | 333 | 416 | FTGLPCLFSPQNNVSLQSCID\LFK NN |
| 3440 | 8937 | A | 3708 | 1 | 1219 | MAAVPELLQQQEEDRSKLRSVSVD LNVDPSLQIDIPDALSERDKVKFTV HTKTTLP TFQSPEFSVTRQHEDFVW LHDTLIETTDYAGLIIPAPTKPDFD GPREKMQKLGE GEGSMTKEEFAK MKQELEAEYLAVFKKT VSSHEVFL QRLSSHPVLSKDRNFHV FLEYDQDL SVRRKNTKEMFGGFFKSVVKSAD E VLFTGVKEVDDFFEQEKNFLINY N RIKDSCVKADKMTRSHKNVADDYI HTAACLHSLALEEPTVIKYLKVA ELFEKLRKVEGRVSSDEDLKLTELL RYYMLNIEAAKDLLYRRTQS/ALI DYENSNKALDKARLKS KDVKLAEA H\QQECCQKFEQLS\ESAKEELNFK VRKRVAAFRKNLIEMSELEIKHARN NVSLQSCIDL FEE |
| 3441 | 8938 | A | 3709 | 527 | 724 | TMKIGLGFSLVSINIFSPVELINFKR KRVA AFRKNLIEMSELEIKHA\RNN VSLQSCIDL VKNN |
| 3442 | 8939 | A | 3710 | 1 | 1220 | QEGGSAGSAGSGADGTGLRQSLAG HVGRPGRGQWGQRGSGDLP GHRPP PARSEHRCVAEG/NLSLYVFGGYNP DYDESGGPDNEDYPLFRELWRYHF ATGVWHQMGTDG\YMPRAELASMS LVLHGNNLLVFGDTGIPFGESNGND VHVCNVKYKR WALLSCRGKKPSRI YGQAMAIINGSLYVFGGTTGYIYST DLHKLDLNTREWTQLKPNNLSCDL PEERYRHEIAHDGQRIYILGDGTSW TAYSLNKIHA YNLETNAWEEIATK PHEKIGFPAARRCHSCVQIKNDVFIC GGYNGEVILGDIWKLNLQTFQWVK LPATMPEPVYFHCAA VTTA\GCMYI HG\GVVNIH\ENKRTG\SLFKIWL VV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PSLLELAWEKLLGAFPNLANLSRT QLLHLGFTQGLIERLK |
| 3443 | 8940 | A | 3711 | 2 | 266 | FLMESRSVTRLECSSTTTAHCNLCPL VSSDSA VSASQVAGTTGMRHHAQL IFVFLVETGFHHVVGQDGLHLL/NIVI HLPRPPKVLGLQA |
| 3444 | 8941 | A | 3712 | 1 | 453 | FKRAMDLVQEEFLQRLDFSQHSWL PARALVEEALAQRQVDPSPGEIVEL AKGACPWKEHLYHLESGLSPPVAIF FVIYTDQ/RWTVANIAGCPLPEPWR GLRDEALDQVSGIPGCIFVHASGFIG GHRTREGALSMARATLAQRSFLPQI S |
| 3445 | 8942 | A | 3713 | 20 | 891 | RWNSRYDHHQRSFTETMSSLSPGK PWQTKLSSAGLIYLFHGAQVLAQL LGTSEEDSMVGTLYDKMYENFVEE VDAVDNGISQWAEAGEPRYALTTTL SARVARLNPTWNHPDQDTEAGFK RAMDLVQKEVSCRD*IFYQHSWLP ARGLGGKSHLPQRIPRWNPSPGKIVE LAKRCHVPWKEHLLPPGNLGLSPS KWPIFFVIYTD/SRL/EQWRIQCVAQ/ VSPTHSQSRAALPEPWRGLRGTRP WT*FSGIPGCIFVHASGFI/SAVNATR EGALSMARATLAQRLIPTNLLV |
| 3446 | 8943 | A | 3714 | 176 | 450 | |
| 3447 | 8944 | A | 3715 | 1 | 472 | |
| 3448 | 8945 | A | 3716 | 418 | 1354 | AAARRATCLGCRSCSGATARRASS WRTAPRVHSVAWKL/DGRRLASGS FDKTASRLLAWRTRFGQKKTIIGG HGG*C/VTSFCWHPNPEPICYGVI/Y GDKTIRIWECEYKNALPLVNIKGE NINICWSPDWQTIAVGNKDDVVTFI *CQDTPFQSRRAVQVPRSTKSPWNH DHNMFLLTNGNGCINILSYPELKA/ VQSINAHPNMCICNQV*PHGESTLP QASCKMLLVSLWDVG*VSVCFGAF SRLDWAC*EPFSFSHDGKMLASASE DHFIDIAEVETGDKLWEVQCESPT/ SQVAWAPQKASAGHLPR |
| 3449 | 8946 | A | 3717 | 1 | 296 | LWDV/EELVCVGAFLDWP/VRTSV SAHDGKMLASASEDHFIDIAEVKTG DKLWEVQCESPTFTVAWHPKRPLL AFACDDQKTANMTSSREAGTVKPV GAS |
| 3450 | 8947 | A | 3718 | 2 | 276 | RSTFALVAPAGVQWHDNRSLOPLL PRFKQLSCLSLSSWDYRCPPPSPA NF/SLFLVETGFRHAGQAGLQLLTS GDLPTSASKSAGITGMGLQ |
| 3451 | 8948 | A | 3719 | 3 | 613 | GLRALRRGQGLPGL*CCSRPQPSR AQGHPSMGGPMQRTVPPRGMASV GPQSYGGGMRPPNSLAGPGLPAM NMGPGRGPWASPSGNSIPYSSSSP GSYTGPPGGGGPPGTPIMPSPGDST NSENMYTIMNPIGQAGRANFPLG PGPEGPMAAMSAMEPHHVNGSLGS GDMDGLPKSSPGAVAGLSNAPGTP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RDDGEMAA |
| 3452 | 8949 | B | 3720 | 134 | 471 | MYAKGGKGSAPSDSQAREKLALY VYEYLLHIGAQKSAQTFLSEIRWEK NIMPSPGDSTNSSENMYTIMNPIGQ GAGRANFPLGPGPEGPMAAMSAME PHHVNGSLGSGDMDG* |
| 3453 | 8950 | B | 3721 | 223 | 692 | MEPSPRAQGHPSMGGXMQRVTPPR GMASVGPQSYGGGMRPPPNLAGP GLPAMNMGPVGRGPWASPSGNSIP YSSSSPGSYTGPPGGGGPPGTPIMPS PGDSTNSSENMYTIMNPIGQGAGRA NFPLGPGPEGPMAAMSAMEPHHVN GSLGSGDMDG* |
| 3454 | 8951 | B | 3722 | 228 | 292 | XLARDDHERVMGRQPRASLRA* |
| 3455 | 8952 | A | 3723 | 1 | 1753 | MYAKGGKGSAPSDSQARENLSAF QAATELTSLDRLALYVYEYLLHIGA QKSAQTFLSEIRWEKNITLGEPPGFL HSWWYGLGCCGVFWDLYCAAP DRREACEHSGEAKAFQDYETPERP AHRHGNAGRAGSSSGMIDVGGSSD PQILRPTTPVCSLTNASSLSHGAGHL QRGGGTPQSAAAAPSPVMGSMAPG DTMAAGSMAAGFFQGPPGSQPSPH NPNA PMMGPHGQPFMSPRFPGGPR PTLRD\GSQPPAGPPWVSPSSPGA MEPSPRAQGHPEHGRPNARGVTPP RG/MGPAWGPWAYGGGMRPPPNL TRPRA CLPMNMGPRKFVGPWAQPP VEYSIPYSSSSPGSYTG\PPGGGGPP GTPIMPSPGDS\TNSSENMYTIMNPI GQGADRANFPLGPGPEGPMAAY\G \GMEPHHVNGSLGSGDMDGLPREF PQAPVAGLSNAPG\TPRDDGEMAA AGTFHAPSSQSENYSP\GMTMSRV NWAAAPGALCGPRLLPRRCLRAK GLKVTPSGTLDLANQGLPMLGGP TRKTLTILLKTQGPRETFFSVWTLPA ICILVPERKALWGGPSSPGRQGGGA H |
| 3456 | 8953 | A | 3725 | 65 | 210 | ATRAGLIFDDSFEDVWQDASSFRL IFIVDGWHPELTPQQRSLPAI |
| 3457 | 8954 | A | 3726 | 2548 | 3800 | NSLILLFFFFRQRSLTECSGVISAH HNLHLPSSSNS/P/ASAS*VAGITGM HRHAWPICIFLVETGFRHVGQAGLE LLTSGDPPAPTSQSM*ATTSGLILL SKILFPFHSTKVFK*SCPS*KILKEEN CSVINEWFNSESSYTSKEKNNLVPN AC*ENTM*VATNCDFT/SLL*RSNY PKLFHNNETTSQKIHLKIKISRPATS GQWILFSLVWWRARKG*GILMIHN GILY*TIC*IKLHRLP*GMDYPNQPD/ MKSGWDKRMSHTL*F*GKEIVDF QNQONKLSTLYLSVQE**HEEFFFR DLKYNKPGSTIKSLVSF/HSLTLFFF FFEARSHSASQAGVQWGNIGSLQPA PPGLKRSSYLSSLSSWDYRRVPPHP ANFCIFCR/GWGFVSPCCPGSSGTP VLKWRAHLSLPNC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3458 | 8955 | A | 3727 | 2 | 217 | SSPSPPHPPASPPSSPSPAPASPPPPSLP LPSPDFPPLSPCSSLSPFSSFSPPPSPP SPPFSRGPSPSDNFH |
| 3459 | 8956 | A | 3728 | 25 | 396 | ISGRSTFSLFSRQGLSALSPRLE\CSV AISAHCNLRPLPGSSN\GTTGA*HHTR LILYF/LAEMGFHHVVGQAGFEVLTS SNPPASASTSARITGMSNRT\GHLFN FHP*MCYKYRCGSLAGRGGSRW |
| 3460 | 8957 | A | 3729 | 80 | 460 | YISLNVTTHLIFFFFFLQRQL\CSV TQAGVQWCNLSLQPLPPRFK\NWDY RCVTPHLANFVFLVEMGF/LPASAS QSAGITGVSHCTQLGVFICICYGSSH GVRQSWHQFCSSKLLVKSGRVGVG LLG |
| 3461 | 8958 | A | 3730 | 1 | 316 | FFFFFETESHIVQAGVQWRDLSSL QPPPPRFKRFSSLSLPSSWDYRHVPP RPA\NFAFLVEMGFHHVVGQAGLELL TPGDPPSSASQSAGMTGVTHCAWP RCLMF |
| 3462 | 8959 | A | 3731 | 3 | 1717 | RPQTLKGHQEKIRQRQSILPPPQGPA PIP\SSTAAGIPRRPRIAWARR/WPLS EPGFRRRESQEEPRAVLAQKIEKET QILNCALDDIEWFVARLQKAAEAF KQLNQRRKKGKKKGKKAPAEVLT LRARPPPEGEF\DCFQKIKLAINLL AKLQKHIONPQRR\DVVHFLFGPLD LIVNTCSGPDIAHSVSCPLFSRDAVD FLRGHLVPKEMSLWESLGESWMRP RSEWPREPQVPLYVPKFHSGWEPPV DVLQEAPWEVEGLASAPIEEVSPVS RQSIRNSQKH/RPHFRAHPPGGCPY HQSAPHILTRGYQPTPAMAKYVKIL YDFTARNANELSVLKDEVLEVLED GRQWWKLRSRSGQAGYVP\GNILG EARPEDAGAPFEQAGQKYLGTQP DPQATPKLPGGT/IDELMQHMDEVN DELIRK\TTSRAQPQRHFRVERSQP VSQPLTYESG\PDEVRA\FLEAKAFS PRIVENLGILTGPQLFSLNKEELKKV CGEEGFRVYSQ\TMQK\AFLEKQQS GSELEELMNKFHSMNQRRGEDQLG PAALGWGLRRGSPPTMHGVFLYV YVFCIK |
| 3463 | 8960 | A | 3732 | 1 | 324 | |
| 3464 | 8961 | A | 3733 | 1 | 581 | MDKLETTYSLQRLSQEEIESLNRTI MSFKTKSVINTIPTKKSPGPDRLTAN FYQMCKEELADIIHGLCIRHEMTPV NPGVGQCCTSSYANRRPCFSSLVVD ETYVPPAFSDDKFIFHKDLCQAQGV ALQTMKQEFLINLVKQKPQITEEQL EAVIADFSGLLEKCCQGQ\NQEVCF AEEGQKLISKTRAALGV |
| 3465 | 8962 | A | 3734 | 39 | 1935 | LATMKWVESIFLIFLLNFTESRTLHR NEYGIASILDSYQCTAEISLADLATIF FAQFVQEATYKEVSKMVKDALTAI EKPTGDEQSSGCLENQLPAFLEELC HEKEILEKYGHSDCCSQSEEGRHNC FLAHKKPTPASIPLFQVPEPVTSCA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YEEDRETFMKNKFIYEIARRHPFLYA PTILLWAARYDKIIPSCCKAENAVE CFQTKAATVTKELRESSLLNQHAC AVMKNFGTRTFQAITVTKLSQKFTK VNFTEIQKLVLDAHVHEHCCRGD VLDCLQDGEKIMSYICSQQDTLSNK ITECCKLTTLERGQCIIHAENDEKPE GLSPNLNRFLGDRDFNQFSSGEKNI FLASFVHEYSRRHPQLAVSVILRVA KGYQELLEKCFQTENPLECQDKGE EELQKYIRE\GQPWAKGSSGFSKK* GEYYLQTGSSLSLQQ*RPPQLTSSEL MAITRKMAATAATCCQLSEDKLLA\ CGEGAADIH\GHL CIRHEMTPGKPL VFGQVPAPPSICPNRRPHASSTWVV DGNIWSPPCISLMTKFHFSP*RDPGG PSLQGW*ALAKPMKAKRFPSLTLV KAKGPQIPGGNNSEAVIARFPQAWL EK\CCQ/GPQEQEVCFAQEGTKLISK TRAALGV |
| 3466 | 8963 | A | 3735 | 95 | 272 | RALQPDTTWE*GSQRRPWLPQVTN KPV*SKTSKS |
| 3467 | 8964 | B | 3736 | 344 | 1420 | MLLKTVLLLGHVAQVLM LDNGLL QTPPMGWLAWERFCNINCEDEPK NCISEQLFMEMADRMAQDGWRDM GYTYLNIDDCWIGGRDASGRLMPD PKRFPHGIPFLADYVHSLGLKLG IY ADMGNFTCMGYPGTTLDKVVQDA QTFAEWKVDMLKLDGCFSTPEEAA QGYPKMAAGLNATGRPIAFSCSWP AYEGGLPPRVNYSLQADICNLWRN YDDIQDSWRSVLSILNWFVEHQDIL QPVAGPGHWNDPDM LLIGNFGLSL EQSRAQMALWTVLAAPLLMSTD LR TISAQNMDILQNPLMIKINQDPLGIQ GRRHKGSWMPKGSCVPGCLRDPG TQDSQGKISHRSVHAASVQQG* |
| 3468 | 8965 | B | 3737 | 49 | 2119 | MALWTVLAAPLLMSTD LR TISAQN MDILQNPLMIKINQDPLGIQGRRIHK EKSLIEVYMRPLSNKASALVFFSCR TELCLIATTSCLGQLNFTG SVIYEAQ DVLLS* |
| 3469 | 8966 | A | 3738 | 139 | 536 | QSLGFIPFRKRQRISISYTFYFETGS YSVAQAGVQWHNLGSLQPRPPGFK QSSCLSPPGSWDHWRA PHQANFA LLVETGSPHAAQASLKLSSSDPSA LASQSTGITGVSHHGQPYISHTLIIFI GKFY |
| 3470 | 8967 | A | 3739 | 1 | 213 | QFSCSLPSSRDYRHEQP/PLIFVFLV ETGFYHVGQAGLELLTSGDPPALAS QSAEITGVSPRTRPNNLKS |
| 3471 | 8968 | B | 3740 | 75 | 729 | MEGTAGGERPSVVNGDSGKSGGVG DPREPLSCLQEGSGCHPTTESFEKSV REDASPLPHVCCCKQDALILQ RGLH HEDGSQHIGLLHPGDRGPDHEYLLV EEAERAMSEREARPNEESVQRNRLI CRTNPYRIFEYLP LSLEEAFFLVYAL GCLSIYYEKEPLTIVKLWKAFTVVQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PTFRTTYMAYHYFRSKGWVPKVGL KYGTDLLLYRKGPFFYHAX* |
| 3472 | 8969 | A | 3741 | 1 | 2649 | |
| 3473 | 8970 | A | 3742 | 41 | 656 | PVPRPCCGLRARSWPSSPRAARAAL PHGESALSRLRALLAARASLDLCL FAFSSPQLGRAVQLLHQRGVVRV VTDCDYMALNGSQIGLLRKAGIQV RHDQDPGYMHHKFA\VDRRVLITG SLNWTQTQAIQNNRENVLITEDDEYV RLFEEFERIWEQFNPTKYTFFPPKK SHGSCAPPVSRAGGRLLSWHRTCG TSSESQT |
| 3474 | 8971 | A | 3743 | 3 | 267 | FNMESQSLASLKCSGAVSAHCNLCF LGSSNSPASASRVSGITGVLYHTWLI FVFLVQTGFHHVGQAGLELL/NLVI HPPRPPKVLGLQA |
| 3475 | 8972 | A | 3744 | 2 | 430 | FFFETGGAFVTQAGVQWPNLSSLQP SPPGFKPSSHLSLPSTWDYRYTPPCP ASFCIF\TDTGFCHVDQAGLELLASC NLPASASRSAGITGVSHHACPFLLFS FFKSGITSPNYPISHHEIESNVAPVF LFEDSTAIYVYYF |
| 3476 | 8973 | A | 3745 | 2 | 316 | EFLFFETEFCSVTRLECSGAISAHCK LCLGSRHSPASASRVARTTGTRHH AQRIF\VFSVETGFHRVSRDGLDLL/ NLVIHPPQPPKVLGIRGREPPCPACF FAF |
| 3477 | 8974 | A | 3746 | 1 | 1053 | |
| 3478 | 8975 | A | 3747 | 1 | 3011 | SLQRLPGLMHNLTQFLLDGNFLQSL PAELENMKQLSYLGLSFNEFTDIPE VLEKLTAVDKLCMSGNCVETLRLO ALRKMPHIKHVDLRLNVIRKLIAD VDFLQHVLTQLDLRDNKLGDLDA FNNIEVLHCERNQLVTLDICGYFLK ALYASSNELVQLDVYPVPNYLSYM DVSRNRLAENVPEWVCESRKLGSF GILGHN\QIC\ELPARLFCN\SSLRKLL GQGHN\QLARLPERLERTSVEVLDV QHNQLELPPNLLMKADSLRFLNAS ANKLESLPPATLSEETNSILQELYLT NNSLTDKCVPLLTGHPHLKILHMA YNRLQSFPASKMAKLEEELEIDLSG NKLKAIPTTIMNCRRMHTVIAHSNC HRGPFPEVM\QLPEIKCVD\LSCNE\ LSEVTLP\ENLPSPNCRSLDLTGNPR PCPLITKPELLNNIRCFKID\QPSTG DG\SGAPAVWASHG\YTEA\SGVKNK LCV\VALSVNNFCDNREALYGVFD GDRNVEVPYLLQCTMSDILAEELQ KKTKEEEYMNVTFIVMQRKLGT GQKLGGAAVLCHIKHDPVDPGGSF TLTSANVGKCQTVLCRNGKPLPLSR SYIMSCEEELKRIKQHKAIITEDGKV NGVTESTRILGYTFLHPSVVP QSVLLTPQDEFFILGSKGLWDSLSV EEAVEAVRNVDPALAAKKLCTLA QSYGCHDSISAVVVQLSVTEDSFCC CELSAGGAVPPPSPGIFPPSVNMVIK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DRPSDGLGVPSSSSGMASVEISSELST SEMSSEVGSTASDEPPPGVALSENSPA AYPSEQRCLHPIWLSNSFQRQLSS ATFSSAFSDNGLDSDDEEPIEGVFTN GRRVEVEVDIHCSRATEKEKQOHL LQVPSEASDEGIVISANEDEPGLPRK ADFSAVGTIGRRRANGSVAPQERSH NVIEVATDAPLRKPGGYFAAPAQPD PDDQFIIPPELEEEVKEMKHHQEQQ QQQQPPPPQLQPQLPRHYQLDQLP DYYDTPL |
| 3479 | 8976 | A | 3748 | 1 | 246 | LPTLECSGMISAHCNLRPGSSDSP ASASQVAGITSAHHYAWLVFVFSV EMGFHHVGQGWRSRLDLVIRPPQP KMLGLQA |
| 3480 | 8977 | A | 3749 | 153 | 527 | LLVFYLPPTSLKGGLRQLDMSLLCQ LYSLYESIQEYKGACQAASSPNWTY ALENGFFDEEEYFPEQNSLHRRD RGPPRDLSPAPPSPAATGFWSPSR GSWEGCDCWEALPTGHA VIICFS |
| 3481 | 8978 | A | 3750 | 2 | 377 | IPAASTFFCFLRQSLTLWPHAGVQW CGLSSLHPPPPGFMLFSCSLPSSWD YRRPPRPAKFSVFLVETGFHRVSQ DGLDLMTSDPPALASQSAGITGVS HCTRPKEAYFYFLALDPRCKDGVR |
| 3482 | 8979 | A | 3751 | 2 | 294 | LFLHADRLEYSGMTISHLQPQTPGA QGDPLTSSLPREVGLQ/CVCHHTQL FFF/CIFVETESHHLA/RAGLKLLGSS DPTASPSQSDGITGMSHHSCPSTF |
| 3483 | 8980 | A | 3752 | 80 | 267 | RQGLTILPRLVLNSC/RLKLSSHLSLP KYWDYRQEPPCLAISIIFFKKSLIYY LNLAILYFKCK |
| 3484 | 8981 | A | 3753 | 1 | 972 | |
| 3485 | 8982 | A | 3754 | 1 | 283 | PKPQEIELPEAKNR/PWIFNKILGTTV KLMELKPNTCYCLSVRAANTAGVG KWCKPYKVSPGKRGALGVERSPPK REPGLWRLGTPLCPHDSSG |
| 3486 | 8983 | B | 3755 | 346 | 472 | XRNMNILQYCPSSDMWTLFETCDV HIRKQQMVSVETIYIVGG* |
| 3487 | 8984 | A | 3756 | 1 | 1346 | MSAEEMVQIRLEDRCYPVSKRKLIE QSDYFRALYRSGMREALSQEAGGP EVQQLRGLSAPGLRLVLDFINAGGA REGWLLGPRGEKGGGVDEDEEMD EVSLLSELVEAASFLQVTSLLQLLS QVRLNNCLEMYRLAQVYGLPDLQE ACLRFMVVHFHEVLCKPQFHLLGS PPQAPGDVSLKQRLREARMTGTPV LVALGDFLGGPLAPHPYQGEPPSML RYEEMTERWFPLANNLPPDLVNVR GYGSAILDNYLFIVGGYRITSQEISA AHFLQGP/RTNEWLQVASMNQKRS NFKLVAVNSKLYAIGGQAVSNVEC YNPEQDAWNFVAPLPNPLAEFSAC ECKGKIYVIGGYSTRDRNMNILQYC PSSDMWTLFETCDVHIRKQQMVSV EETIYIVGGCLHEARGPNRRSSQSED MLTVQSYNTVTRQWLYLKENTSKS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GLNFDLCAP |
| 3488 | 8985 | A | 3757 | 3 | 358 | TNSMPPMMSMSYRICAMLKGE/DV QALRRAHQRNVKHMRLQLLMDRGL PCHPLPPANINPIRVR/DPHPCPIALS HPIYSWSLTLPNKPTSVAVFNILLS CLTIPFIASFVSLFEKLSAILD |
| 3489 | 8986 | A | 3758 | 1 | 164 | GSTTPAMEFASLFKKILLIDCRD/RG LALLPRLVLSSWPQVIFLPWPPKFL GLRT |
| 3490 | 8987 | A | 3759 | 3 | 280 | FFFETESHSAVARLEYRGITLAHCILC RQGSSNSPASDPQVAGTTGTRHRA QLTFVFLVQMGFHHFGQAGLELPN LGIHPTSASPKCWDLPA |
| 3491 | 8988 | A | 3760 | 3 | 516 | AQHQP MNIFYPVGVHAPLMNIQR NPFNIHPQLPLHLHTGVPLMQVATP TSVSQGLPPPPPPPPSQQVNYIASQ PRWKRNCTKLQIQEKAQAQEVKLAI KPFYQNKDITKEEYKEIVRKA VDKV CHSKSGEVNSTKVGNLVKAYVDQ YEYSRKGSQRKLWEGPVSTGKN |
| 3492 | 8989 | A | 3761 | 173 | 411 | |
| 3493 | 8990 | A | 3762 | 438 | 789 | LTWSTPVLPAPTAAPGKYGNFGQ PSSGNTSSSSHSQRPLMAAVKLAES KVSVAVEASADSSKTDKKLQIQEK AAQEVKLAIKPFYQNKDITKEEYKE IVRKA VDKCVLLECSIQKM |
| 3494 | 8991 | A | 3763 | 1097 | 4669 | ILGTSCGYALAHQTQEGEEKKQTS GTSNTRGSRKPAMTTPTRRSTRNT RAETASQSQRSPISDNGCDAPGNS NPSLSVPSSAESEKQTRQAPKRKSV RRGRKPPLLKKKLRSVA APEKSSS NDSVDEETAESDTSPVLEKEHQPDV DSSNICTVQTHVENQSANCLKSCNE QIEESEKHTANYDTEERVGSSSSESC AQDLPVLVGEEGEVKKLENTGIEA NVLCLESEISENILEKGGDPLEKQDQ ISGLSQSEVKTDVCTVHLPNDFPTC LTSESKVYQPVSCLSDLSENVESV VNEEKITESSLVEITEHKDFTLKTTEE LIESPKLESSEGEIIQTVDRQSVKSPE VQLLGHVETEDVEIATCDTFGNED FNNIQDSENNLLKNNLLNTKLEKSL EEKNESL TEHPRSTELPKTHIEQIQK HFSEDNEMIPMECDSFCSDQNESE VEPSVNADLKQMNENSVTHCSENN MPSSDLADEKVETVSQPSESPKDTI DKTKKPRTRRSRFSPTTWSPNKD TPQEKKRQSPSPRRETGKESRKSQ SPSPKNESARGRKKRSQSPPKKDIA RERRQSQRSPKRD TTRESRRSESL PRRETSRENKRSQPRVKDSSPGEKS RSQSRERESDRDGQRRERERRTRK WSRSRSHSRSPSRCRTKSKSSSFGRI DRDSYSPRWKGRWANDGWRCPRG NDRYRKNDEKQENENTRKEKNDIH LDADDPNSADKHRNDCPNWTEKI NSGPDPRTRNPEKLKESHWEEENRN ENSGNSWNKNFGSGWVSNRGRGR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GNRGRGTYRSSFAYKDQENENRWQ NRKPLSGNSNSSGSESKFVEQQSY KRKSEQEFSFDTPADRSGWTSASSW AVRKTLPADVQNYYSRRGRNSSGP QSGWMKQEEETSGQDSSLKDQTNQ QVDGSQLPINMMQPMNVMQQQM NAQHQPMMNIFYPVGVHAPLMNIQ RNPFNHPQLPLHLHTGVPLMQVAT PTSVSQGLPPPPPPPPPSQQVNYIAS QPDGKQLQGIPSSSHVSNNMSTPVL PAPTAAPGNTGMVQGPSSGNTSSSS HSKASNAACKNWQKGKVSVAVEA SA\YSSKTDKKFAKFQEKAAQVVKI WAKPFYQNKDITKEEYKEIVRKA VDKVCHSKSGEVNSTKA\ANLVKA YVDKYKYSRKGSLLKKTLEEPRVTE KDLG |
| 3495 | 8992 | A | 3764 | 108 | 253 | |
| 3496 | 8993 | A | 3765 | 2 | 283 | RRLFFFFETESRSV\SRLECSGVISAHC NLH/LPGSSNSPGSASRVAGITGACH HAQLIF\VFLVETGFHHVGQAGLEL L/NLMICPPQPPKVLGLQA |
| 3497 | 8994 | A | 3766 | 1 | 290 | RSTFFFFFLERVYCSVT\SRLECSGTNIS AHCNLRPLPGSSGSHASVSQVAGITG AHHHTQPIFVFLVETGFHHIGQAGL ELL/NLMIHPPRPPKVLGLQV |
| 3498 | 8995 | A | 3767 | 234 | 1449 | EPGTHDPHLFLQGLLFWQAGGGEG GDGTGPAGGRQICVPPAALAHVRV PGEFLAQVAAAA*AIHDEQRPGKLH HPPG/ELMQRGVASESYMIVAPPMP SSWSSSGTNGPPSPTNLT*PIVHFIFS APTP/TKKTTTNTAMKTATHIPDVQ SAFCSPHSGTQRGDGLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNCLEAEAAAGAAAE DSGAARGSLQPAPAQPPGDPAQA SVSNGEDAGGGAGRELVDLKIIWN KTKHDVKFPLDSTGSELKQKIHSIT GIPPDESPRRGGPAGPYQQSQRLLE YAQATEALLKTGAAYPCFCSPQRLE LLKKEALRNHQTPR |
| 3499 | 8996 | A | 3768 | 1 | 8157 | |
| 3500 | 8997 | A | 3769 | 1126 | 1355 | |
| 3501 | 8998 | A | 3770 | 1 | 1611 | MGSRCNLNPPPPAHSDTTGKDSFGNI RGAETGQGASACSVTSARVTCGAG SEPHSHRNPGISAQVGLAPSYGAAR GRRRPLALQQSPQERRHVGWNSTR GLLPASLPGTASSQSASATASAALP LKVTGPLARNPTPPWTAAAALATR GQRPEKGLFPGPAPFSLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNCLEAEAAAGAAAE DSGAARGSLQPAPAQPPGDPAQA SVSNGEDAGGGAGRELVDLKIIWN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KTKHDKFPLDSTGSELKQKIHSIT GLPPAMQKVMYKGLVPEDKTLREI KVTSGAKIMVVGSTINDVLAVNTP KDAAQQDAKAEENKKEPLCRQKQ HRKVLDKKGPELVMPVSKGAQERL PTVPLSGMYNKSGGKVRLTFKLEQ DQLWIGTKNGTEKLPMGSIKNNVVS DPIEGHEDYHNDGRFQLAPTEASY YWVYWVPTQYVDAIKDITVLGKW QYF |
| 3502 | 8999 | A | 3771 | 482 | 631 | AGGWGPQAPDTPWVGPAGQAGRL HPLRSTKRS/MSVPATRTTVPLTVM Q*RRVCRWCWGPLGHWEAHGFLV SGDVNHFGGPAALL |
| 3503 | 9000 | A | 3772 | 1 | 1579 | |
| 3504 | 9001 | A | 3773 | 3 | 486 | DRYMLTRDYLTVKVWDLNMEARP IETYQVHDYLRSLCSLYENDCIFD KFECAWNGSDSVIMTGA YNNFFRM FDRNTKRDTVLAESRESSKPRAVL K\PRRVCVGG\KRRRDDISVGQLGTF TKKILHTAWHPAENIHLFFAATNN LLHLSRGKVNSDMH |
| 3505 | 9002 | A | 3774 | 72 | 1317 | KLLPAPRQPPRPTNGSPRDPTPAQV* VEAPAGSSQ*TAP/ARRPLRAARTLP AAEAAGLTLRGCFHGDRGRACAAL RRWPWRQLRGWGFEVPAPPLLRT AELVG/RSPEPRCPGKVSMAEFLTEF LEIPPFNKQYTESQLRAGAGYILED NEAQVDVLESQFSQLLHQINSTRDF ESIRLAHDHFLSNLLAQSFILLKPSP VEEKSEPQDFQEADSWGDTKRTPG VGKEDAAEETVKPGPEEGTLEKEE KVPPPRSPQAQEAQVNIDEGLTGCTI QLLPAQDKAIVFEIMEAGEPTGPILG AEALPGGLRTLPEPGKPKDEVLR YPDRSLSPEDAESLSVLSVSPDTAN QEPTPKSPCGLTEQYLHKDRWPEVS PEDTQSLSLSEESPSKETSLDVSSKQ LSPKALAPFQLGN |
| 3506 | 9003 | A | 3775 | 1 | 350 | FGTRKPGAVGAGEFVSPCESGDN GEPALAEQGRPLPLNKTFLGYAF LLTMATTSKDLASRSKLPDGPTGSS EEEEEFLENPPFNKQYQESQLRAGA GYILKEFKEAQVRSFFV |
| 3507 | 9004 | A | 3776 | 3 | 318 | RRGLTLSSRLEYSGIUKTHWNHLL GSSNPPTSASQVAGTTGTCHHAQLN FF/CLTFLVATRSHDIAQAGLELLDS SHPPASASHSAGTTGVNHHA WPAV ALLWIN |
| 3508 | 9005 | A | 3777 | 4 | 378 | ARNHDLCLCFKAILFFEMESCSVSQ AGVQWRVFGSLQAPPPGFLPFS/CY RCQPPSPANFFLYFLVETGFLF**RQ GFTVLDRMVSIS*PRDPPALASQSA GITGVSPRTRQEGHS*R*EENGIG |
| 3509 | 9006 | A | 3778 | 19 | 418 | VEMGFCQADQAGLELLTSGDPPAS VSQSTGITVLSLSFFFETESRSVAQA GVQWRDLGSLQRPPPGFTPFSCLSL PSSWDYRRPPRLANFFVFSVETGF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HRVSQDGLDLLT/S/GDPPASASQSA GDTGVSQAPV |
| 3510 | 9007 | A | 3779 | 3 | 331 | CFIFYFILFYFETESRSVAQAGVQWR HLDLQAPPPGFTPFSCSLPSSWDY RRP/PPRPANFFVLLVQTGFHRVSQD GLDLLT/S/GDPLASASQSAGITGLSH RARPAQVS |
| 3511 | 9008 | A | 3780 | 659 | 1092 | AYNIFQFANRTNTGENLPKTLVIKYI SSTFRSFFFFFFFLRQSRVAQAGVQ WRNLGSLQPPPPGFTPFSCSLPSSW DYGRPPRPANF/SVFLVETGFHRVS QDGLDLLT/S/GDPPTSASQSAGITG VSHCARPHSVLIKEITQT |
| 3512 | 9009 | A | 3781 | 8 | 295 | GRVSLRHQAGVQWRSLSLQAPPP RFTPFSCSLLSRWDHRRPPRPANL LYFLVETGFHRVRQDGLDLLT/S/GD PPALASQSAGITGVSHRAHPTY |
| 3513 | 9010 | A | 3782 | 1474 | 1870 | SARGITGVSHCTRPFSSFFFFFFFETE SHSIAQAGVQWRYLGSLOPLPPGFK QFACLSLSSSWDCRHAPRPANFLF LVEMGFHHL*LELLISSDPPASAFKS ARITGVSHRAWPIRFFLLKNIFKFLN FC |
| 3514 | 9011 | A | 3783 | 60 | 560 | SDNYEKSHNIQEMTGLQSTLLVNN RVQLNFKWELNFFLSFLKQSSTLVA QAGVQWHDLSLQPPPPGVKRFSC LSLPSSWDYRHVPPCLANFVFLFFL VETGFLHVGQAGPELLTSGGPPASA SQSAGITSVTHRPLPEDSAFYQCRL NLWQRSPLECRCSLVLKT |
| 3515 | 9012 | A | 3784 | 3 | 230 | FFFKTESRSVTRLECSGAVLAHCNL QLPGSSNSPASASRVAGITRHVPPH RLIFVFLVETGFHHVGQDGLDLLTL |
| 3516 | 9013 | A | 3785 | 3 | 4117 | |
| 3517 | 9014 | A | 3786 | 1 | 457 | FPVRNLDLSTYCIGQKEEQLPSEYEL YADINHYGGMIGGHYTACAPLPND RSSQRNDVGWRLFDDSTLTTRDQS QAVTRYAYVLFYRRRNSPVERPAPK AGHSEHHPDLGPAAEAAASQ/ATRP WPGPRGG/APRGQPLNASPPLWIGQ TPPLKQT |
| 3518 | 9015 | A | 3787 | 1 | 298 | NNQESCSVTEAGVQWHDLSLQPP PSGFKQFS/CAQLLSSQDHRHMPPCP ANFYVFLIAEMGFYHVSQAGLELL TSSDLPALASQSAGIIGVSHRAWAK |
| 3519 | 9016 | A | 3788 | 3 | 286 | FFFLLFETQSHSHIRLECSGVISDYC NLCLPSSSDSLVLASGVAGTMGVR HNARLIFVFLVKMRFHVGPRLGP QIPWTGIWIPSHFGPPQSA |
| 3520 | 9017 | A | 3789 | 1 | 1422 | |
| 3521 | 9018 | A | 3790 | 353 | 470 | IPGVSLYSLFSLLAQNIPQSTEILKKL MTTNEIQSNIYT |
| 3522 | 9019 | A | 3791 | 1328 | 1615 | VSLFHAGVQWCDLSSLQPPPPGFKR FS/RLNLLSSWDYRRPLPHPSTFCKF VEMGFHHIGQAGLKLLTSGDPPASA SQSARITGVSHRARNCFYVT |
| 3523 | 9020 | A | 3792 | 2 | 114 | CQPGFVMKGPPAHRVQCQALNKWE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TELPSCSR\VCLPEA |
| 3524 | 9021 | A | 3794 | 1940 | 2062 | |
| 3525 | 9022 | A | 3795 | 785 | 892 | |
| 3526 | 9023 | A | 3796 | 1 | 2745 | |
| 3527 | 9024 | A | 3797 | 1 | 3297 | |
| 3528 | 9025 | A | 3798 | 1 | 2202 | |
| 3529 | 9026 | A | 3799 | 1 | 2868 | |
| 3530 | 9027 | A | 3800 | 1 | 3237 | |
| 3531 | 9028 | A | 3801 | 1 | 2001 | |
| 3532 | 9029 | A | 3802 | 1 | 2982 | |
| 3533 | 9030 | A | 3803 | 1169 | 3269 | VHCRFWILALCQMSRLQKSPLLFI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPTVSAQNLLK LMSNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSGLPFTITSKRITYLGI QLTRDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGGRINLVKMAILP KVIYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRALIAKSSLSQKNKTGGI TLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNYLIFDK PDKNKQWGKDSL FNKWCWENWL AICRKLKLDPFLTPYTKINSRWIKDL HVRPKTIKTLEENLGNTIQDIGMGK DFMSKTPKAMATKAKIDKWDLIKL KSFCTAKETTIRVNRQPTWEKIFA TYSSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYAAKK HMKKCSSSLAIREMQIKTTMRYHLT PVRMVIKKSGNNRCWRGCGEIGTL LHCWWDCKLVQPLWKS VWQFLRD LELEIPFDPAIPLLGIYPEDYKPCCYK DTCTRMFIAALFTIAKTWNQPKCPT MIDGIKKMWHIYTMEYYAAIKKDE FMSFAGTWMKLETILRKLSQGQK TKHRMYSLIGGNLTMRFTGHSAGS HHTPGPIMRCGAGGGIALGEIPNVN DELMGTANQHGT CIPMQQNCTLCT CTLKLV |
| 3534 | 9031 | A | 3804 | 2821 | 5793 | |
| 3535 | 9032 | A | 3805 | 2 | 256 | KRSLSLPSRLECSGVILAHCKLRLLG SRHSPPSDSGAAGTAGARHHARLFF LYFLVFHRVCLDGLDLL/NLVHLP SPK VWGLQA |
| 3536 | 9033 | A | 3806 | 1 | 2406 | |
| 3537 | 9034 | A | 3807 | 139 | 6503 | |
| 3538 | 9035 | A | 3808 | 1 | 3204 | |
| 3539 | 9036 | A | 3809 | 77 | 277 | PHPTPCSCFPWSASSPLT*THQALT EEDEW*QAKNSGQAAQGQTPALPL GNLGQVTAPLCPRFIC |
| 3540 | 9037 | B | 3810 | 21 | 219 | MMPRSSRTKSCRSSCVAWSSCMKE NKELRAEAERLGHELQQAGLKTKE AEQTCRHLTAQVRS LGGTX* |
| 3541 | 9038 | A | 3811 | 1 | 6359 | MTLHATRGAALLSWVNSLHVADP VEAVLQLQDCSIFIKIIDRIHGTEEGQ QILKQPVSERLDFVCSFLQKNRKHP SSPECLVSAQKVLEGSELELAKMT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MLLLYHSTMSSKSPRDWEQFEYKI QAELAVILKFVLDHEDGLNLNEDLE NFLQKAPVPSTCSSTFPEELSPPSHQ AKREIRFLELQKVASSSSGNNFLSGS PASPMGDILQTPQFQMRRLKKQLA DERSNRDELELELAENRKLLTEKDA QIAMMQQRIDRLALLNEKQAASPL EPKELEELRDKNESLTMR LHETLKQ CQDLKTEKSQMDRKINQLSEENGD LSFKLREFASHLQQLQDALNELTEE HSKATQEWLEKQAQLEKELSAALQ DKKCLEEKNEILQGKLSQLEEHLSQ LQDNPPQEKGEVLGDVLQLETLKQ EAATLAANNTQLQARVEMLETERG QQEAKLLAERGHFEEEEKQLSSLIT DLQSSISNLSQAKEELEQASQAHGA RLTAQVASLTSELTTLNATIQQQDQ ELAGLKQQAQEKQAQLAQTLOQQE QASQGLRHQVEQLSSSLKQKEQQ KEVAEKQEATRQDHAQQLATAAEE REASLRERDAALKQLEALEKEKAA KLEILQQQLQVANEARDSAQTSTVT QAQREKAELSRKVEELQACVETAR QEQHEAQAQVAEELQLRSEQQKA TEKERVAQEKDQLQEQLQALKESL KVTKGSLEEEKRRAADALEEQQRCI SELKAETRSLVEQHKRERKELEER AGRKGLERLQQLGEAHQAETEV RRELAEAMAAQHTAESECEQLVKE VAAWRERYEDSQQEEAQYGAMFQ EQLMTLKEECEKARQELQEAKEKV AGIESHSELQISRQQNELAELHANL ARALQQVQEKEVRAQKLADDLSTL QEKMAATSKEVARLET LVRKAGEQ QETASREL VKEPARAGDROPEWLE EQQGRQFCSTQAALQAMEREAEQ MGNELERLRAALMESQGQQQEERG QQEREVARLTQERGRAQADLALEK AARAELEMRLQNALNEQRVEFATL QEALAHALTEKEGKDQELAKLRGL EAAQIKELEELRQTVKQLKEQLAK KEKEHASGSGAQSEAAGRTEPTGP KLEALRAEVSKLEQQCQKQQEQAD SLERSLEAERASRAERDSALETLOQ QLEEKAEQELGHSQSALASAQRELA AFRTKVQDHSKAEDEWKAQVARG RQEAERKNSLISSLEEEVSILNRQVL EKEGESKELKRLVMAESEKSQKLEE RLRLLAQETASNSARAAERSALR EEVQSLREEAEKQRVASENLRQELT SQAERAELGQELKAWQEKFFQKE QALSTLQLEHTSTQALVSELLSA\KH LCQQLQAEQAAAEKRHREELEHSK QAAGGLRAELLRAQRELGELIPLRQ KVAEQERTAQQLRAEKASYAEQLS MLKKAHGLLAENRWLGERANLG RQFLEVELDQAREKYVQELAAVRA DADTRLAEVQREAAQSTARELEVMT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AKYEGAKVKVLEERQRFQEERQKL TAQVEQLEVFQREQTKQVEELSKK LADSDQASKVQQQKLKAVQAQGG ESQQEAQRLQAQLNELQAQLSQKE QAAEHYKLQMEKAKTHYDAKKQQ NQELQEQLRSLEQLQKENKELRAE AERLGHELQQAGLKTKEAEQVTCR HLYLPRLRSLEVAQVAHARPSSFRD LGKFQVATDALKSREPQAKPQLDL SIDSLDLSCEEGTPLSITSKLPRTQPD GTSVPGEPAISPISQRLPPKVESLESL YFTPIPARSQAPLESSLDSLGDVFDQ SGRKTRSARRRTTQIINTMTKKLD VEEPDSANSSFYSTRSAPASQASLR ATSTQSLARLGSPDYGNSALLSLP GYRPTTRSSARRSQAGVSSGAPPGR NSFYMGTCQDEPEQLDDWNRIAE QQRNRVCPPHLKTCYPLESRPSLSL GTTDEEMKTGDPQETLRRASMQPI QIAEGTGITTRQQRKRVSLEPHQGP GTPESKKATSCFPRPMTPRDRHEGR KQSTTEAQKKAAPASTKQADRRQS MAFSILNTPKKLGNSLLRRGASKKA LSKASPNTRSGTRRSPRIATTTASAA TAAAGATPRAKGKAKH |
| 3542 | 9039 | A | 3812 | 241 | 6884 | LSGITKMTLHATRGAALLSWVNSL HVADPVEAVLQLQDCSIFIKIIDRIH GTEEGQQILKQPVSERLDFVCSFLQ KNRKHPSSPECLVSAQKVLEGSELE LAKMTMLLLYHSTMSSKSPRDWEQ FEYKIQAEALAVILKFVLDHEDGLNL NEDLENFLQKAPVPSTCSSTFPEELS PPSHQAKREIRFLELQKVASSSSGN NFLSGSPASPMGDILQTPQFQMRRL KKQLADERSNRDELELELAENRKL LTEKDAQIAMMQQRIDRLALLNEK QAASPLEPKELEELRDKNESLTMRL HETLKQCQDLKTEKSQMDRKINQL SEENGDLDFKLREFASHLQQLQDAL NELTEHASKATQEWLEKQAQLEKE LSAALQDKKCLEEKNEILQGKLSQL EEHLSQLQDNPPQEKGEVLGDVLQ LETLKQEAATLAANNTQLQARVEM LETERGQQEAKLLAERGFHEEEKQ QLSSLITDLQSSISNLSQAKEELEQA SQAHGARLTAQVASLTSELTTLNAT IQQQDQELAGLKQQAQKEKQAQLAQ TLQQQEASQGLRHQVEQLSSSLK QKEQQLKEVAEKQEATRQDHAQQ LATAAEEREASLRERDAALKQLEA LEKEKAAKLEILQQQLQVANEARD SAQTSVTQAQREKAELSRKVEELQ ACVETARQEQHEAQAQVAEELQL RSEQQKATEKERV AQEKDQLQEQL QALKESLKVTKGSLEEEKRRAADA LEEQQRCELSLKAETRSLVEQHKRE RKELEEERAGRKGLEARLLQLGEA HQAETEVLRRRELAEMAAQHTAES |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ECEQLVKEVAAWRDGYEDSQQEE AQYGAMFQEQLMTLKEECEKARQ ELQEAKEKVAGIESHSELQISRQON KLAELHANLARALQQVQEKEVRAQ KLADDLSTLQEKMAATSKEVARLE TLVRKAGEQQETASRELVKEPARA GDRQPEWLEEQQGRQFCSTQAALQ AMEREAEQMGNELERLRAALMES QGQQQEERGQQEREVARLTQERGR AQADLALEKAARAELEMRLQNAL NEQRVEFATLQEALAHALTEKEGK DQELAKLRGLEAAQIKELEELRQTV KQLKEQLAKKEKEHASGSGAQSEA AGRTEPTGPKLEALRAEVSKLEQQC QKQQEQADSLERSLEAERASRAER DSALETLQGQLEEKAEQELGHSQSAL ASAQRELAAFRTKVQDHKAEDW KAQVARGRQEAERKNSLISSLEEV SILNRQVLEKEGESKELKRLVMAES EKSQKLEE/RLRLLQAETASNSARA AERSSALREEVQSLREVEAEKQRYA SENLRQELTSQAERAEEELGQELKA WQEKFFQKEQALSTLQLEHTSTQA LVSELLPAKHLCCQLQAEQAAAEK RHREELEQSKQAAGGLRAELLRAQ RELGELIPLRQKVAEQERTAQQQLRA EKASYAEQLSMLKKAHGLLAEENR GLGERANLGRQFLEVELDQAREKY VQELAAVRADAETRLAEVQREAQS TARELEVMTAKYEGAKVKVLEERQ RFQEERQKLTAQVEELSKKLADSD QASKVQQQKLKAVQAQGGESQQE AQRFAQLNELQAQLSQKEQAAEH YKLQMEKAKTHYDAKKQQNQELQ EQLRSLEQLQKENKELRAEAERLG HELQQAGLKTKEAEQTCRHLTAQV RSLEAQVAHADQQLRDLGKFQVAT DALKSREPQAK\POLDSLIDSLDLSC EEG\TPL\SITSKLPRTQPDGTSVPGE PASPISQRLPPKVESLESLYFTPIPAR SQAP\LESSLDSLGDVFLDSGRKTR SARRRTTQIIN\TMTKK\LDV\EEPDI SAPNLSFYS\TRSAPASQASLRATSS TQSLARLGSPDYGNSALLSLPGYRP TTRSSARRSQAGVSSGAPPGRNSFY MGTCODEPEQLDDWNRIAEQQRN RVCPPHLKTCYPLESRPSLSLGTITD EEMKTGDPQETLRRASMQPIQIAE GTGITTTRQQRKRVSLPHQGPGTPE SKKATS\CFPRPMTPRDRHEGRKQS TTEAQK\KAAPASTKQADRRQSM\ AFS\LNTPKKLGNSLLRTG*PQRKA LSK\ASPNTTRSG\TRRSRPIATTTASA ATA\AAIGCHPSRPRGKGKALKGPV PVSGPHLCSPMVAVTWSSAYCPSQ CLLSAPRPTVAKPLETVMPARTLA WSLVLHWRLLGAGPGGLEHGGCG RSPYLASFFLKAKSLLHHNQI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *~Stop codon; /~possible nucleotide deletion; ~possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3543 | 9040 | A | 3813 | 1 | 3466 | EKEKAAKLEILQQQLQVANEARDS AQTSTVTAQREKAELSRKVEELQA CVETARQEQHEAQAQVAEELQLR SEQQKATEKERV AQEKDQLQEQQL ALKESLK VTKGSLEEEKRRAADAL EEQQR CISELKAETRSLVEQHKRER KELEEERAGRKGLEARLQQLGAEH QAETEVLRRELAEAMAAQHTAESE CEQLVKEVAAWRERYEDSQQEAAQ YGAMFQEQLMTLKEECEKARQELQ EAKEKVAGIESHSELQISRQQNELA ELHANLARALQQVQEKEVRAQKLA DDLSTLQEKMAATSKEVARLETLV RKAGEQQETASRELVKEPARAGDR QPEWLEEQQGRQFCSTQAALQAME REAEQMGNELERLRAALMESQGQQ QEERGQQEREVARLTQERGRAQAD LALEKAAARAELEMRLQNALNEQRV EFATLQEALAHALTEKEGKDQELA KLRLGLEAAQIKELEELRQTVKQLKE QLAKKEKEHASGSGAQSEAAGRTE PTGPKLEALRAEVSKLEQQCQKQQ EQADSLERSLEAERASRAERDSALE TLQGQLEEK AQELGHSQSALASAQ RELAAFRTKVQDHSTAEDWKAQV ARRRQEAERKNSLITILEEEVSILNR QVLEKEGESKELKRLVMAESEKSQ KLEERLRLQAETASNSARAAERS ALREEVQSLREEAEKQRVASENLR QELTSQAERAEELGQELKAWQEKF FQKEQALSTLQLEHTSTQALVSELL PAKHL CQQLQAEQAAAEKRHREEL EQSKQAAGGLRAELLRAQRELGELI PLRQKVAEQERTAQQRLAEKASYA EQLSMLKKAHGLLAEENRGLGERA NLGRQFLEVELDQAREKYVQELAA VRADAETRLAEVQREAQSTARELE VMTAKYEGAKVKVLEERQRFQER QKLTAQVEQLEVFQREQTKQVEEL SKKLADSDQASKVQQQKLKAVQA QGGESQQEAQRLQAQLNELQAQLS QKEQAAEHYKLQMEKAKTHYDAK KQQNQELQEQLRTLEQLQKENKEL RAEAERLGHELQQAGLKTKEAEQT CRHLTAQVRTLEAQVAHADQQLRD LGKFQVATDALKSREPQAKPQLDL SIDSLDLSCEEGLPLSITRSGGSLPPY VCLWSACCLSGCILVR |
| 3544 | 9041 | A | 3814 | 35 | 266 | |
| 3545 | 9042 | C | 3815 | 383 | 628 | MDPSAGVTIVTCLASLFSGRLVRFR CSHDWRNYTERVLLFQWVELKTKC WRHTEAGLKPSHYFLEKMKKTLRE SQATYDRI* |
| 3546 | 9043 | A | 3816 | 2 | 513 | DIYGGDYERFGLQGS AVASSFGNM MSKEKRDSISKEDLARATLVITNNI GSTA\WLCALNENIDRVVFGNFLR INMVSMKLLAYAMDFWSKGQLKA LFF/VEHQGYLGAVGALLGTVQND |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LMTSRRRGSGRETASQKGQRTKKL LLEKVKVALGRKPSHLWQMNLGFC |
| 3547 | 9044 | A | 3817 | 29 | 175 | KSRPGTVAHACNPSTLGSRGGRIIPA QEFKTSLGNTVSEAPCLYLKNN |
| 3548 | 9045 | A | 3818 | 171 | 419 | KFFPFQSLWWERRAFPLKGEDMAA LLCQDEKKDQVERSSTAFHGEIFGT SVPENGWHPKKQSDGMEEYKTFGL GLTNVKKNR |
| 3549 | 9046 | A | 3819 | 2 | 1209 | WPSKETAFNNTTQMPCQLQSASTWS SYEHNSSEYLLREHVSELDSSFHSV LSLPSDVPLHFHFETLLKKTEIKGNL AENKFVDEYIISPSPVHSTLNQWRN GYSPICKPQIRSESSAQLLQGRKKRH LSETALGERTKLKEFDHHTESGSH SNFTAVSNVNLRSIQNSSRNTARR R\LRSESSYDIDNTV\IPMSLVAPAK LEKLQYKEILTPSWRMVVLQPLDE YNLGKEEIEDLSDEVFSLRHKKYEE REQARWSLWEQSKWHRNSRAYS KNVEGQDLLLKEYPNFSSSQQCA AASPPGLPSENQDLCAYGLPSLNQS QETKSLWWERRAFPLKGEDMAALL CQDEKKDQVERSSTAFHGEIFGTSV PENGHHPKKQSDGMEEYKTFGLGL TNVKKNR |
| 3550 | 9047 | A | 3820 | 7 | 447 | |
| 3551 | 9048 | A | 3821 | 1 | 373 | EQQVLRSTCLGVGAKV/L/VEGMVL QYSTQKGILT/ENHIQEINAQ/TTGLR /KTMLLLDILPSRGPKAFDT/FLDSLQ EFPWVREKLKKAREEAMTDLPAGL EEKGRTGRRMGWGAGEEKGQKCQ TVGMRT |
| 3552 | 9049 | A | 3822 | 1 | 708 | TPVWWNSLWGRFPNSQDSGCSFSP PPQRYVVADGEMEARDKQVLRSLR LELGAEVLVEGLVLQYLYQEGILTE NHIQEINAQTTGLRKTMMLLDILPSR GPKAFDTFLDSLQEFPPWVREKLKK AREEAMTRPCLAVDRLTGIP\SHILN SSPSDRQINQLAQRLGPEWEPMVLS LGLSQTDIYRCKANHPHNVQSQVV EAFIRWRQRFQKQATFRTLDNGL\R AVEVDPSLLLHMLE |
| 3553 | 9050 | A | 3823 | 791 | 1090 | HFLHGPLAQEDKSERERWQHLAD\ LADFALA\MKDTLTNNNQSFNNFM LRIGEHTPAGLPSRLPSHAGAWPP TRRDMRLRTTEAIRVGRFTHSQGKE T |
| 3554 | 9051 | C | 3824 | 172 | 243 | MRPSHGPEQLCSTLSPPIKPRPT* |
| 3555 | 9052 | A | 3825 | 1 | 615 | |
| 3556 | 9053 | A | 3826 | 1 | 596 | PGWEKRMSRSSVVNTQEALPTAAIP RDAKGRVYYFNHITNASQWERPSG\ NS\SSGGKNGQGEPVVRC\SHLLV KHSQSRPSSWRQ\EKITRTKGGGP GSLINGLHPEDSSSGEEDF\ESLASQF SDCK/SSAKARG\DLGAFQKQVRLQ KPFLKTPRFAL\RTGGDERGPCFTD\ T |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SGIHILPHLSEGGEPRPGLGAGQGG |
| 3557 | 9054 | A | 3827 | 1 | 295 | ETVFHSVTQSGMQWHNLASLQRLP LRLKQTSHLSLLSSWDCRHMPPNL A/NF/CVLRDKISPFPCPGWASNPPG LKQCIGILKYPQALTPYELINIWEGI |
| 3558 | 9055 | A | 3828 | 131 | 771 | MGVILEPSGTTVPLVSSV*LLVWDH GPTRIVGLIIRLGPR/YPLVSSSSKSG RTMPNILDIIASA VENKIPPSKTSKI NVKPELKEEPEESIISA VDENNKLYS DIPHSWICDALQKAFTDKEELLKQQ ASNLHEQKKAGVIFEAEVITLLTS VLKTSSASRTSLSSRHQFAPGATVL YKGDKMVLNLD RSRVPTECIEKIEA ILKELEKPAP |
| 3559 | 9056 | A | 3829 | 1 | 655 | MPVNAGGKVQESQKPPTLIPEPKDS QANFKSSSEQSLTEMWRPNNLSK EKTEWHVEKSSGKLQAAMASVIVR PSSSTKTDSMPAMQLASKDRVSERS SAGAHKTDCLKLAEAGETGRILPN VNSDSVHTKSEKNFQAVSQGSVPSS VMSAVNTMCNTKTDVITSAADTTS VSSWGGSEVISS/CIKYHFGLYIIRM CIFKKCQSASGSKTRMQGYLE |
| 3560 | 9057 | A | 3830 | 1 | 515 | LTLNQIKEEREQDNSESPNGRTSPL VSQNNEQGSTLRDLLTTTAGKLRV GSTDAGIAFAPVYAMGAPSSKSGRT MPNILDIIASVVENKIPPSKTSKINV KPELKEEPEESIISA VDENNKLYS DIP HSWICEKHILWLRIIIA VIGSF SKNV GNKDSLQWFLVCIRK |
| 3561 | 9058 | A | 3831 | 6 | 226 | RKGGFFVDLFVR\VSNQVAVNMYK QLGYSVYRTVIEYYASNGEPDEDA YGKLPSMAVSPRSRNSYILSTDCSI |
| 3562 | 9059 | A | 3832 | 37 | 611 | SGGGAMTTLRAFTCDDLFRV/FNNI NLDPLTETYGIPFYLAHWPEYF IVAEAPGGELMGYIMGKAEGSVAR EEWHGHV\ALSVAPEFRRRLGLAA KLMELLEISERKGGIFLVDLFVRV SNQVA\VNMYK\QLGYSVYR\TVNE YYFGPATGEP**GTLIDMRESTFPRD TGERNPIIP\LPHPGGGLEDH |
| 3563 | 9060 | A | 3833 | 1 | 191 | MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWPQLST/FQQMWISKQEY DESGPSIVHRKCF |
| 3564 | 9061 | A | 3834 | 2 | 1203 | LSRRCQLSHSVLPPLRRRVSLPVAM EEEIAALVIDNGSGMCKAGFAGDD APRAVFPSIVGRPRHQGVMMVGMGQ KDSYVGDEAQSKRGILTLKYPIEHG IVTNWDDMEKIWHHTFYNELRVAP EEHPVLLTEAPLNPKANREKMTQIM FETFNTPAMYVAIQAVLSLYASGRT TGIVMDSGDGVTHTVPIYEGYALPH AILRLDLAGRDLTDYLMKILTERGY SFTTTAEREIVRDIKEKLCYVALDFE QEMATAASSSSLEKSYELPDGQVITI GNERFRCPALFQPSFLGMESCGIH ETTFNSIMKCDVDIRKDLYANTVLS GGTTMYPGLADRMQKEITALAPST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *—Stop codon; /—possible nucleotide deletion; \—possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MKIKIAPPKYSVWIGGSILASLST FQQMWISKQEYDESGPSIVHRKCF |
| 3565 | 9062 | A | 3835 | 3 | 412 | SRFPEGLFQPFPGVMKSCGIHETTF HSH/IKFDVAIR\KDLYANTLLPGGN HQVSGALLTGMQKEIHAPAAQATL RFKIIAPPGSASTRW/VGSGVGSILASL STFQ\QMWISKQEYDESGPLHSSTA KCFLNGLSQIA |
| 3566 | 9063 | A | 3837 | 3 | 480 | SHITVLTNLVNGLNAPVKRHRLAN WIKSQDPPVCFIQETHLTCDTHRL KIKGWRKIYQANGK/QKKAGVAIL VSDKTDFKPTKI/KRQGHYIMVKGS MQQEEQVLRDPQRDLDSHTMIMGD FNTLLSILDRSTRQKVNKDIQELKSA LHQADLIDIYRTLH |
| 3567 | 9064 | A | 3838 | 1 | 834 | MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEIITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNLLNDYWYKQPSN KHLANKLENLEEMDKFLDTYTLPR RLNQEEVESLNRPIRSEIEAITNSLP T/KKSPGPDGFTAIFYQMLEVLAR AIRQEKEIKGIQLVKEEVKLSLFADD MIVYLENPIVSAQNLLKLIGNFSKVS GYKI/NVQKSQAFLYTNNRQTESQI M |
| 3568 | 9065 | B | 3839 | 1 | 543 | MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEIITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNLLNDYWYKQPSN KHLANKLENLEEMDKFLDTYTLPR RLNQEEVESLNRPIRSEIEAITNSLP TKK* |
| 3569 | 9066 | A | 3840 | 1 | 1470 | MEQSWVENDFDELREEGFRRSNFS EVKEESRTQPKEAKNLARRDTHRL KIKGWRKIYEENGKQKKAGVPILVS DKTDFKPTKIKRDKEGHYTMVKGSI QQEELTILNIYAPNTGAPRFIKQVLR DLQRDLDSHTIIMEDFNTPLSTLDRS TRQKVNKDIQELNSALQQVDLIDIC RMLHPKSTEYTFFSAPHHTYSKIDH RVGSKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTENRSTAYNLNLL NDYGVHNEMKSEIKMFFETNENKD TTYQNLWDTFKAVEIQTIREYYKH LYRNKLENLEEMDKFLDTYTLPRV NQEEVESLNRPIRSEIEAITNSLP KSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYDASILIPKPG KDTTKKENFRPISLMNIDAKIMNKIL ANQIQQHIKKLIHHDQVGFIPGMQV WFNIGKSINVIQHINRTKDQK\NHRH SIDAEKAF |
| 3570 | 9067 | A | 3841 | 2807 | 4148 | |
| 3571 | 9068 | A | 3842 | 2 | 1516 | WRKIYQANGK/QKKAGVAILVSDK TDFKPIKIKRDKEGHYIMVKGSIQQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | EELTILNIHAPNTEAPRFIKQVLSDL QRDLDSHTIIMGDFNTPLSTLDRSTR RKVNKDTQELNSALHQVDLIDIYRT LHPKSTEYTFLSAPHHTYSKTDHIV GSKALLSKCKRSDIITNCLSDHSAIR LELRIKKLTQNRSTTWKLNNLLND YWVHNEMKAEIKMFFQTNENKDT TYQNLWDTFKAEEVKSLNRPITGSE IVAINSLPTKRSPGPDGFTVEFYQR CRKAFDKIQRPFTLKTNLKLAIDGM YLKIIRAIYDKPTANVILNGQKLEVF PLKTGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLRKEKVKLSLFVD DMIVCLENPIISVQKLLKLISNFSKV SGYKINVQKSQAFLYINNRRQTESQI MSELPFTIASKRIKYLGIQLTRDVKG LFKENYKPLLNKIKEGTNKWKNVP CSWIGKINIMKMAILPKETPSHMQR HT |
| 3572 | 9069 | A | 3843 | 3 | 120 | FIIDKKQKQLKSPSIDEWIK\KMWYI HKIEYHSAIKGIKF |
| 3573 | 9070 | A | 3844 | 2 | 244 | SRLSFPSSWDYICAPPHLANFCIFLV ERSVAMLPRLVSSSWAQAILPPWP PKAQGFTGMGHHAQSAAGLYIFSG LGSNAI |
| 3574 | 9071 | A | 3845 | 1 | 2616 | |
| 3575 | 9072 | A | 3846 | 1 | 773 | QTSPMIPSIVVHCVNEIEQRGLTETG LYRISGCDRTVKELKEKFLRVKTP LLSKVDDIHAICSLKDFLRNLKEPL LTFRLNRAFMEAAEITDEDNSIAAM YQAVGELPQANRDTLAFLMIHLQR VAQSPHTKMDVANLAKVFGPTIVA HAVPNPDPVTMLQGHQGVQPKVV EARLLFLGLWEYWEFSFMDGWEQG GTFDPLHVIENSNAFSTPQTPDIKAV PGGGLCVHFTAGEAEIQKGPPSCGQ NKSTAAFN |
| 3576 | 9073 | A | 3847 | 1 | 422 | CGRVRACGRVREPSSQIHNNMANL FIRKMNPLLYLSRHTVKPRALSTF LFG\SIR\SAAPRGCGNPGAAVR\SL SPGLPA/HHLPACGWGFKKQDCPLR KRCKDCYLVKRRGRWYVYCKTH PRHKQKTRCRTLFPPEST |
| 3577 | 9074 | A | 3848 | 1959 | 4060 | RFFSFFFFFETESHVAQAGVQWCN LGSLQAPPPGSRHSPASASRVAGTT GAHHHARLIFVFLVETGFHRISQDG LDLLTS*SARLGIPKCWDYRCEPPH LASI |
| 3578 | 9075 | A | 3849 | 1 | 1320 | |
| 3579 | 9076 | A | 3850 | 1239 | 1733 | ALFFSFFFFFETESRSVAQAGVQW RDLGSLQAPPGPSRRSPASASRVAG TTGARHRIFFVFLVEMGFHRDLDFP TS*SA\QGLQA*ATAPGPFLFFFFFF LRRSLTLLPRLECNGAILARC�LYL LGSSNSPASASRVAGIAGMHHR LIFCILVEMGFHHL |
| 3580 | 9077 | A | 3851 | 131 | 436 | VTHLHQKKGSVFFFFFFFETESCPV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AQAGVQWRDLRSLQAPPPG\SRHSP ASASRVARTTGAHHYTRLIFVCLV ETGFHHVSQDGLDLQDQFPWSLFLF CPP |
| 3581 | 9078 | A | 3852 | 56 | 192 | KFLFSPKALNSVRKFFQYFPPPKKR/ CPSQNSQVG/CLKSPP*GEKF |
| 3582 | 9079 | A | 3853 | 1 | 230 | FQLHQHLLNPKHDYRGWAKWNR NSLYEKMKEGERRK\RRSAIPYLQG QRLDNVVAKKSVPQFFPLRVRDPG VKSSC |
| 3583 | 9080 | A | 3854 | 3 | 126 | SCCGVGNQFKGPGGGGG/RGGG/RR NVSGGGAGGRGWKNERKER |
| 3584 | 9081 | A | 3855 | 1 | 1021 | MPRLEAFVNNQTCPKKECGAASEG DTIGKQSELSFGKAKMARETHWPK KVGKLRSTVVKQLPKTFQAISSTET KDQGPIVPAPVKGEGPIVPAPVKDE GPMVSAPIKDQDPMVPEHPKDESA MATAPIKNQGSVMSEPVKNQGLSG/ PGPVKDQDVVPEH*KGHDSA\LV APW*RIKGP\VVPRSPVKNQDPILPV LVKDQGPTVLQPPKNQGRIVPEPLK NQVPIVPVPLKDQDPLVPVPAKDQE P/TLPG/PLGSETAAPVPAHSHSPPPA GSSPAPPRAPGSGRLRLPCSLAPRDLG TRDRAGTVSGALRTMRHPTGGLCQ KGPCWVPPPPLLQIQHFGPP |
| 3585 | 9082 | A | 3856 | 1 | 448 | SSRKDQGLVVSGPVKDQDVVPEH QRSRFSCQVAPVKNQGPVVPESV KNQDPILPVLVKDQGPTVLQPPKNQ GRIVPEPLKNQVPIVPVPLKDQDPL VPVPAKDQGPVPEPLKTQGP/KGT LSLPTVSPLPRVMIPTAPHTEYIESSP |
| 3586 | 9083 | A | 3857 | 1 | 573 | DPQFISGSPESPIRLWCVGLGNTKVT FTNPKNPVRAVVIHPRHYTFASGSP DNIKQWKFPDGSFIQNLSGHNAIINT LAVNFDGGLVFGAANGPMHLWDW ETWAPIFKRVHA\AVQPG\SLDSESG IFACAFDQ\SESRL\TAEADKPAKV YREDDTATEETHPVSWKPEIKRKR FLMNVEFFLSLFFSF |
| 3587 | 9084 | A | 3858 | 1 | 589 | EDLRKCTFIFIIGGPGSGKGTQCEKL VEKYGFTHLSTGELLREELASESER SKLIRDIMERGDLVPSGIVLELLKEA MVASLGDTRGFLIDGYPREVKQGE EFGRRIGDPAQLVIGKE\CSPDT\MTN RL\QRSRSSLPVDDTTK\TMAKRLE AYYR\ASIPVIAYYETKTQLHKINAE GTPEDVFLQLCTAIDSIF |
| 3588 | 9085 | A | 3859 | 1 | 557 | KLLSPKQPLLRAQLKTLVRLLCFSH AFVGLSKITTWYQYGFVQTQGPKA NILVSGNEIRQFARFMTEKLNVSHT GVPLGEEYILVFSRTQNRLILNEAEL LLALAHEFQMKT\TVTPWRTTPLTD VVRLVSNASMLVSMHGAQLVTTLF LPRGATVVELFPYAVNPDHYTPYK TLAMLPGHGTSSM |
| 3589 | 9086 | A | 3860 | 323 | 656 | NEELMPKGRLYPPLANIQEV SINIAI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KVTEYLYANKMGFPDTQEPEDKA KYVK/EKGTWAEWNMDSLLPDVY EWPEICNQAPPVNTIEALPLINTFV CSRGTPFFQTRKR |
| 3590 | 9087 | A | 3861 | 1411 | 1799 | GYLQFSFSFFLFFFFFFFLRWSLTLS PRLECSSVISTHCNLRPLGSSDSRAS ASQVAGTTGAHHARLIVCVLVER VFHHVGQAGLEVLTSGGPPTSASQS ARJTGMSHHTRPVICSFQFSDLPHEY F |
| 3591 | 9088 | A | 3862 | 1 | 1007 | MDGGHLFSNLTGKEEVIHKGAKLH PNGYRMAQGSETLVARGGPCRSVE PSAASPQELRGWWEAQALKRWGL MGGVWVMEVDPSWLGAISAIVSSS ASRLKSVWHIPCPHLLLRPOLKE AQRKKQLEERCERVEESIGNAVLT WNNILPNWETMWCSRKVRDLWW QGIPPSVRGKVWSLAIGNELNITHEL FDICLARAKERWRSLSLSTGGSEVENE GLCVAVCAQQGHVGVMMGFGSDEP SAVSPCEKGKSLAAWVLIFVDFRVG LQKSFQKRKERESTKLQQLWSWCL MLTYFAAFEVFFEENLPKLFAHFKK NNLTPDIYLID/W*FRLLVGC |
| 3592 | 9089 | A | 3863 | 1 | 1857 | |
| 3593 | 9090 | A | 3864 | 1 | 840 | GIPAADREASLELIKLDISRTFPNLCI FQQGGPYHMLHSILGAYTCYRPD VGYVQGMFIAAVLILNLDTADAFI AFSNLLNKPCQMAFFRVDHGLMLT YFAAFEVFFEENLPKLFAHFKKNNL TPDIYLIDWIFTLYSKSLPLDLACRI WDVFCRDGEEFLFRTALGILKLFED ILTKMDFIHMAQFLTRLPELPAEE LFGPSIATIQMSRNKKWAQVLTAL QKDSREMREGKSVPTLRLQREFAL GTNQSPMPRPLCCFRLTPGQPRRTD AL |
| 3594 | 9091 | A | 3865 | 3 | 288 | FFEMESLYVTRLNCSGTITISVHC NLCFPGSSDSPASASQIAGITGTRHH AQLILVFLVEMGFC/HISTKQMEVIH PPWPPKVLGLQVVTHDVL |
| 3595 | 9092 | A | 3866 | 285 | 489 | |
| 3596 | 9093 | A | 3867 | 3 | 425 | GSSDPPASAFQVAGSISVCHHTQLIF VFLVEVEFHHSQASLQL/RDLSLPS SWDYRRPPRPANFFVFLVEMGFH HLNKAIKSFACNEIQPLSAVSARA GWGVFEYVSVYFLCSNSDYFSSNPS IANWMREWPLRLSLF |
| 3597 | 9094 | A | 3868 | 1 | 156 | APHPANFAFLVEMEFHDVGQGD QLLASSDLPASASQSAGITGVSHCN WI |
| 3598 | 9095 | A | 3869 | 1 | 526 | LAESGEGVLVSGGSLRLPACIASRFIF SSYYMSGVRQAPGKGLEWVSFIRA TSVRGRFTMSRDESKNITYLQMKSL RRGMFRGDLGWDWPGGDGHWGAL RIWEPLWIFRCLWKMGLRLGASDG VTEPGGLGSHIWTRCLNKPGVLVM |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *~Stop codon; /=possible nucleotide deletion; ~possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AEECVSGAVSVGLQDRCTAANRAI FSLEL |
| 3599 | 9096 | A | 3870 | 2 | 353 | |
| 3600 | 9097 | A | 3871 | 136 | 315 | FKYVLSFLFLASGDGESLDEDESEFTL ARDFEIGHFFRERIVPRAVLYFTGE AIEDDDNV |
| 3601 | 9098 | A | 3872 | 132 | 1552 | GDKNIQMADHSFSDGVPSPDSVEAA KNASNTEKLTQVMQNPRVLAALQ ERLDNVPHTPSSYIETLPKAVKRRIN ALKQLQVRCALIEAKFYEEVHDLE RKYAALYQPLFDKRREFITGDVEPT DAESEWHSENEEEKLAGDMKSKV VVTEKAAATAEPPDPKGIPEFWFTIF RNVDMLSELVQEYDEPILKHLQDIK VKFSDPGQPMSEVLEFHFEPNDYFT NSVLTKTYKMKSEPDKADPFSFEGP EIVDCDGCTIDWKKGKNVTVKTIK KKQKHKGRTVTRITKQVPNESFFN FFNPLKGKSVASGDGESLDEDESEFT LASDFEIGHFFRERIVPRAVLYFTGE AIEDDDNFEEGEEGEEEEELEGDEEG EEDDDAEFNPVKVLIFFVLLIHTFSRR DPSQPAECKQQYEAEGA WQTGCR DSRPVGGASVLAQAQSRGQSLHL TRFQVHDFHFHFSFFLIILINLYSGN |
| 3602 | 9099 | A | 3873 | 171 | 324 | |
| 3603 | 9100 | A | 3874 | 3 | 383 | |
| 3604 | 9101 | A | 3875 | 2 | 314 | FFFFISALKALFAFLQILLFQVNVLR TAHIVISFINLLSVTPSKAFLLLAFIF CREDYSFTAYATISYLKIGPKANLL NNEAYVITMQVTKSTQNSFRVNG Y |
| 3605 | 9102 | A | 3876 | 3 | 319 | TESRSVPQLGVQWRDLGSLQPPPPG FTRFSCSLPSSWDYRHTPPRPANFL VFLVETGFRHVGQTGLELLTSGDPP ASASQSAGILCVLCTSTLGNHREHI YRMV |
| 3606 | 9103 | A | 3877 | 118 | 1341 | |
| 3607 | 9104 | A | 3878 | 1 | 214 | GFTSSLACMQMGEMFMGFTCQTH LLALGCALFTAYLGVGMANFMAE GTCERRIVGKKKASITKDHQORRI |
| 3608 | 9105 | A | 3879 | 1 | 176 | MRTFALLTAMLLLVA/HAQAEPLQ ARADEAAAQEQPGADDQEMAHAF TWHESAALPLSA |
| 3609 | 9106 | A | 3880 | 3 | 125 | AASTFLFPNLKNSLRG\SLRTFSSVT NVRKTALTWLNSQDI |
| 3610 | 9107 | A | 3881 | 1169 | 1512 | YTQKNWHLFCFIFLRWSFVLVAQP GVQWCNLSSLQPLPPRFR*FSCLSL SSWDYRCAPPRPANF/SVFLVETGF HHVGQADLELLTSGDLPTSASQSAG ITGVSHCTWPDILYEI |
| 3611 | 9108 | A | 3882 | 43 | 347 | AGVQ*CDLG*LQLLPLGFK*FSCLSL PSSWDYRRLPPRPANF*FLVETGFH HVGQADLELLTSGDSPASASQSAGI TGMSHRAGPI*KSFLKYSTNKLRTT |
| 3612 | 9109 | A | 3883 | 10900 | 11295 | KPWVNETGKLFQDSYSSHHLSGF SFPSFFSETESCSVTQAGVQWHDLS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SLKPLPPGFKQFSCSLPSSWDYRR VPTRPANF/SVFLLETEFHRVSQDGL DRLT/S/GDPPSSASQSAGITGVSHRA RPHSPHF |
| 3613 | 9110 | A | 3884 | 3 | 227 | RFSCSLSSSWDYRAPPPRLANFCI LVETGFHHAGQTGLELLTSGDPPAS ASEIAGITGMSHHTQPGQLLWECC |
| 3614 | 9111 | A | 3885 | 2 | 296 | KWSSALVAYAGVTWHHLGSLRSP PGFKRFCCLSLPSSWDYRHAPPPA/ NFFVFLVKTGFLHVGQAGLELPISG DPPALAPKQSAWIRGVSHRAQPQN |
| 3615 | 9112 | A | 3886 | 1 | 162 | LGGLVFPSEVVCK/RKLDGMQLIKV HLDKAQQNNVENKAETFSGVCKK HRDLMA |
| 3616 | 9113 | A | 3887 | 2 | 474 | |
| 3617 | 9114 | A | 3888 | 2 | 592 | STGKFSQEKAMFSSSAKIVKPNGEK PDEFESGISQALLEMNSDLKAQL RELNITAAKEIEVGGGRKAIIFVPVP QLKSFQKIQVRLVRELEKKFQWES MSVFIAQRRILPKPTRKSRTKNKQ KRPRSRTLTAVHDAILEDLVFPSEIV GKRIRVKLDGSRLIKVHLDKAQQN NVEHKVETFSGVYKKHRDLMA |
| 3618 | 9115 | A | 3889 | 1 | 93 | GFTMLP/RLVLNSWVQMICLPWPPK MLSLQA |
| 3619 | 9116 | A | 3890 | 1 | 252 | PTLEQYAMRAFADALEVIPMALSE NSGMNPIQTMTEVRAR/QDMKQQH VIETLIGKKQQISLATQMVRMILKID DIRKPGEESE |
| 3620 | 9117 | B | 3891 | 18 | 1121 | MASMGTLAFDEYGRPFLIKDQDRK SRLMGLEALKSHIMAAKAVANTMR TSLGPNGLDKMMVDKDGDTVTVN DGATILSMMDVDHQA KLMVELSK SQDDEIGDGTGTVVVLGALLEEA EQLLDRGIHPRIADGYEQAAARVAIE HLDKISDSVLVDIKDTEPLIQTAKTT LGSKVVNSCHRQMAEIAVNAVLT ADMERRDVDFELIKVEGKVGGRL DTKLIKGVIVDKDFSHPMPPKKVED AKIAILTCPFEPKPKTKHKLDVTSV EDYKALQKYEEKFEEMIQQIKETG ANLAICQWGFDDDEANHLLQNNLP AVRWVGGPEIELIAIATGGRIVPRFS ELTAEKLGFAGLDKRISFGDT* |
| 3621 | 9118 | A | 3892 | 1 | 282 | LPSSHTIPGYPNPLHPRFPSSRLPP GIIGGEYDQRPTLPYVGDPISLIPGP GETPSQFPPLRPRFDPV/GPNDRFPF RPSRGRPTDGRLSFM |
| 3622 | 9119 | A | 3893 | 3 | 166 | PRPFPKSRLPPGIIGGEYD\QRPNPILP \GRGGPNDRFPF\RPSRGRPTDGRLS FM |
| 3623 | 9120 | A | 3894 | 101 | 1926 | SPVRGRRRLGRELLGPAAPVPAAS GSRPLGPPAAVMRLRVLLKRTWP LEVPEPTEPTLGHLRSHLRQSLCTW GYSSNTRFTITLNYKDPLTGDEETL ASYGIVSGDLICLILQDDIPAPNIPSS TDSEHSSLQNNEQPSLATSSNQTSM |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QDEQPSDSFQGQAAQSGVWNDDS MLGPSQNFESAESIQDNAHMAEGTG FYPSEPMLCSESVEGQVPHSLETLY QSADCS DANDALIVLIHLLMLESY IPQGTEAKALSMPEKWKLSGVYKL QYMHPLCEGSSATLTCVPLGNLIV NATLKINNEIRSVKRLQLLPESFICK EKLGENVANIYKDLQKLSRLFKDQ LVYPLLAFTTRQALNLPDVFGLVLP LELKLRIFRLLDVRSVLSLSAVCRDL FTASNDPLLWRFLYLRFDRDNTVR G\QD TDWKEL YRKRHIQRKESPKGR FVMLLPSSHTIPFYFNPPLHPR\FP SSRL\PPGNGGEYDPKTNTFPMLGD PISSLIPWVLGETPQPSFPPTETHALN PSWPPISRDPNPQSCPGAEGGPPN/R TRFPPLRPQPGGRANLMAGLVISCG LDLLIFISWSLPPFVFCFLNYRCQRPW GADLRVLFS |
| 3624 | 9121 | A | 3895 | 2 | 442 | LSQLCGDPQRFDDFLRAYVEKYKF TSVVAQDLLDSFLSFFPELKEQSVD CRAGPPLAEPDLSQGSSLTRPVEAL FQL/WTAEPDQAAASASAIKSKW RTFQTALFLDRLLDGSPLPQEVVMS LSKCYSSLLDSMNAEIRIRWLQIV |
| 3625 | 9122 | A | 3896 | 1 | 1035 | GEFLVIDVIHEVAHSWFGNAV TNAT WEEMWLSEGLATYAQRRTTETYG AAFTCLETAFRLDALHRQMKLLGE DSPVSKLQVKLEPGVNPSHLRNLF YEKGYCFVYYLSQLCGDPQRFDDF LRAVYGEYKFTSVVAQDLLDSFLS FFPELKEQSVD CRAGLEFERWLNAT GPPLAEPDLSQGSSLTRPVEALFQL WTAEPDQAAASASAIKSKWRFTQ TALFLDRLLDGSPLPQEVVMSLSK CYSSLLDSMNAEIRIRWLQIVVRND YYSLT/FHRVRRFPGRARCHACYTIP LYEDLCTGALKSFALEV FYQTQGR HPNLRRAIQILSQGLGFQHRARP |
| 3626 | 9123 | A | 3897 | 2 | 912 | CSRSSRTGGWWPAPCSAASRRPTPG PAAAAAATTD/VVTAGCGFGKDFR KGLLKKGACYGDDACFVARHRSA DVLGVADGVGGWRDYGVDPQSQS GTLMRTCERLVKEGRFVPSNPIGILT TSYCELLQNKVPLLGSSTACIVLD RTSHRLHTANLGDSGFLVVRGGEV VHRSDEQQHYFNTFPQLSIAPPEAE GVVLSDSPDAADSTSFQVQLGDIILT ATDGLFDNMPDYMLQELKKLKNS NYESIQQTARSIAEQAHELAYDPNY MSPFAQFACDNLNVRGGKPDIT VLLSIVA EYTD |
| 3627 | 9124 | A | 3898 | 2 | 220 | YMSKKFSALLQSQERNCLIINWCSS LCLRVRLYLRQVTVIPRICKVSDSP CAPEADAMFAFNADGVGDAKG |
| 3628 | 9125 | A | 3899 | 1 | 346 | SANATTKTSETNHTSRPRLKNVDRS TAQQLAVTVGNVTVIITDFK\EKTRS SS\TSSSTVTS\SAGS\EQQN\QSSSGV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QRAPDKGLPPRSLPTPKGDMSAVN DEIFPEIATWNCEKL |
| 3629 | 9126 | A | 3900 | 76 | 368 | |
| 3630 | 9127 | A | 3901 | 1 | 1182 | MFAKGRGSAVPSDGQAWKELASY VYEYLLHVRVQKSAETFLSEIRWEK NITLGEPPGFLHSWWCVFGDLYCA APQRRDTCEHSSEAKAFHDYSAAA APSPVLGNIPPNDGMPGGPIPPGFFQ GPPGSQSPHAQPPPHNPSSMMGPH SQPFMSPRYAGGPRPPIRMGNQPPG GVPG\TQPLL\NSMDPTRQQGHP\N MGGSMQRMNPSRPLGPMGPRPHR ITGSGMRPPPNSLGPA\MP\GINMGP GAGRPWPNPNSANSIPYSSSSPGTY VGPPGGGGPPGTPIMPSPADSTNSS DN\YTMI\NPV\PPGGSRSNFQMGP STGPMDSMGGMEPHHMIG\SLGSG DIDGLPKIFPNNISGISNPPGTPRDDG ELGGNFLHSFQNDNYSPSMTMSV |
| 3631 | 9128 | A | 3902 | 2 | 470 | IPTFGLPGSIQSDNGP\SFISQITQQVS QSLGIQWRLHIPCWPTSGKVERAN GILKAQLTKLTLEVQKPWDLALLPH RHWESIRRP/GPKGTLLSFSSIWSLIY GTPFPLT\NRPPSNSQLGGIPSQQSSL MEVIFLWPTRPTRAFPKPHGGGLPIP K |
| 3632 | 9129 | A | 3903 | 69 | 523 | PLGCASSQSIASRNTLCTTASSCCP QVLAHSKAAEYMTRWKVQQMPH SQDRALQSVFCAPFHS**LVALPTG HR*MTPAQFSECFQATSGGSD*DPF LAPSFL\VPGLPVAPGLLLPLGPVHS RATMEEGQATHEELTVFIGLRPGVR GS |
| 3633 | 9130 | A | 3904 | 101 | 1469 | RTHPTFPHPGTGPTSAPPSGALEGTA GTITSNEWSSPTSPEGSTASGGSQAL DKPIDNDGEGVWSPDIEQSFQEALA IYPPCGRRKIILSDEGKMYGRNELIA RYIKLRTGKTRTRKQVSSHQVLAR RKAREIQAKLKDQAAKDKALQSM AAMSSAQIISATAFHSSMRLARGPG RPAVSGFWQGALPGQAETSHDVKP FSQQTYAVQPPLPLPGFESPAGPAPS PSAPPAPPWQGR\SVASSKLWMLEF SAFLEQQQDPDTYNKHLFVHIGQSS PSYLRPYLEAVDIRQTYDKFPEKKG GLKDLFERGPSNAFFLVKFWADLN TNIEDEGSSFYGVSSQYESPENMIT CSTKVCSFGKQVVEKVETERYE NGHYSYRIHRSPLCEYMINFIHKLK HLPEKYMMSVLENFTILQVVTNR DTQETLLCIAVFEVSASEHGAQHH IYRLVKE |
| 3634 | 9131 | A | 3905 | 1 | 1290 | |
| 3635 | 9132 | A | 3906 | 2 | 270 | ISLADLKEGPHTHLKPPDYSVAVQR SKMMHNSLSRLPPASLSSNLVACVP SKIYVTPQRHNLQPFHPKLGDVTD DSEED\ENEQVSAV |
| 3636 | 9133 | A | 3907 | 2 | 288 | RWGLALSLR/AGAQWFHHGSLQPQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PPMLKSSSRSLPSSRNHRHTQPCPA NFFIFVEMGFHHVAQAGLELLSS\LT VWASQSAGITGVSHRTHPLLS |
| 3637 | 9134 | A | 3908 | 3 | 222 | FFFETESRSVT\RLCSGTISAHCKLH LPGSCHSPASASRVAGTTGAHCHTQ RIFVEMGFHRVSQDGLDLKNL |
| 3638 | 9135 | A | 3909 | 3 | 175 | GTSPKDCVDRDFCPSEGLYST*WGG SILPSLDT/FKKMWVSKKKYEEDGA RSIHRKTF |
| 3639 | 9136 | A | 3910 | 2 | 533 | RAAEFFFETFNVPALFISMRAVLSLY ATGRTTGVLDSGDGVTHAVPIYE GFAMPHSIMCIDIADRDVSRFLRL YLRK\EGYDFHSS\SEFEIVKAIKERA CYLSINP\QKDETELEKAQYYLPD GSTIEISAPQERLYSTWIGGSILASLD TFKKMWVSKKEYEEDGARSIRKTF F |
| 3640 | 9137 | A | 3911 | 1 | 1213 | EFGALRRTRLGSSFPRRRDSSAMES YDVIANQPVIDNGSGVIKAGFAGD QIPKYCFPNYVGRPKHVRVMAGAL EGDIFIGPKAEHRGLLSIRYPMEHG IVKDWNDMERIWQYVYSKD\QLQT FSEEHPVLLTEAPLNPRKNRERAAE VFFETFNVPALFISMQAVLSLYATG R\TTGVVLDSGDGVTHAVPIYEGFA MPHSIMRIDIAGRDVSRFLRLYLRK EGYDFHSSSE\FEIVKAIKERACYLF HKTPKRD\ETLETEKASVTTWLDGS TIEIGPFR\FRAP\ELLFGPRI*LEKESE GINHEVPGVRPFRKSDMGPAGARLF SNIVL/SQGGSTPVQKFSSLPISGFGD RLLC*VKKLAAPKDVKIRISAPQERH VYPRGLGGSILASLD\TFKKMWVLQ KGDMR*DGSTIEIGPFRIPGPLSCSSG PEFDWKRKVKASHEVPGVRPFRKS DMGPAGARLFSNIVLFREALPLFKS SPLCPFQVLVTGSFVIVKKLSSKRCE DQDICTSGETCISTWIGGLHPCLPGH HLRRCGCSKKEI |
| 3641 | 9138 | A | 3912 | 2 | 262 | LEKRSHSVTKLGYSGVIIAHCSLNF LSSSQPPTSASQTAGTTGICHSTQLIF KIFLVEMG/LHYVAQAGLDLLGSSN VEPPKVLLGL |
| 3642 | 9139 | A | 3913 | 1379 | 2175 | TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGGCVAHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN |
| 3643 | 9140 | A | 3914 | 1 | 387 | TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGLLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MLQLSPEEKGKLAAVAQGLQETSIP KKK |
| 3644 | 9141 | A | 3915 | 360 | 885 | NVFLLEANQRTSTVTLATVSASGQ MPSTFGGLDSSIQKLIAlAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSFQTLF |
| 3645 | 9142 | A | 3916 | 1669 | 4914 | |
| 3646 | 9143 | A | 3917 | 1379 | 2175 | TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGCVAPHHSW PWQVSLRTRSPRPSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLSPNYVVA DRTECFITGWGETQEHFYFN |
| 3647 | 9144 | A | 3918 | 1 | 387 | TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGLLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK |
| 3648 | 9145 | A | 3919 | 360 | 885 | NVFLLEANQRTSTVTLATVSASGQ MPSTFGGLDSSIQKLIAlAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSFQTLF |
| 3649 | 9146 | A | 3920 | 1669 | 4914 | |
| 3650 | 9147 | A | 3921 | 1 | 246 | FLETEFHSVAQAGVQWCHLGSLOP PPPGFKQLS\CLSLPSSWDYRGTPPY LANFCIFSRDGVSLCWPGWSQTPDL KQSSGNL |
| 3651 | 9148 | A | 3922 | 10 | 476 | DRVLLSVAQAGLQWRDLGSLQPPP P/GFKRFSCLSLPNSWDYRCVPPCLA NFFVFLVETGFHHVQGAGLELLTSG DPPLPQPPKVLGAGITGMSHHTWLI SLIFYQTKWRQTAIASVGIPGSPLCH PLPLIRKGVAGKAVLCPRKDGHTH KTQLRP |
| 3652 | 9149 | A | 3923 | 2 | 465 | ARARADSARAARAEFEDIMKRNRA ISSSPISKAVSGASAGDYSDAIETLLT AlAVIKQSRVAK\DERCRVLISLKD CLHG\IEGQVPTVWGAQLGALSRRK HPFPGERSP\SRSRERSRRHRDLLHN EDR\HDDYFQERNREHERHRDRER DRHH |
| 3653 | 9150 | A | 3924 | 3 | 218 | LPPPLSNIHSTLSTPFLPPPAPL/SP/YP SRASPPSTYSPLPTPPPLPTSQPSTPT LPLPTPPCSTPSGQALFF |
| 3654 | 9151 | A | 3925 | 1379 | 2175 | TTAGIQMPIKAPGVLPQTPASGGST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWCY TTNPRKLYDYCDVPQCAAPSFCG KPQVEPKKCPGRVVGGCVAHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN |
| 3655 | 9152 | A | 3926 | 1 | 387 | TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGLLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK |
| 3656 | 9153 | A | 3927 | 360 | 885 | NV FV LLEANQRTSTVTLATVSASGQ MPSTFGGLDSSIQKLI AIAHFILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQEQRHFYFLNM RF/DDSLLGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRSAFQTLF |
| 3657 | 9154 | A | 3928 | 1669 | 4914 | |
| 3658 | 9155 | A | 3929 | 1 | 1542 | |
| 3659 | 9156 | A | 3930 | 3 | 1771 | |
| 3660 | 9157 | A | 3931 | 2 | 1869 | RLVVVEAKMAAQAAAAA QAAAA QAAQAEAAADSWYLALLGFAEHFRT SSPPKIRLCVHCLQAVFPFKPPQRIE ARTHLQLGSLVLYHHTKNSEQARSH LEKAWLISQQIPQFEDVKFEAASLLS ELYCQENSVDAAKPLLKAIQISQQ TPYWHCRLLFQLAQLHTLEKDLVS ACDLLGVGA EYARVVGSEYTRALF LLSKGMLLLMERKLQEVHPLLTL C GOIVENWQGNPIQKESLRVFFLV LQ VTHYLDAGQVKS VKPCLKQLQQCI QTISTLHDDEILPSNPADLFHWLPKE HMCVLVYLVTVMHSMQAGYLEKA QKYTDKALMQLEKLKMLDCSPILS SFQVILHEHIMCRLVTGHKATALQE ISQVCQLCQQSPRLFSNHAAQLHTL LGLYCVSVN CMDNAEAQFTTALRL TNHQELWAFITVNLASVYIREGNRH QEVVLYSLLERINPDHSFPVSSHCL RAAAFYVRGLFSFFQGRYNEAKRF LRETLKMSNAEDLNRLTACSLVLL GHIFYVLGNHRESNNMGGPAMQL ASKIPDMSVQLWSSALLRDLNKAC GNAMDAHEAAQMHQNFSSQQLLQD HIEACSLPEHNLITWTDGPPP VQFQ AQNGPNTSLASLL |
| 3661 | 9158 | A | 3932 | 2 | 614 | |
| 3662 | 9159 | A | 3933 | 1 | 4992 | VSSNNVLLNSQADDRVVINKPESAG FRDVGSEEIQDAENSAKTLKEIRTL MEAENMALKRCNFPAPLARFRDIS DISFIQSKKVVC FKEPSSTGVSNGDL LHRQPFTESPSSRCIQKDGTQTNL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KCRRG IENW EFISSTTVRSPLQEAE KVSMAL EETLRQYQAAKSVMRSEP EGCSGTIGNKIIIPMMTVIKSDSSSD ASDGNGSCSWDSNLPESLESVSDVL LNFFPYVSPKTSITDSREEEGVSESE DGGGSSVDSLAAHVKNLLQCESSL NHAKEILRNAEEEEESRVRAHAWNM KFNLAHDCGYISSELNEDDRRKVEE IKAELFGHGRTTDL SKGLQSPRGMG CKPEAVCSHIIIESHEKGCFTLTSE HPQLDRHPCAFRSAGPSEMTRGRQ NPSSCRAKHVNLSASLDQNNSHFK VWNSLQLKSHSPFQNFIPDEFKISKG LRMPFDEKMDPWLSSELVEPAFVPP KEVDFHSSSQMPSPPEPMKKFTTSITF SSHRHSKCISNSSVVKVGVTEGSQC TGASVGVFN SHFTEEQNPPRDLKQK TSSPSSF KMHSNSQDKEVTILAEGR RQSQKLPVDFERSFQEEKPLERSDF TGS HSEPSTRANCSNFKEIQISDNHT LISMG RPSSTLG VNRSSSRLGVKEK NVTITPDL PSCIFLEQRELFEQSKAP RADDHV RKHHSPSPQH QDYVAPDL PSCIFLEQRELFEQCKAPYVDHQMR ENHSPLPQGQDSIASDLPSPISLEQC QSKAPGVDDQMKNKHHFPLPQGQD CVVEKNNQHKPKSHISNINVEAKFN TVVSQSAPNHCTLAASASTPPSNRK ALSCVHITLCPKTSSKLD SGTLDERF HSLDAASKARMNSEFNFDLHTVSS RSLEPTSKLLTSKPVAQDQESLGFL GPKSSLD FQVVQPSLPDSNTTITQDL KTIPSQNSQIVTSRQIQVNISDFEGHS NPEGTPVFADRLPEKMKTPLSAFSE KLSSDAVTQITTESPEKTLFSSEIFIN AEDRGHEIIEPGNQKLRKAPVKFAS SSSVQQVTFSRGTDGQPLLLPYKPS GSTKMYYPQLRQIPSPDSKSDTT VESSHSGSNDALAPDFPAQVLGTRD DDLSATVNIKHKEGIYSKRVTKAS LPVGEKPLQENADASVQVLITGDE NLSDKKQQEIHSTRAVTEAAQAKE KESLQKDTADSSAAAAAEHSAQVG DPEMKNLPDTKAITQKEEIHRRKKT PEEAWPNNKESLQINIEESECHSEFE NTTRS VFRSAKFYIHPVHLPSDQDI CHESLGKSVFMRHSWKDFFQHHPD KHREHMCLPLPYQNMDKTKTDYT RIKSL SINVLGNKEVMDTTKSQVR DYPKHNGQISDPQRDQKVTP EQTT QHTVSLNELWNKYRERQRQROPE LGDRKELSLVDRLDRLAKILQNPIT HSLQVSESTHDDSRGERSVKEWSG RQQQRNKLQKKKRFKSLEKSHKNT GELKKS KVLSHHRAGRSNQIKIEQI KFDKYILSKQPGFNYISNTSSDCRPS EESELLTDTT NILSGTTSTVESDILT QTDREVALHERSSSVSTIDTARLIQA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FGHERVCLSPRRIKLYSSITNQQR\RYLEKRSKH\SKESAGLTGHPLVTSEHTRRRHIQPPTSATACRQPLMTFCFYGFAYSGPFI |
| 3663 | 9160 | A | 3938 | 2 | 354 | NRILVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIFPEKPLALSGKSFLQLEALLPPRQKVRITDDMDQVELKEFCPNEQNWRQHREAYEEDEDGPQAGVQFQTA |
| 3664 | 9161 | A | 3939 | 204 | 374 | DHGFLIPLTQGDQKGPPRVHPL*ACYHWNQREKVISSCIGCICMSQIKDPLVKKKKK |
| 3665 | 9162 | A | 3940 | 39 | 385 | AGVQWRDLSSPQPPPPGFKRVSCSLPSSWDYRPPQRLANFC/DFLVEMGFCHVDQ\AGLELLTSGDPPASASQSAGITGVSHRTQPCLLFLKTKTWGKWEKDGMFWEMNGAQDQQE |
| 3666 | 9163 | A | 3941 | 1 | 200 | FETGSYSVT\RLVFSVQISAHCNLCLPGSPDPPTSASEVVGTSVCHR\TQLI VIYPLQLPKLFRLQV |
| 3667 | 9164 | A | 3942 | 2 | 458 | LFYGVYFLFPLNSCILFVSFTVNHQLIFFFGGGMKSWSVRRLECSGVILAH CNLRLPGSSDSPASASRVAGTTGTC HRARLIFVFLVEMG\FHHVG/RRDGLGSPDLVIHPPR\TPKGVGGGLQGVSHCGPGPSPQGFYLIKELGSSQGGEQFP |
| 3668 | 9165 | A | 3943 | 1 | 2499 | |
| 3669 | 9166 | A | 3944 | 855 | 2479 | PGGSGPGFPTLEGSSKAGRELIGYEPGSSGVGAPLTPHKMKKRKELNALIGLAGDSRRKKPKKGPSSHRLLRTEPPDSDSESSSEEEFEFGVVGNRSRFAKGDYLRCCCKICYPLCGFVILAACVVACVGLVWMQVALKEDLDALKEKFRTMESNQKSSFQEIPKLNEELLSKKQLEKIESGEMGLNKVWINITEMNKQISLLTSAVNHLKANVKSADLISLPTTVEGLQKSVASIGNTLNSVHLAVEALQKTVDEHKKTMELLQSDMNQHFLKETPGSNQIIPSPSATSELDNKTHSENKQDILYLHNSLEEVNSALVGYQRQNDLKLEGMNETVSNLTQRVNLIESDVVAMSKVEKKANLSFSM MGDRSATLKRQSLDQVTNRTDTVKIQSIQKEDSSNSQVSKLRE*LQLISALTNKPESNRPPETADEEQVESCTSKPSALPKFSQFLGDPVEKGCPKLRTYSP*QGVSKH*KIFQDLFR\KTGQDV\DGKLT\YQEIWTSLG\SAMPEPESLRAF D\SDGDGRYSFLELRVALGI |
| 3670 | 9167 | A | 3945 | 336 | 519 | AALPCEPAFSPLQEVQRGLQDRGQNQTQRPFFL\NVVQA\VSQEG\ACV\YAVSELRK EWGRPQ |
| 3671 | 9168 | A | 3946 | 252 | 2104 | LCASSCFPICPIRPSVCPPAAPLLGCRAMARGYGATVSLVLLGLGLALAVIVLAVVLSRHQAPCGPQAFAHAAVAADSKVCSDIGRAILQQQGSPVDA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TIAALVCTSVVNPQSMGLGGGVIFT IYNVTTGKVEVINARETVPAHAPS LLDQCAQALPLGTGAQWIGVPGEL RGYAEAHRRHGRLPWAQLFOPTIA LLRGGHVVAPVLSRFLHNSILRPSL QASTLRQLFFNGTEPLRPQDPLPWP ALATTLETVATEGVEVFYTGRLGQ MLVEDIAKEGSQTLQDLAKFQPEV VDALEVPLGDYTLSPPPAGGAIL SFILNVLRGFNFSTESMARPEGRVN VYHHLVETLKFARGQRWRLGDPRS HPKLQNASRDLLGETLAQLIRQQID GRGDHQLSHYSLAEAWGHGTGTSH VSVLGEDGSAVAATSTINTPFGAMV YSPRTGIILNNEILLDCERCPWGSCT TPSPVSGDRVGGAPGRCWPPVPGE RSPSSMVPSILINKAQGSKLVIGGAG GELIISAVAQAIMSKLWLGFDLRAA IAAPILHVNSKGCVEYEPNFSQEVQ RGLQDRGQNQTQRPFFLNVVQAVS QEGVACVYA\VSDLARKSGEAARS |
| 3672 | 9169 | A | 3947 | 2 | 97 | GLGRWLT/PVIPTLWEAKKGRSPEV RSSRPVKS |
| 3673 | 9170 | A | 3948 | 3 | 308 | PEDSDEKSLSSSVVHVRRPSRRVP RMPRGSRSRTSRMAPPASRAPQMR AAPRPAPVAQPPAQPCLYEIKQFLEC AQNQGDIKLCEGFNEVLKQCRLAN GLA |
| 3674 | 9171 | C | 3949 | 38 | 154 | MXSNSFWSPRTRVTSSSVRVSMR CCYDFILCELIRIKS* |
| 3675 | 9172 | A | 3950 | 1 | 192 | GSNAEP/ARPDLY/QEP/QGTQPAQ QQQPCLYEIKQFLECAQNQGDIKLC VGFNEVLKQCRLANGLA |
| 3676 | 9173 | A | 3951 | 1 | 254 | LMARMQTLKLAVLWASAIGHTWV HAFTGAFSGGSNAEPARP/DITYRSL YEIKQFLECAQNQGDIKLCEGFNEV LKQCRLANGLA |
| 3677 | 9174 | A | 3952 | 1 | 142 | |
| 3678 | 9175 | A | 3953 | 1 | 325 | FFFEMESCSVAHAGVRWA/DLSSLQ SPFPGFKRFSCLLGLSSWDYRRLPP HPANFYFLVDTGFHHVGQAGLELL T/S/GDPPASASQSAGITGTSHRAPT VNTFNRPPAS |
| 3679 | 9176 | A | 3954 | 3 | 304 | HEGREKRRVLGAEAGGGRSCEIGV PLEWWRPLMRVRVRMCC\MLML RWGASFAWYCCFLSFCNWL\SSDT TGLMITFMLRISALLMRS\QNPEAM TLPW |
| 3680 | 9177 | A | 3955 | 3 | 961 | LLLNSRPRRRDRLVTLESWANDPD YLKRQVGFCQWSLDNLFLKEGRQ LTYEKNLSSIRAMLNSNDVSEYK ISPHGLEARCDASSFESVCC\SFCVD AGVWDYEVTVVTSGVMQIGWATR DSTFLNHEGYGIGDDEYSCAYDGC RQLIWYNARSKPHIHPCWKEGDTV GFLDLNEKQMIFFLNG/TPA/RPPEE QVFSSTVSGFFAAASFMSYQQCEFN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FGA\SPFKYPPSMKFSTFNDYAFLTA EEKIIL\PRHRLALLKQVSIRETAGS LCCDEVADTQLKPCGHS DLCMDCA LQLETCPLCRKEIVSRIRQISHIS |
| 3681 | 9178 | A | 3956 | 4 | 101 | RQSLAMLSRLA\LSWPQVILLPWP PKVLGLQA |
| 3682 | 9179 | A | 3957 | 21 | 338 | HPVLAITLSIFIFVAFAYAEELDEIQ P/CIMMKTLNKLGIEMCLNSIKAIY /DKSNANFILNKEKLKAFFLRSGTRQ IRPNFQ/PLLFNIVLEVLAKEIRQEEEI KV |
| 3683 | 9180 | A | 3958 | 90 | 360 | ALICLV DIESGENSTTRPRFASHDQV CIALLRTA\GILCLET FIDSPSHGSRH FLFVLSSPPLTLFPLLHIYLLAVVPI VSPLLSLSDPP |
| 3684 | 9181 | A | 3959 | 1 | 424 | CGRRFSTRSDLT\KHRRTD TG\EKPN\ RCELCGKRFTCVSNLNVHRRNHAG HKPHKCPECSKAFSVASKLALHRKT HLGERPAECARVGQVLQPQPAPLS QHQRGPHAPPAPLPPLPSSPAVGHC PQSFEGGRLEQEKA KGS L |
| 3685 | 9182 | A | 3960 | 153 | 328 | SIASYFTLVCHLLRKCHPRLGTVAH TYPSTLGGGRGRWIMR\QEFETSLT NMVKPCRY |
| 3686 | 9183 | A | 3961 | 1 | 936 | |
| 3687 | 9184 | A | 3962 | 1 | 1023 | |
| 3688 | 9185 | A | 3963 | 15 | 337 | RINNTISWLIYVCKFCLSSFSIYLIIIII IIFFETESHVAQAGVQWRNLGSLQ PPPPRFKRFSCLSFPSSWDYRCPPPR PANFCIF\SRDGVSPCWPGWFRT PDL R |
| 3689 | 9186 | A | 3964 | 3 | 1105 | HASALTPVVCMLSAIAFSNVFEHYL GDDMKRENPPVEDSSDEDDKRNQG NLYDKAGKVRKHATEQEKTEEGLG PNIKSIVTMLMLMLLMMFAVHCTW VTSNAYSSPSVVLASYNHDGTRNIL DDFREAYFWLRQNTDEHARVMSW WDYGYHIAGMANRTTLVDNNTWA NNSHIALVGKAMSSNETAAYKIMR TLDVDYVLVIFGGVIGYSGDDINKF LWMVRIAEGEHPKDIRESDYFT PQG EFRVDKAGFPTLLNCLMYKMSYYR FGEMQLDFRTPPGFDRTRNAEIGNK DIKFKHLEEAFTSEHWLVRIYKVKA PDNRETLDHKPRVTNIFPKQKYL SK KTTKRKRGYIKNKL VFKKGKKISK KTV |
| 3690 | 9187 | A | 3965 | 1 | 181 | ANVVFTQLLIWYGVDVRSRDARGL TALAYARRAGSQECADILIQHG\CS AEGCGLSSTCY |
| 3691 | 9188 | A | 3966 | 640 | 961 | DGVSASCCPGLGVQWVRFLGSL\QP SASWGFKQFSCLSLPSSWDYRRALP PPRPANF/SVFLVKMGFLHVG\QAG LELLTSGHPAASASQSAGITGVSHR TRPAASIL I |
| 3692 | 9189 | A | 3967 | 2 | 334 | VGLYGRIEASSPMGEGNRW*SGTPA NQG*QEQGIARPKPRGEPGLRNEGG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PGAILPGRWAGV*GPTGQEGR*RG QESCPCPAQSSCSHRVAGLDVGGSH GHSAAFPATP |
| 3693 | 9190 | A | 3968 | 1 | 361 | ARARLRHLRDLRAPAGPVGGLCAA GTACGWPGPGPLLGERVRAFLRR* RAQHLLHHHRVRAPLPGWREAAG GAPPFLGTYPESQVRLRDAVVPEA GGQDSGSSGSASLRPRSSFSCSCS |
| 3694 | 9191 | C | 3969 | 151 | 373 | MPTAVXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXVLPFLV LEV MQCLCPVLLLYYDPNSKTRYV FFKTR* |
| 3695 | 9192 | A | 3970 | 50 | 441 | IPSPPDGFFSNLGTRKPFPCNFSCQ NILLTRKILLKSFLYPFFFLRWSLA LPPAVLSAHCNLCPPGSSDSLASAS* VAGITGVHHQAWPVLPLVLEVMQ CLCPVLLLYYDPNSTPRYVFFKTRT FIA |
| 3696 | 9193 | A | 3971 | 3 | 224 | FLRWSLALPPAVLSAHCNLCPPGSS DSLASAS*VAGITGVHHQAWPVLPL LVLEVMQCLCPVLLLYYDPNSFV |
| 3697 | 9194 | A | 3972 | 1 | 214 | PIQFKQRLPFGFLVFVF*EGVLLCH PGWTAVTEDRSWLTATSTSWAQVI LQSSCLSLPGS*DYRQCLPGV |
| 3698 | 9195 | A | 3973 | 154 | 341 | KNFFRGQFWFVA*AGVQWGHFRSL QPQPSGVKQFFPLGLPKPLDCRCES HRVPFLFLGLETL |
| 3699 | 9196 | A | 3974 | 3 | 379 | FALVAQAGVQWCSFDSLQPPPPGF K*FSCLSLPSSWNYRHLPPRLANFV FLVEMGFHYVGQASLELLTSGDPPA SASQSAGIRGLSHCTWPHVSGFIMQ YEYTLCFMVFIMSFWRNCRKVAKY LK |
| 3700 | 9197 | A | 3975 | 2 | 35 | LKQAPCLCLPSS*DYRHLPPCLSNF* NFL*R*GLSLLPRLVSNS*PQAICPRR PPKVLRL*AQTSPLPLPTK |
| 3701 | 9198 | A | 3976 | 1958 | 2316 | IHSSPTKATFFLRQSLALSPRLEYSG AISAHCNLCFPGSSDSRALAS*AAG TTGACHHIRLIFFLVFLVETGFHH VGQAGLELLVSSDLPLVSLSARITG VSHHAQPPPKLLNALL |
| 3702 | 9199 | A | 3977 | 2 | 80 | SLCICMCVCACIRTHA*MYVCVCV HTHACMNATSPSWVF |
| 3703 | 9200 | A | 3978 | 123 | 452 | KTGSNFAPQLEAQGGNLG*LNPWP PG*KQFSGLTLLITWINGAPPPPRAN FGIFNKKGVTPCGQGGPKTRDLGIG PSKPPKGLEFRAQPPEPALMGKFYP MVNLSNVPPF |
| 3704 | 9201 | A | 3979 | 3 | 250 | AIAAH*NLHLLGSSNSSASVSRVAGI TGARHHTQLIFVFLVETGFHHVCQA GIEFLTSGDTSTSASQSARITGMSHH TWPQKQ |
| 3705 | 9202 | A | 3980 | 2 | 257 | PRSSPTCPACLCVQVNPPAQDPEDP APQLSPQPQDPAKPPQPYNPYPY PNLGCGL*PQNYCIIVCMVSIVYYH MGIIETVKSQ |
| 3706 | 9203 | A | 3981 | 2 | 147 | LVEMGFHHVSQAGLKLLDSGNLSA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | S*RSAGITGISHRAHPPNSTNIYA |
| 3707 | 9204 | A | 3982 | 3 | 446 | QVVRGFGGRVSKQMGIPTANFPEQV VDNLPADISTGIYYGGASVSGSDVH KMVVS I*WNPYYKNTKKSMETHIM HTFKEDFYGEILNVAIGD*LRPDKN FDCLESLISPVQGD TD*AKIRLELPE HLRI*EDTFFQVSLNRTMIVTDDK |
| 3708 | 9205 | A | 3983 | 1 | 162 | FFFRVKASICCPGWSTVAQ**LTAA SDSWAQKSSCFSLWSSWDNRRGLP HLANK |
| 3709 | 9206 | C | 3984 | 131 | 442 | MNIPLSMSLVVSNSMQDVFWXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXX* |
| 3710 | 9207 | A | 3985 | 141 | 429 | TGSHFVAQAGMQWCNLWSMQLLP AGLR*FPYLSLPSSWDYRHAPPCST HFLYFFVEMGFCHVAQVGLELLAS SDVPTYASQSAGITGVSNHPRPF |
| 3711 | 9208 | A | 3986 | 1577 | 1879 | |
| 3712 | 9209 | A | 3987 | 1 | 219 | EM*SCRVTQAGVQWCNLSSLQLPS PGFKQFSCLSVPSGWGYRCMPHP ANFCIFSRDRASPRWPGWSQTPDLR |
| 3713 | 9210 | A | 3988 | 1 | 414 | FF*TGSCFVSQAGTQQQDHSSLQP* TPGLKPSSHLCLLSSWDNRHLIFKFF VEMGSRHVAQAGLQLLGSNNPPTL AS*SARIISWSHRAQPTCTLCSWLC DSGAGTAESFLWQPALSRVANRGC CRRPGKLKEKQGT |
| 3714 | 9211 | A | 3989 | 3 | 666 | FFVETGFCHVGQAGLELLGSGNLPA AASQSAGITGMSHRVRQHS*YETHR KVFYS |
| 3715 | 9212 | A | 3990 | 1 | 436 | FFFFFLRQNLTLSPL*CSGTILAH NLQHPGSSDSPASASQVAGITGVRH HIWLIFVFLVEMRFHHVQGASLELL NSGYLPTSASQSAEITGVSHCAQLQ PGILMHGLRRLTDLDDNVHHPRSRL KVTSSSAHPGAASSSFLHL |
| 3716 | 9213 | A | 3991 | 167 | 563 | SESASEFSIFYLFIIIIIIIIETRSCSVA QTGVQWCDHGLLQPRPPWFRPSCH LSLLSSRDYR*APHPANTFNFFLLE IGSHYVAWGSLELLGSSDPASASQ SVEIIGVSHRGPD SQKSFIHLSPRFP |
| 3717 | 9214 | A | 3992 | 3 | 456 | |
| 3718 | 9215 | A | 3993 | 78 | 129 | |
| 3719 | 9216 | A | 3994 | 96 | 251 | MDQYSRNSPLEVNGQQLLGWYQH ALRCKWNF*APLCYCSHTVFNSQPT HTEE |
| 3720 | 9217 | C | 3995 | 94 | 351 | MKRISTTQYYHCQDYDLRHSKHM CLVSTAFQKVPLYKYLEILQENLD PQGKDSRWFSVISSPRSQNVKVWR HLQSCLTSHCKH* |
| 3721 | 9218 | B | 3996 | 1 | 431 | MAVASTKSRWETGEVQAQSAAKT LSCKDIVAGDMSNKSFWQKGGSK TSSTITAQIAFLQGERKGQENLKKD LVRMIRMLEYALKQKRAKYHKLK YGTELNQGAMKPPSYDSDEAQQQA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MRSVHGPLHLSAPPASQQKRPTE * |
| 3722 | 9219 | A | 3997 | 772 | 1391 | IANNKDALARKTWNPKFTLRSHFDGI RALAFHPIEPVLITASEDHTLKMWN LQKTAPAKK*EYSTLTLEFYFK*HA |
| 3723 | 9220 | A | 3998 | 3215 | 3491 | SAKVLRPTFFFFFFFFFFFFFAIESHCVT QAGVQWCNLASLQSPTEFK*FSCL GLPSSWDYRCVPPHPANFYIFSRDR VSPCWPGWSKTPDLK |
| 3724 | 9221 | A | 3999 | 1 | 779 | MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEK VPETTTRFWAPGVEAPGDDAERRR REASGPATRHSPPLTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSTVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCHDQ SAWHVGRAEIRKLLPYCSTQGGLK YSDVTSGMVKDPPDVL/DRQKCLD ALAALRHAKWSSEIRF |
| 3725 | 9222 | A | 4000 | 1 | 1286 | MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGPPGGLLGV RPGMPPQPQGPAPLRPDSSDDRYV MTKHATITYPTEEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLISR IAE NLPKQLAFISPEKYDIKCAVSEAAI LNSCVEPKMQVTITLTSPHREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCVHIR ILRDLQCRVPTWSDFPSWAMELLV EKAISSAS\SPQSPGDAL\RRVFECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PDPASRED/LSTSQCHSLPLETS LAFPPRYHKVLGMDPITRK*AQRF NIHNNRKRRRD\SDGVDGF AEGK KDKKDYDNF |
| 3726 | 9223 | A | 4001 | 2 | 379 | DLPASATQONAGITGVSHHIWPRIIFL LW*KTFTILTFLSVQYSSSNYIHPVC NRALELFKSYKTETKLNFPSPPPPI VNLHCIFFF*GLTFLGFFSLPKYRG FTNFVSPCTVAMLTRGGGGGEF |
| 3727 | 9224 | A | 4002 | 229 | 445 | RPGPNFGLLETLTWGLKGTWLWNP PKNWELGAHPPTPGNFWIF*KGGF WNVSQGGSKTRGLRELPPFSWKKG |
| 3728 | 9225 | A | 4003 | 192 | 529 | HEVLNFLTSCVLTTLVFLIADIWLS CRTRSLPFVATTLEVLPLSLIGLCHH TILVFISNAFFI*KAYFVTSSFIMFP*S FFLFNISVLSYMYLTFSHLTSFVIAY FSYSHI |
| 3729 | 9226 | A | 4004 | 330 | 754 | SDLSQKESSSSLSKFLVTEKNSSLGS GGCDMANKENELACAGHLPEKLH HDSRTYLVNSSDSGSSQTESPSSKYS GFFSGGFLRDHETMAQVLF SRDMR LNVALTFWRKRSISELVAYLLRIED LGVVVDCLPVLTNCLQE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3730 | 9227 | A | 4005 | 296 | 861 | VSQDHETMAQVLF SRNMRLNVALT FWRKRSISELVA YLLRIEDLG VVVD CLPVL TNCLQEEKQYISLGCCVDLL PLVKSL LKSKFEE*CY*WVLTGLQA VIKRWWSELSSKTEIINDGNIQLKQ QLSGLWEQENHL TLVPGYTGNIAK DVDA YLFPVTIEGFHLLKSIWFFKTS LELYNLQKKKVS V |
| 3731 | 9228 | A | 4006 | 2 | 265 | NNFFSFSETESHSVTQAEAQWYDNS SLQP*ILGLKQSFCLSLPSNWDHRC APPHPQFSFLIPGLYVSQFILGNKPSS LPCQMFKSAV |
| 3732 | 9229 | A | 4007 | 3 | 295 | HFNLSHRSAQAKGNRYKEAEALTN AAVHVDDMPNALNALIDLRAHNLG QDPVNFKRLSHCLLVTLAAHLLAEL TPAVHA*LDKFLASVSTVLTSKYT |
| 3733 | 9230 | A | 4008 | 1 | 1077 | |
| 3734 | 9231 | A | 4009 | 3 | 285 | ETESRLATQAGVQCCDLGSLQPLSP GFK*FSCFSLPSSWDYRYPPSCQAN FCILVEMGFHHVGQASLELLTSGDP PASASQSARITGVSHRAQ |
| 3735 | 9232 | A | 4010 | 1 | 338 | VIATYHGGLCTQKSQPPPPQALWSA STSTINLMVSTEPLALTETHICKLPK D*GTCRDFILPWDYDSNTKSCARF WYGRCSANENDFGSQSECEKVCAP VLCKPGVISEMAT |
| 3736 | 9233 | C | 4011 | 269 | 526 | MLARLVSNLSPQVIHHTQPRVGSPT RIPTLSLNLPLPLALTSLRWDRHQLR GQGHWGAQELRAITGFKDHQVWQ TLNCSLCVPPK* |
| 3737 | 9234 | A | 4012 | 2 | 51 | |
| 3738 | 9235 | A | 4013 | 83 | 5229 | |
| 3739 | 9236 | A | 4014 | 3 | 45 | EVVHALRCRWW SWGLKLDLLTPEP EPICGPALLSRSSLRGSHPTAFLLP QVSQ*RGELGPSTFRAFRAEFPTS RG SKDNKEKNQQEQDMAKPATGTGQ G*GADGGAGA |
| 3740 | 9237 | A | 4015 | 3 | 323 | LLWKVESSWRDQKDIMSWEWDR RRRHHLTDRSQLCSKVKFQVDCDLI EWGTWIINLKQYNAYHCEGECHNP VG*KFHQSNHAYIQVGCQVLGGEE AVIWHWGTGL |
| 3741 | 9238 | A | 4016 | 2 | 279 | FFFFEAKSHSVTRMLECNGAISAPC NLHLP GSSDSPASASQVVGITGVYH HTQLIFISVETGFCHVGQDGLNLPD LMIHPPWPPKVLG*QA |
| 3742 | 9239 | A | 4017 | 166 | 939 | |
| 3743 | 9240 | A | 4018 | 2 | 225 | KELTGRRCAEPPHPRPSPQLLTEEPF TKGRFSGEWRGRNAASMTGPFAE HSNQLWNISAVPSWSKVNQGLIRM YKAEP*EGADRKALCRASPPPIPPV TDRGAIYKRPI LWGVERQERSVYED WPICRALQPAVEHQRRPFLVQSEPG SHPHV |
| 3744 | 9241 | A | 4019 | 142 | 1336 | KARGDCKHPGRCWPEQMAEGERQ PPPDSSEEAPPATQNFIPKKEHTVP DMGKWKRSQAYADYIGFILTLNEG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VKGKKLTFEYRVSEAIEKLLALLNT LDRWIDETPPVDQPSRFGNKAYRT WYAKLDEEAENLVATVVPHTLAA AVPEVAVYLKESVGNSTRIDYGTG HEAAFAAFLCCLCKIGVLRVDDQIA IVFKVFNRYLEV MRKLQKTYRMEP AGSQGVWGLDDFQFLPFIWGSSQLI DHPYLEPRHFVDEKAVNENHKDY MFLECILFITEMKTGPFAEHSNQLW NISAVPSWASKVNQGLIRMYKAECL VEKFPVIQH/FSKFGSLLPIHPVHVGL GGAKPKEPPRGTVSCCLPFPTPAVA PPSPPSVSSRLMRGCLLGLGGEMG LRGLRA |
| 3745 | 9242 | A | 4020 | 80 | 283 | |
| 3746 | 9243 | A | 4021 | 61 | 626 | DLICVIGVPEEEKETGAKNIFKEIMG ENSPHLVKDVIVHIEEHSQIDEN*** Q*KSYK**QKGIIKLRVDLLETMEA KCSRTPSLKCLGKESFGESWESRILH PAEISHRNECHMKIILDFKSEKGPDA VAHTCNPSILGGHTAGGSLEARSFE TNLPETLSLLKKNLKEKEFVASYP PLVEMLK |
| 3747 | 9244 | A | 4022 | 18 | 161 | TSFKNPPPPPPGGLKKIPSPPPKKK KFKDVS*PTYFLYL NASSVT |
| 3748 | 9245 | A | 4023 | 30 | 262 | NRRQAGPFPKLG RPS PKGGFPNFF KSSSSKSSF*KNPKGQGWGFPLIPG FQGPQVGGSLGAPGLKPPWGTPQN PF |
| 3749 | 9246 | C | 4024 | 193 | 366 | MYNRSIPKNKYTYTYTKSYPNKIF SRLILYIPLGTVSQISTLNCVPRFVLL TWKAL* |
| 3750 | 9247 | A | 4025 | 3 | 258 | TIDSLKGLPCKQNEPWHTIQCGYL GNSSKWN I*YQSGKDFIRIAFCVCIC I/CYF*E*IYSCT*IPVRNTLNELNPLA KCPCPFH |
| 3751 | 9248 | C | 4026 | 164 | 313 | MEGTRIFGKWVKLIQSIPNRNSCTTI DLFLKINIHIHTQKAILMKSFPD* |
| 3752 | 9249 | A | 4027 | 9 | 373 | DRVSLCRPTLEVQWRDLGSLQPPSP QVQSNPALSLPSSWDYRRVPPCPS *FFVFLSRRWRFRHVGQTALFLIKM MGKKILKIKSNYTLGLYVGPSYSER MIKPQEFESSLGQHCKTPSQK |
| 3753 | 9250 | A | 4028 | 1 | 336 | DRILLHRPCWSTLARS*LTIPSNHLG SVFPPSALLES*DCRHTPTTPD*FLKI FL*RRGLTVFPRLVLNAWTQAIQPL PLKALGLQDTFFKNINCDRLKVSEY YSDTEIEI |
| 3754 | 9251 | A | 4029 | 514 | 742 | LPKC*DHRHEPPHQAKFFNFFVEMG SCHVPQSGQLLLGSSDLPASAFYSA GIAGMSHHTWPPYLFKSRHKS RFCP S |
| 3755 | 9252 | A | 4030 | 1 | 264 | QAQGKHPSFGPPFAGLKGFPGGLGF PRTGNSGGFPQGGKYKGFLIKNGVP PSFQGGF*IPGPGSHQRLGFRG*VGR AL*TPGFRATLF |
| 3756 | 9253 | A | 4031 | 7 | 417 | RQDLALSPRLECSDTIIAHCSIKLLG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SNGAPSAAS*VAGTTGTRHHAQLIF LKIFVETRSLYVAQASCVFPASSNPP TSASQSTGITGMSCCARPTSYVPGS DLSVLCILTHLILKIPLYRRYYYFVS LTYSKAEVQ |
| 3757 | 9254 | A | 4032 | 123 | 376 | KTGSNFVPQAEAQGGNSG*LNPLPP G*KQFSGLTLLITWINRAPPPRANF GIFKKKGVSPCC*GGLKTPNSGFSPF KPPKGLE |
| 3758 | 9255 | A | 4033 | 3 | 292 | QWHKHGLLQPQPPGLK*SSHLSLPR SWDHRHVSPCLTNFF*FSVSMGSCY VAQAGLKHLASSDPPASASVGTIG MSTT*SKTTLYTEKLANIILTK |
| 3759 | 9256 | A | 4034 | 1 | 230 | FFF*TDSCSVAQAGLQWRDYRPEPP CPANFITIKQVQNKSVTFPARNLNK MRGASIMLYPIGLSLNDLMQLLSEG F |
| 3760 | 9257 | A | 4035 | 3 | 189 | SWDYRRLP HARLIFVFLVGTGFHHV VQAGLELLTS*FTRLGLPCWDYRR EHIAPGHIWY |
| 3761 | 9258 | A | 4036 | 2 | 148 | PGSSNPPTSASQLAGTAGTHHHA*LI FVCLVETGFCHVA*AGV*VKFF |
| 3762 | 9259 | A | 4037 | 348 | 696 | AEEQDKKGRQ*ERGKEWERETETK IYSRIKGNREGQAKKKWGHGELIH KTKDEKRKKSEEDKKLRWRKR*TN SQKD*IRKRLHKETANSER*EEKHK ERKQWRRGPKARRAISRG |
| 3763 | 9260 | A | 4038 | 1 | 295 | QNQFFIFIYFKTESGSVTRLEYSGVIS AHCNLCHPGSSQSPASAS*AAGTTG AHHHIQLLFVFLVETGFHHVGGQAG LELLTSSDLPASASQSAWGLQV |
| 3764 | 9261 | A | 4039 | 6 | 151 | SQGLALLPRLISNPWVQAILLPWPP KVLGL*AEIAQNMKQK |
| 3765 | 9262 | A | 4040 | 101 | 318 | SNHTLGTS*HFFETVSCCIMLHRVE CSGAVIAHCNLELLGSSDSPASTS*V AGTTAVYHHTGLSWLLNHLH |
| 3766 | 9263 | A | 4041 | 210 | 306 | SWPGTVAHICNPSALGGQGGWIA* GQAFRQA |
| 3767 | 9264 | A | 4042 | 2 | 147 | DFSVKTL*ARREWDRIFTVMKEKNF YPRKVYALKIPFKNEAETKKVEV |
| 3768 | 9265 | A | 4043 | 160 | 525 | NTQTRSFGNRLMAPAQSSHKALTK KVMTCNPSETVHDSQECFFVLFFET VLVCLPGWSAVMLVRCSLCLLSSW DYRRVPPHLG*FLYF**R*CLTMLA RMVSNS*PQVIHLPRPPKLLGLQA |
| 3769 | 9266 | A | 4044 | 3 | 72 | KTQVHFQGWQHSHVHIITHPCWEKL ALSITPLR*DNRKLQAWNSPRLGPT CLFPRLALMCVLMML**NIHEYNSFQ RVLWVLLVNC*ISKVGSTLCISSHIP AGRS |
| 3770 | 9267 | A | 4045 | 313 | 358 | |
| 3771 | 9268 | A | 4046 | 7 | 308 | AGGRRARAPHLGGRGAARGRL*RV RGHRERGLRAAPVPRPQQLRRGA AAGAVQPGQGVGRAGPPEGSEGSV AGVGLDLDSscyHHSSDFYICHMP ISS |
| 3772 | 9269 | A | 4047 | 92 | 390 | ETGSHSVNLAGLQWCDHNSLQP*T |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PGLKQSSYLSLLSS*DYRWVPPCPA NF*IFFVEIRSCHISQAGLDLPRPSDP PVWGSQSAGTIGMSHHAQPREIC |
| 3773 | 9270 | A | 4048 | 65 | 375 | SQLTATSTSRVQ*HDLSSPQPPPPGF KRFSCLSLPSGCDYRHPPPHLANFL YFLVETGFCHVGQAGLELLTSSDLP ALASQSAGITGVRYCAWPTFLIMKT CIPSFPLPSTSPIPLP |
| 3774 | 9271 | A | 4049 | 12 | 292 | DIVSPVA*TRMQWHNLGSLQPPPPR FKQSLCFSLPSSWDYRCVPPCPAIF VFLAEMGFCHIGQAGLELLASSNPT TLASQSAEPPHLAATDF |
| 3775 | 9272 | A | 4050 | 40 | 343 | SSSSLILSSSVIYLLLNLSIDFLVLLLY FLVFRFSVCSFCFQFFVKNFNLFYF FKHIKNICFKVCV*RLGFLDPLCAYF GCLLFL*VFSHVLSLHIPDDL |
| 3776 | 9273 | A | 4051 | 97 | 282 | |
| 3777 | 9274 | A | 4052 | 3 | 336 | FFETGSRFVTHAGVKWHNHDSLHP QPPRLK*FSYFSLLSWDHRHVPP RPANLVYLL*RGGPSMLPRASLEF PGLQVNSSLPSALPKVLGITG*GHRP RPKVTFHQRG |
| 3778 | 9275 | A | 4053 | 3 | 294 | CCFGDGVSLCRPGWSIECSGNHSSL QAVEPRLR*SSRLSLLGSWDPSHV PLHLANF*TFCTHGVLA MLPLAGLK TPWAQTIPPHLSLPKVLGLQG |
| 3779 | 9276 | A | 4054 | 16 | 308 | MPQPN*SNPPVNCRLPRGPSQVP PRIHLSPKYSPSEASAPDLQKKGNL QAPRRPGEVLETPRKPESSCMKFP* REIKPLPPPRLTPSVHSMVL |
| 3780 | 9277 | A | 4055 | 445 | 448 | IS*HCDASASIFRKKQRKQINKHPTL ASRVLGLAMEMQDETWC SGQSET VN*SQTAQNHPQPGS*PAGVCLWV ASSQHFTPQLKKKPNPDSAKLNSA SDSLTEVILCKIFSAWQTDK |
| 3781 | 9278 | A | 4056 | 3 | 284 | CLSLSSWDYKCLPPRLGYFLYF** RRGFTVLARMVSISRMVSISRMVSIS *RRDPPASASQNAGITGVSHCARPK EQKLFYPEVSCLYLGLY |
| 3782 | 9279 | A | 4057 | 428 | 636 | DYHIVSLLHLF*FLETGSHSVTQAGI QWCDHSSL*PRTPLKQSSCLSLPE* LGLQE*VTVPGSYSLFF |
| 3783 | 9280 | A | 4058 | 2 | 113 | FFGRDGVSLCCPDWS*TPGLKGSSC LGLPKCWDYRRE |
| 3784 | 9281 | A | 4060 | 36 | 359 | RSGVQNGFHHQAEVLSVRLCFSTEAL GQNPMFPAPPGATSSPGPRPSCHL HSQKL/TLLHAQTLVTPLPL*GLGLS AWRTL AGGAPGLHPFTTHALSTPET IPGAYRRT |
| 3785 | 9282 | A | 4061 | 17 | 168 | APGMVSGVLSACVVNGWSPGAPPA SVLQA/PQT*PF*SRPHVTSQPLLKA PH |
| 3786 | 9283 | A | 4062 | 2 | 375 | FFFFFENHTNLLSYSSRGSGVQNGF HQPEVLSVRLCFSTEALGQNPMFP APPGATSSPGPRPSCHLHSQKLPLLH AQT LVTPPL*WPPWITQGPPQST GHLPTTEILKLKHRRRVPFCHAR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3787 | 9284 | A | 4063 | 309 | 620 | |
| 3788 | 9285 | A | 4064 | 3 | 218 | LRQSYSVTQAGVQWRNLGSLQPLP PGFKRFSCLSLRKS*DYRRPRLPNFC ILVKTGVHPCWSGWSQTLDLR |
| 3789 | 9286 | A | 4065 | 1 | 170 | NPKATPPQIVNGDQYCGDYELFVE AVEQNTLQEFLKLA*VKPVQSSPAG LHHHTPL |
| 3790 | 9287 | A | 4066 | 29 | 483 | RRLPAVQLPLTAALCPPARLSTPSM SGPARSTARRATGFREIKVPSKSEVT RILÆGKRIQYQLVDISQDNALRDEM RALAEQPQGHPTPDLSTGDQYCGD Y/DASFVEAVEQNTVAG\FPGSLGL KFKPCSRVSPCWDSHHQHSPPAFQP GQ |
| 3791 | 9288 | C | 4067 | 33 | 236 | MRHHAWLIFVLLVETGFHHVGQAG LEHLISGGPPTSASQSAGITGVSHHA WPIYLFILLSGPSRLCF* |
| 3792 | 9289 | A | 4068 | 1 | 205 | AIGTDKGTRWPSEDDPGNLPEIFLFI LGPTADYV*RERQRSIELESFYRRV WGSPGGEGTGDLDEFDF |
| 3793 | 9290 | A | 4070 | 2 | 44 | LSSWDYRHVPPRLANFCIFSRDGGF TMLARLVLNS*PQVIHPPQPP*VL*L QACATTPG |
| 3794 | 9291 | A | 4071 | 173 | 369 | CSTLI*IRKVWLGAHAHAYNPNTLR GRGGRIA*GQVFKTSLGNNVKTCLF LPSPHNQQLSGFLL |
| 3795 | 9292 | A | 4072 | 1 | 336 | |
| 3796 | 9293 | A | 4073 | 1 | 200 | |
| 3797 | 9294 | A | 4074 | 11 | 392 | |
| 3798 | 9295 | A | 4075 | 1 | 191 | |
| 3799 | 9296 | A | 4076 | 84 | 264 | |
| 3800 | 9297 | A | 4077 | 2 | 446 | DSARNSRVDGCE/IDRQKGTNDSLM MLMRELEDRFASEASGYQDNIARL EEEIRHLKDEMARHLREYQDLLNV KMALDVEIATYRKLLERGEESRINLP QTYSALNFRETSPEQRGSEVHTKK TVMIKTIETRDGEVVSEATQQQHEV L |
| 3801 | 9298 | A | 4080 | 3 | 196 | SRAKGPKNYNFGQGPPTKVKGPLA SPFFPLLPPFPRPPWFPPPF*NPIFPW W*KGPKKPFLN |
| 3802 | 9299 | A | 4081 | 1 | 187 | SIRLFFFCFFF*AETGFRHIGQAGFGL LTSSVPPALASQSAGIIGVSHRARPC SSLIVLHL |
| 3803 | 9300 | A | 4082 | 156 | 326 | KLEICRRARVSLKIGFIRPGTVAHAY NPSTLEGRGRQIT*DQEFETSLANM VKPCLY |
| 3804 | 9301 | A | 4083 | 3 | 448 | |
| 3805 | 9302 | A | 4084 | 1 | 4249 | AAATIRYLKTTMAWKTLPIYLLLLL SVFVIQQVSSQDLSSCAGRCGEGYS RDATCNC DYNCOHYMECCPDFKR VCTAELSCKGRCFESFERGREDCD AQCKKYDKCCPDYESFCAEVHNPT SPPSSKKAPPPSGASQTIKSTTKRSP KPPNKKKTKKVIESEEITEHSVSEN QESSSSSSSSSSSTIWKIKSSKNSAA NRELQKKLVKDNKKNRTKKPTP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KPPVVDEAGSGLDNGDFKVTTPDT STTQHNKVSTSPKITTAKPINRPSL PPNSDTSKETS LTVNKETT VETKET TTTNKQSTSDGKEKTTSAKETQSIE KTSAKDLAPTSKVLAKPTPKAETTT KGPALTTPKEPTPTTPKEPASTTPKE PTPTTIKSAPTTPKEPAPTTT KSAPT PKEPAPTTTKEPAPTTTPKEPAPTTT EPAPTTT KSAPTTPKEPAPTTPKKPA PTTPKEPAPTTTPKEPTPTTPKEPAP TKEPAPTTTPKEPAPTAPKKPAPTTPK EPAPTTTPKEPAPTTTKEPSPTTPKEP APT TTKSAPT TTTKEPAPTTT KSAPT PKEPSPTTTKEPAPTTTPKEPAPTTPK KPAPTTPKEPAPTTTPKEPAPTTTKK APTAPKEPAPTTTPKETAPTTPKKLTP TTPEKLAPTTPEKPAPTTPEELAPTT PEEPTPTTPEEPAPTTPKAAAPNTPK EPAPTTTPKEPAPTTTPKEPAPTTPKET APTTPKGTAPTTLKEPAPTTTPKKPAP KELAPTTTKEPTSTTSDKPAPTTPKG TAPTTPKEPAPTTTPKEPAPTTPKGTA PTTLKEPAPTTTPKKPAPKELAPTTTK GPTSTTSDKPAPTTTPKETAPTTPKEP APTTPKKPAPTTPETPPPTTSEVSTPT TTKEPTTIHKSPDESTPELSAEP ALENSPKPEGVPTTKTPAATKPEMT TTAKDKTTERDLRTTPETTTAAPKM TKETATTTEKTTESKITATTTQVTST TTQDTPFKITTLKTTTLAPKVTTTK KTITTEIMNKPEETAKPKDRATNS KATTPKPQKPTKAPKKPTSTKKPKT MPRVRKPKTTPTPRKMTSTMP ELNPTSRIAEAMLQTTTRPNQTPNSKLVE VNPKSEDAGGAEGETPHMLLRPHV FMPEVTPDMDYLPRVPNQGIINPM LSDETNICNGKPDGLTTLRNGTLV AFRGHYFWMLSPFSPSPARRITEV WGIPSPIDTVFTRCNCEGKTTFFKDS QYWRFTNDIKDAGYKPIFKGFGGL TGQIVAALSTAKYKNWPESVYFFK RGGSIQQYIYKQEPVQKCPGRRPAL NYPVYGEMTQVRRRRFERAIGPSQT HTIRIQYSPARLAYQDKGVLHNEVK VSILWK\GLPNV\VTSAISLPNIRKPD GYDYYAFS\KDQYYNIDVPSRTARA ITTRSGQTL SKVWYNCP |
| 3806 | 9303 | C | 4085 | 258 | 362 | MFYRNLMKVRAELNCSAILIEIKA KVLTLFHSN* |
| 3807 | 9304 | A | 4086 | 2 | 236 | QSYNSDSLFFLRRSFALVTQAGVQ WRDLGSLQLPSPGFK*FSCLSLPSS WVYRCPPDPANFLVLVETGFHHV GQGS |
| 3808 | 9305 | A | 4087 | 224 | 464 | KIFLFFFFFKRQGLTLCRLDCSVQ *HNHYPLQSRTPELKQSSCLSHPKY WD*RHEPLCLAPKKEDTLQEQLAIR LLIY |
| 3809 | 9306 | A | 4088 | 129 | 315 | ILKILWIFRIFLLSIKCF*TNMHVCV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SCLFIFLTVSFIEQTF*ISFFYASWIML LMSFFF |
| 3810 | 9307 | A | 4089 | 1 | 190 | FFF*IGPHSVAQAGVRWCDLGSCSL NLPGSSDPPASASQVAGTTGVHYYT QLIFKFFIEMRAP |
| 3811 | 9308 | A | 4090 | 1 | 5229 | |
| 3812 | 9309 | A | 4091 | 1 | 7044 | |
| 3813 | 9310 | A | 4092 | 170 | 422 | |
| 3814 | 9311 | A | 4093 | 1 | 3230 | |
| 3815 | 9312 | A | 4094 | 3 | 151 | DTATCCAKWNTEDKVSHVSTGGG AS*ELLEGKALPGVDATSTIYYFPAF |
| 3816 | 9313 | A | 4095 | 2 | 1446 | SLRSARRQSAPSLTESPTSLPSCISK MSLSNKLTLDKLDVKGKRVVMRV DFNVPMKNNQITNNQRIKAAVPSIK FCLDNGAKSVVLMShLGRPDGVPM PDKYSLEPVAVELKSLLGKDVFLK DCVGPEVEKACANPAAGSVILLENL RFHVEEEGKGKDASGNKVKAEPK IEAFRASLSKLGDVYVNDVAFGTAHR AHSSMVGVNLPQKAGGFLMKKEL NYFAKALESPEPFLAILGGAKVAD KIQLINNMLDKVNEMIIGGGMAFTF LKVLNNMEIGTSLFDEEGAKIVKDL MSKAENGVKITLPVDFVTADKFD ENAKTGQSTWA\SGITPG\WMGLDC CPSS\RYAE\AVTRAKQMVWNGP VGYFE\WEAFARGTKALMDEVVK ATSRGLSPS*GGWRPLPTCCAQM ETREDKSQPM*ATGGWCPVWQLLE G*SPFLGVDALSQYLGTFPALLSPC AQPPKVNLGIFLHLPLGH |
| 3817 | 9314 | A | 4096 | 1 | 747 | MDSSRARQQLRRRFLLLPDAAEQ DREGDAGPETSTAVEKKEKPLPRLN IHSGFWILASIVVTTYVDFFKTLKEN FHTSRSPESPAPRRGGVRASVPQKL AEMLSQYGLIVFVAGLLLLLLAWA VHAAGVSKSDLLCFLTALMLLQL/P VDAVVRGPQLRAPPLPPQGHARG CRLAARQRPPTVSTGRGEHVDSPPP AQRSSYLPLRLRGAEFASEPPSAPA HRAATPPPVEVTPTEAGRRFRQAKG ALS |
| 3818 | 9315 | A | 4097 | 1103 | 1295 | EQEGTGLERRRGSPMSKDWPPPHL TPPQGPGGIPVHSLSPPSFS\PGPRNS K*ARRSTAPVDCK |
| 3819 | 9316 | A | 4098 | 1 | 1302 | MVAGSDNYHEVSLHDGVIGARGCP PPSPSARGARSPRPPGGCARQPTEA GRDAEQPVWADRVRGGAAAAAGL GRARRGLAESDLLCFLTALMLLQM LWYVGRSSAHRRLFRLKDTHAGAG WLHRLWLWPPAFGCRPEYDNGLEEI VFGFEPWIIVVNLAMAFSIFYAMHA AASLFEVYSGISETSVLGDWSKPSTF DSKASGLRHLKTSKGKSSLVNASIP TPPSPFRPSQPSEPASQPAKPAKPAK PVSQPSQPSQT\PGKPAKPAKPPKPA KPPASQASQASQPGMPAKPAKPAK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | K/PPKPGMPAKPARQPSQPAKTAKPA NQPSQSASQASQPASQPSRPACQPT KSARQPRQPSLPAAKRANATYQRS HSASQDRHASEPTSQPSSQHSAARP AATSQPDRAANQSAVEQARQPSA KHSGKQQADSEAAAGS |
| 3820 | 9317 | A | 4099 | 684 | 902 | |
| 3821 | 9318 | A | 4100 | 143 | 551 | TNEFPFHSRSPPIQTS*AHFPHLITD PDLLSPLSPSHHRSRPPEPTSPISPIQ TC*AHFPHLITDPDLLSPLSPSHHRS RPPEPTFPISSPVISWAPASFPNCCC KQTATDSSGFHFCLIVLIAKSPKRISP G |
| 3822 | 9319 | A | 4101 | 14 | 209 | ASFKVWLIWE*RPWHGTYPSCKNW GKFASGSVTIWFKLPSGPLALSGIL MRLLLLSLSLHENSVS |
| 3823 | 9320 | A | 4102 | 126 | 265 | |
| 3824 | 9321 | A | 4103 | 74 | 196 | NLGMLAHAYNSRNLGGQVRTII*G QKFETSHENISRCLV |
| 3825 | 9322 | A | 4104 | 1 | 217 | NIYMFLICFVLIFNFLNELIT*KHIVIF ICWILSLLLLTLH*FWCHKFHVSW NLEFCIFYFGFKIKLDTFT |
| 3826 | 9323 | A | 4105 | 3 | 268 | DRVLLCCPGWSAVSQS*LTAPQTPG FK*SSHLSPSSWDYRHIPPHLAKK QKYFK*RWSLPVLPRLV*NSWAQAI FPCQPPKGLGLQA |
| 3827 | 9324 | A | 4106 | 3 | 263 | DSLALSLRLECSGVISAHCNLCFLGS NNSPAAASRVAGTTGACH*DWLIFE FLVETGFHHIGQAGLELLTEVICLP WPPKVLGLQM |
| 3828 | 9325 | A | 4107 | 22 | 208 | SFSIQGPLLLKPNS*PGVVAHSYNPS TSGGQGRCT*QGEFESSLVHMAKP HLYQKIQKICR |
| 3829 | 9326 | A | 4108 | 122 | 339 | EKGFWFCAQGGKNLPGGNSLEPSA SGLKEIFGLNLLNNWE*RGGPKTPG NFWIWKKGGV*PLWPGWG*NPGL |
| 3830 | 9327 | A | 4109 | 2 | 210 | KEKIFSPGFKHPPPPFF*KTPLKGG RIFFSPPRKNWPPQRIFKKAPPSSSSS SSSSSSSAQI*SFNSP |
| 3831 | 9328 | A | 4110 | 3 | 76 | ATSESLDVMA SQKR*SRSGSPMARR |
| 3832 | 9329 | B | 4111 | 1 | 2142 | MGGAGSPQVILVSHTPQSASAACEE IAYQVAGVSGNLAPGNQPEKEGRA HQCLECDRAFSSAAVLMHHSKEVH GRERIHGCPVCRKAFKRATHLKEH MQTHQAGPSLSSQKPRVFKCDTCE KAFAPKPSQLERHSRIHTGERPFHCT LCEKAFNQKSALQVHMKKHTGERP YKCA YCVMGFTQKSNMKLHMKRA HSYAVAVAMGGTAQCPPGATACL GTAICPSGLRAQRPSNLSVPEAAKP KSGRNRKIEAPT WALSTSKDPQTEG LRNPQTCVQIRSNPFCAFAQGFS LIS ELRTLNC FVGLCDSQSGKQQLGFYS GQPATEAWQKYS LAVCILRSEQEIS ATRLGLKNTNVNKL DGGCGAWNF LGGMSEHNSPPSGRAILLPVVFTEV FPGPWTPEQSGSHICRMNLAPTQAF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LPKTGFPIDPQELLQGPIERTIWPGT VYTFRSAIVTARAVWVRPRMDRRA DLSSATQSASAEKFGGRVSAGHCA LPLPARPV TASVYGR LARLRGCLED SYPSALSAQVFLDSPAVGCGLETRL FIEAALGPPCRATVTSRGHLLDISIT KSPGRPCFLSVCLHGSDQOKRKA AATAKRKSKGGGVNVEGRLCTWPP EDPPKSWSLAFGPLQEKTTTELNLHP RCWARCLSHWELPPGPRGRAQAPD WTGSKSFREQLLTFTLWGVQEKISK HQANQGKEAPAYTGLEDSDPGGLC AV* |
| 3833 | 9330 | A | 4112 | 1 | 551 | |
| 3834 | 9331 | A | 4113 | 3 | 288 | CIGLGVAHACGPGTLGGRGGRIT* AREFGTSLGNIARSHLYKKRKNSES QMSLHLLTLDLTPYISAAFASPVDA DTQLSACTFQLKETPMPSF |
| 3835 | 9332 | A | 4114 | 3 | 344 | VQYYGPAT*VQDGS*GYRTHMYMI NQIWLQAVLKIITNKTGRALTILTQ QETQMRNAIYQNRLALDYLLAAEG EVC RKFN LINCCLHIDNQGQVFEDI VRDMTKLAHVPMQV |
| 3836 | 9333 | A | 4115 | 6 | 185 | LAGHDRVRL*SQLFRRLRREDCLSS GGRGCSEP*SHHHTPVWKTCLGPV SKEKKYNQIV |
| 3837 | 9334 | A | 4116 | 1 | 176 | QSIFQICIFFKFTVYMFKTFLKFQTV FLCGRCWFL*KGLIIFFTLYFKTFHH IVRGIK |
| 3838 | 9335 | A | 4117 | 1 | 312 | GGEKNQDFTFKMESPSDSA VVLPST PQASCLSLPSN*DYRHPPPCPANFCI FSRDWVSTHVGPWSRTPDPQVIH RLGLPKTIRGSEEGIPDEYQLKGTLYKL |
| 3839 | 9336 | A | 4118 | 1 | 112 | GKTFKQKQKQEKKQK*ELK*KAM GKGPLAAGEIKKS |
| 3840 | 9337 | A | 4119 | 3 | 355 | SQSTKNLPSLARDMDIQIEAQRSP KRSPPRHIIFELTKVKDKEKNPKVPV EKHQVIYKGFIRITAETSQARKKW DDISKFLKEKKKYRSKILCTANQSIR N*VEIASHSGSCL*SMILTA*PATVA HAYNP |
| 3841 | 9338 | B | 4120 | 638 | 3862 | MKGTCVIAWLFSSLGLWRLAHPEA QGTTQCQRTEHPVISYKEIGPWLRE FRAKNAADFSQLTFDPGQKELVVG ARNYLFRLQLEDLSLIQAVEWECDE ATKKACYSKGKSKEECQNYIRVLL VGGDRLFTCGTNAFTPVCTNRSLSN LAEIHDQISGMARCPYSPQHNSAL LTAGGELYAATAMDFPGRDPAIYR SLGILPPLRTAQYNSKWLNEPNFVS SYDIGNFTYFFFRENA VEHDCGKTV FSRAARVCKNDIGGRFLLEDTWTF MKARLNC SRPGEVPFYYNELQSTFF LPELDLIYGIFTTNVNSIAASAVCVF NLSAIAQAFSGPFKYQENSRSAWLP YPNPNPHFQCGTV DQGLYVNLTER |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NLQDAQKFILVHEVVQPVTTPVPSFM EDNSRFSHVAVDVVQGREALVHIY LATDYGTIKKVRVPLNQTSSSCLLE EIELFPERRREPIRSLQILHSQSVLFV GLREHVVKIPLKRCQFYRTRSTCIG AQDPYCGWDVVMKKCTSLEESLS MTQWEQSIACPTRNLTVDGHFV WSPWTPCTHTDGS AVGSCLCRTRS CDSPAPQCGGWQCEGPGMEIANCS RNGGWTPWTSWSPCSTTCGIGFQV RQRSCSNPTPRHGGRVCVGNREE RYCNEHLLCPPHMFWTGWGPWER CTAQCGGGIQARRRICENGPD CAGC NVEYQSCNTNPCPELKKTPWTPW TPVNISDNGDHYEQRFRYTCKARL ADPNLLEVGRQRIEMRYCSSDGTSG CSTDGLSGDFLRAGRYSAHTVNGA WSAWTSWSQCSRDCSRGIRNRKRV CNNPEPKYGGMPCLGPSLEYQECN TLPCPDGVWSCWSPWTKSATCG GGHYMRTRSCSNPAPAYGGDICLG LHTEALCNTQPCPESWSEWSDWS ECEASGVQVRARQCILLFPMGSQCS GNTTESRPCVFDSNFIPEVSVARSSS VEEKRCGEFNMFMIAVGLSSSILG CLLTLLVYTYCQRYQQQSHDATVI HPVSPAPLNTSITNHINKLDKYDSVE AIKAFNKNNLILEERNKYFNPHLTG KTYSNAYFTDLNNYDEY* |
| 3842 | 9339 | A | 4121 | 3 | 124 | NVNRPVSSNEIKIIKSLPVKKSP*LN GFNAEFTKHVKNL |
| 3843 | 9340 | A | 4122 | 1 | 197 | GFKQLS*LSLPNSWDHRHTTTTPRE MGFHHVGQAGPELPISGDPPAPASQ SAGITGVSHRTRPRI |
| 3844 | 9341 | A | 4123 | 1 | 268 | QLYHLSLQSSRDHRCEPPRPANFLII CRDEVYVAQAGLKLPSSSDPPASAS KSAGSTGVSHCTQAKFYFF*NLMG EMRGKNNKHLTSFK |
| 3845 | 9342 | A | 4124 | 3 | 301 | TEEIHGVLSWNLVPDNYPPYYHPPP PSYTYGAQHLLRLFVKLPEILGKMT FSDKNLKALLKHFDLFLKHLAEYH DDFFPE*AYVAACEAHYCTHNPRSI |
| 3846 | 9343 | A | 4126 | 2 | 214 | FFFFKEMGSHYVA*AAVKWLFTGA IITL*SLKLLDSNNTPALSECKLIITQ EASVLKIKKVEIKKTKNRN |
| 3847 | 9344 | A | 4127 | 2 | 382 | TMVLSPADKTNVCAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLVT LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR |
| 3848 | 9345 | A | 4128 | 2 | 253 | |
| 3849 | 9346 | B | 4129 | 317 | 683 | AHKLRVDPVNFKLLSHCLLVTLAA HLPAEFTPAVHASLDKFLASVMHR ADLQIPLSWSLATGCQKLIIEVDDER KLRTFY* |
| 3850 | 9347 | A | 4130 | 1 | 82 | VDGWVDGWVDG*MDR*VGRWID |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GWVDG |
| 3851 | 9348 | A | 4131 | 1 | 240 | ASTFFFFSIDRVLLCCPGWTRTPGFI* SSCFGLPKCWDYRSEPPCLATFFFIK KKYKEEHFILILCQIVNMILILYQPT Q |
| 3852 | 9349 | A | 4132 | 3 | 180 | REPPLPAANFVFFVEMRSHHVRQA GPEPPSSDLPASASQSAGITGVHCH AWP*YTYL |
| 3853 | 9350 | A | 4133 | 2 | 238 | SPCAGILEDDRADYQGTRKTSEYSS VTP*EACHT*EGPIAFISWP*KVPIQL TFNERNRARGFQVPYGTYDRGLPG TH |
| 3854 | 9351 | A | 4134 | 7 | 259 | IVTAALFTLAPNQK*SKYPSSGKLIN KFWYIYKME*TSISNKQVSTTYSMQ AWVNLKSITLS*RHKGVIYII*SHLYD ILEKTEL |
| 3855 | 9352 | A | 4135 | 141 | 309 | AFDEAIAKLYSVNE*SYKGSTVIMQ LVRVNLAVSATSTGFIVSFVFTYPIIP CYLQ |
| 3856 | 9353 | A | 4136 | 113 | 205 | HNLLMLFDLCLLYWL*LIFLIHELAE NLLN |
| 3857 | 9354 | A | 4137 | 3 | 215 | FETGSCSVTQAGVHWRDHSSLQP*S LGFKQPSNLSLPSSWDYRCTPPHLA NLCIFCKDRVTSYCPGWHPV |
| 3858 | 9355 | A | 4138 | 3 | 386 | |
| 3859 | 9356 | A | 4139 | 1 | 255 | IRLMKEGRMKGQAFIGLPNEKAAA KALKEANGYVLF GKPMVVQFARSA RPKQDPKEG*RKKRTWLFNKVGK WELAPKPMGLDFSL |
| 3860 | 9357 | A | 4140 | 78 | 153 | |
| 3861 | 9358 | A | 4141 | 1 | 293 | LRLPGSSHSPASVS*VAGIAGACHH AWPNFCVFSRDQGFTHVGRAGLGA PDPLDPALPWSPKVMGFTRCEAHP CPSPRMRFLKYVSVPMVMVGRPE |
| 3862 | 9359 | A | 4142 | 3 | 48 | PLPRKSVEPGGGTKYKTEQKKRQE RRDRGSK*RKQQAATSEEQQRK* AKTQEDGGTKRSPDGEEDPEKKIHR NREGTRKKGQDPRNGVNNKNREK EQN*RTHTS*SQKVRRTRRGNEV |
| 3863 | 9360 | A | 4143 | 1 | 276 | GTRDSV*GGLKLIPFLMDFWKEPL GPALAHQLQYPGRD*SSDIWIRTA SLHTLPVGPHELLGLASFCITLLTPD PCQHVPRSRADTVEMG |
| 3864 | 9361 | A | 4144 | 1 | 154 | LVWS*EASKIPGGAEAAHPPTTF |
| 3865 | 9362 | A | 4145 | 2 | 231 | FFFESGSRSVTQAGVQ*HSLGSLQPL PPRFK*FSCLSLPSSWDYTHVPTSPA NFCIFSGDGVSSCWPGWSRTPNLR |
| 3866 | 9363 | A | 4146 | 1 | 303 | GTRGSVKEGAKYTSHRDMGLSTFD RDADQWKENCANVYG*GCRYNNC QAANLNGIYYPGGSYDPRNNSAYE TDNGVVWSFTGAHYSRAARMKI RPLVTQ |
| 3867 | 9364 | A | 4147 | 3 | 372 | HAGLGAHPLHHPVIOEGFLPAPRG FGYRSEVD*IRIPAESTGQNSQCQLR K*KDDSYFHCGYFCGCVCTCRGRL QSSTSHQCAAL*LLLPVCLTMLRC ISSLIYT*NLKTVHSVRLNFIYN |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3868 | 9365 | A | 4148 | 2 | 98 | RRPFFFFFFASCI*NLISPNVQLSNFT CILRN |
| 3869 | 9366 | A | 4149 | 1 | 230 | SGRPFLFFFQGKERVYFIPVVVLFYT VVVQ*LRKNVVRWQKTMEPPRSW LMQLGHTTEEGPGYPLLGETETKLFR TA |
| 3870 | 9367 | A | 4150 | 1034 | 2354 | DRV LAPVAQTGVQWHDLSSLQPPP PGFKRFFCLSLPSSWDYRRPP*RPAN FC*FLVETGFRHVGQAGLGLLTSGD PPASASQSSRITGVSHRARTMGLSR ALYRIPALKVWLLINVELKKQMMA HVDVTCLINKSPSLTRPMGKRLSAE TGKGQKEKQKQTGAGCAVLPSRGF PPKAHHGRQPLTLAPSPPPRTFSPSP PHTHTHTHTCSPICPRQSRSFQGPR MPDPDPGDATCGAGPGGSAPARAA GPRSAPRAKARVQARVQARAQAR WVRALTLLAAHPRLQVPARIARR AAQSSSSPPPATPAKSPPEASGAAA PPALGLERFPGASPNHLTRSTCALR HVGAGGAALGGPGAPRLPHRLEVG REEGRGRRGDGLGHGGCVEPAWEP GWRLPSTIKLFIKSKVSSEALEMPFL CICEHLLSYTYSRKHRNVI |
| 3871 | 9368 | A | 4151 | 387 | 478 | |
| 3872 | 9369 | A | 4152 | 757 | 1477 | HKENRNSLELRQNOSSPIWALPLHG LERKGLGRDHSSPHLPLLPSERL*K ASASQGPEWCCPSRAAGPESGRCD QLWESPMASATWKPYRPQPSRSPQ RQRVVLPLLVKGKTPPLFKLLQESV PGDLLPGELSL*PWEKPI*NNFAFNF SQQCKGMFKFPQFRSLARGSNPTSL TGVGPLPLPREFPGEEREGAPQIFKQ NTANGLGSA*MRAGTAQGCWES* GGNTAPGPGAVNTAN |
| 3873 | 9370 | A | 4153 | 32 | 255 | SRRHDSLHRVTFCISDPHYRKWTNP DGTTSKIFGFVAKKPASPWENVCHL FAKLDPY*PAGAIVTFITNVPTAP |
| 3874 | 9371 | A | 4154 | 1 | 265 | CDTVLLCHPGWSAVAQSQLTTTSA SQIKRFSCNLNPSSQNTRRASPHAN FFYF**R*GFTMLVRLVSNSCPQVIH PPLPPKVLGLQA |
| 3875 | 9372 | A | 4155 | 92 | 333 | FLSFFFF*MGCHSVTQCGVKWHDLS SLQPPHLTFKWFSRLSLLSGWDYRC LAQHQAACCIFSRDGISPF*PCWYQT PDLR |
| 3876 | 9373 | A | 4156 | 16 | 181 | ICSLPSTVDVIEFLDYVVKVSLKL*SI IKICDSKHTHIHTYGYVYIFSPPGK PV |
| 3877 | 9374 | A | 4157 | 1 | 355 | TVSLSCSVAQAGVQWHNLGSLQPL PPGFK*FSCLSLPSSWDHRCPPPCA NFCIFL*RWGFARFCHVGEAGLELL TSSDLHTSDSQSAGIIGTSHHAWPH LLVLTCVCAHTLFRHFYL |
| 3878 | 9375 | A | 4158 | 1 | 194 | FFFFFTISYIFYTLTTCWEFKQLAGN I/HL*GTVAFFYLKLLKLQDRLTNSF SSATTNVLAENS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3879 | 9376 | A | 4159 | 112 | 270 | ILGNSLFKNYK*YLSPA AVTHACNP NTLGGQGGPVT*AQEFETSLGNIVR PCL |
| 3880 | 9377 | A | 4160 | 1 | 211 | RFSCSLSS*DYRRVPPRAIFVFL VETRFHYVGQDGLDFLTSCSARLYL PKCRDYRRELLCPAPASLL |
| 3881 | 9378 | A | 4161 | 2 | 253 | ETDSCSVAQTRVQWYDLGSLQQPP PRFKRFSCSLSPNSWDYKCVPTPI* FFLFLVEMEFHCAGQADLELLGSGD PPASASPK |
| 3882 | 9379 | A | 4162 | 198 | 276 | KPFMAQCSF*TYEAFSCTSSEIRY |
| 3883 | 9380 | A | 4163 | 3 | 193 | HFGRPRRADCLRSSV*DQPGQHGET PSTKNTKISQAWWWVPVPTT*EA EAGESLEPGGQRLQ |
| 3884 | 9381 | A | 4164 | 2 | 515 | DTEKMSPWDMELIPNNAVFPEELG TRVPLTDGECKTLIYKPLDGEWGTN PRDEECERIVAGINQVMTLDIASTFV APVDLQAYPMYCTGVAYPTDLSSI KQRLNRFYRRVSSLMWEVRYIEH NTRTFNEP*KPNGRPAKSGTDLLH FIKDQTCYNIPLYNMCKKVL |
| 3885 | 9382 | A | 4165 | 3 | 418 | HEADKTNVVTGKTEVGAHAGEYG AQALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGKKVADALTNVTRIK EMRNALCTLSDLAHKLLGDSCTL *LLSHCMLVTLAN*PSSEFTPVAHTL VAKILAFVSTELTSKY |
| 3886 | 9383 | A | 4166 | 1 | 191 | CLETECRYVSQAGMQWHYPG*LQP *PPGYKLSSHLSPSSWDYRHVPEH PTNFVYFFVERKSH |
| 3887 | 9384 | A | 4167 | 3160 | 3732 | |
| 3888 | 9385 | A | 4168 | 2 | 326 | PRSGSESFSCQLSPFFFFGDRVSLC GPG*SAVV*LQLM*PGPPKLKQSSC LCLPSSWDHRWAAPHLA*FFKFFFI ETGSYHLPQLVSNPWAQASLLPWP PKVLGLQV |
| 3889 | 9386 | A | 4169 | 2 | 163 | LIFVFIVGTGFHHVGQAGLECLTSS DPSASASQSAGITGVNHHTRPSPAF GC*T*GTGFHHVGQAGLECLTSSDP SASASQSAGITGVNHHTRPSPAFGC |
| 3890 | 9387 | A | 4170 | 126 | 348 | HISIFETGSYSVTQAGAQLDHGSL QP*PPGLK*SSCLSLPSSWDYRHMP CPANFYIFCRDGVSPRCGSCNF |
| 3891 | 9388 | A | 4171 | 1659 | 1970 | MLKGGAKIRSRRKTGVSHSLHSDL NFFFFWDKSIASHRLEYNGAISAH CNLRLLGSSDSPASAS*VARITGMR HHTQLILVFFSRNGVLPCWPGWSRT PDLR |
| 3892 | 9389 | A | 4172 | 153 | 278 | MRPDTVAHTCNPSTLGGQGGRIT*T HEFETSLGDMMPYLYK |
| 3893 | 9390 | A | 4173 | 3 | 254 | LQYLVFISSKAWPS*KLEDGET*SA GENNNYNTIL*LDLFSHREGKWSKI PYV*AFFALQNNRKLCCQCIIDLALI AVISSQT |
| 3894 | 9391 | A | 4174 | 3 | 225 | SLTHLTATSILLK*FSCLGLPSSWDH RCPPPRLANFFAFLVETDFTMLARL V*NS*PEVIRSPRPSKVLGLRA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3895 | 9392 | A | 4175 | 1 | 344 | GGALSGGTPGFSPSPPGKTAAPGQS GNPPGGF*RVSPSGGSQRGGFPGNT PAPGPLPSSSSSSKGGFGDCTPRDKS RKGGKPPFS*GGFFPQGSAPVKHLA APTNRYSFHPQK |
| 3896 | 9393 | A | 4176 | 2 | 201 | QPGQYGKHPVLIKNSKIKPFWGDPP VVPNAREG*A*KMVEPGKVRVQSA QIKALEFNLGPKKKVPF |
| 3897 | 9394 | A | 4177 | 39 | 225 | KSIQSYAI*YNVTCGFFKSALNGVG SVAFCSHHAEHFLGFVFINHEKSQ FCQMLLLCMTR |
| 3898 | 9395 | A | 4178 | 322 | 451 | INSTDWAPWLTLVISALWEAEAA/G SRGQEIETILANTVKPRLY |
| 3899 | 9396 | A | 4179 | 234 | 383 | |
| 3900 | 9397 | A | 4180 | 86 | 216 | KQTLGQAWWLTPIIPALWEAEVGR S*DQEIETILPNTVKPHRY |
| 3901 | 9398 | A | 4181 | 1 | 4123 | MEEVEEDRFKENLEGALAGQLLGD EATQALQVLAVELDVVPGALHPQ RLHRLGAALVERQPVREVDHLVLP AVDDEHGRRLDGHLLDVREGVEA VGLLGVAEGDAHARGERRVQHHR GTLVARGQVHGGHRADALPVQDD AVRADAVPGGAGAGSAAASNARA PFPPAGVPGPSSGCDPPVSPLSQVSA HWELCGPHILNASYLPARVRKPFLV HWPGQRTLFLPAALAHPLGHEEFR QLCPQMSPPNFGLSESPRPVRCQCN PGQHRGWLRRWHPLPPAPSLGSG QVLGHLSTTSSHGAPSPPGHWCAA PDPADPAPVTRPPRAQSQARGTHLP PCPCRDPTTLLPHALGSDPRQTPSC KAGAWAGRSPQLPPGCHHSNERDT SPVEALGTLWPPPHGSGPRFLQDKG AAGQMAEQTEL RAGHGRMAKLRS HRASWASPPDLDAASPHLAPSAA SADGLPATRAQTPRPPPTPSRQAELP PGSPSPGAQGLPGGVDVGIEVPLGR PARAGTVAGGVVGEDVAVEAGAQ ANVEAAHLAQVHGIAVREEDRVPG TRHAANIHAGDTVAAGALGGEDLD GVQLALAVLEVGTLRQGFWWTLR GTDVETYPFSAPRAASHGVGRHEEL PDPTGPCGGRLSLTIHGVTIRYHAL LWARGPIMSKSQVLGEWEPVQGGK SENDKWTMSDPGAEAPTCSRAAS GVDKEQQGRWQGLWNSHIKPLKIR MVKQNNIIPGETQILLRFTGWESKV NAKKQLPVGIKCEPMDQENEQTGG HETDGHRIVSVLHFPLISILSYATW GLSLLECIPGSPVCTLLVRFSNVGTR WSLEVRGSPCGFGSNKVCVMTPEI KMVCVCEGKAGKAVGSGGVEGTK EVSTGNAEGPVRHEAVDGGVHLAF ALLQGLLWSLLGPPGLAGWGGGE LDAVPDSTSSATNVSMVVSAGPWS SEKAEMNILEINEKLRPQLAENKQQ FRNLKERCFLTQLAGFLANRQKKY KYEECKDLIKFMLRNERQFKEEKLA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; v=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | EQLKQAEELRQYKVLVHSQERELT QLREKLREGRDASRSLNEHLQALLT PDEPDKSQGQDLQEQLAEGLDWH STLSKSSAQKMTKMRMCMFK/CEE DEKVLESSAPREVQKAEESKVPEDS LEECAITCSNSHGPCDSIQPHKNKIT FEEDKVNSSLVVDRESSHDGCQ/EC SKHSPSPWPHLFCHKRQHGG/DQPA LCPARRQR*TF*KSMRNCA/HQLAE KKQQFRSLKEKCFVTQVACFLAKQ QNKYKYEECKDLIKSMLRNERQFK EEKLAEQLKQAEELRQYKVLVHSQ ERELTQLREKLREGRDASRSLNEHL QALLTPDEPDKSQGQDLQEQLAEG CRLAQHLVQKLSPENDEDEDVQ VEEDEKVLESSAPREVQKAEESKVP EDSLEECAITCSNSHGPCDSIQPHKN IKITFEEDKVNSSLVVDRESSHDGC QDALNILPVPGBTSSATNVSMVVS GPLSSEKAEMNILEINEKLCPQLAEK KKQQFRSLKEKCFVTQVACFLAKQ NKYKYEECKDLIKSMLRNERQFKE EKLAEQLKQAEELRQYKVLVHSQ REL TQLREKLREGRDASRSLNEHLQ ALLTPDEPDKSQGQDLQEQLAEGC RLAQHLVQKLSP |
| 3902 | 9399 | B | 4182 | 1 | 799 | MLQIPKQQQNEKYQVPQFDQSTIKN IESAKGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDADDTIYM FYQKVGDNISIDSWKNAGRVFKDSD KFDANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHGKQSLTTAQI HFPLISILSYATWGLSLLECIPGSPVC TLLVRFSNGGPPMDPGSERKGFCRF RNHHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHPGAQ YANRLSPRVGRFINAAGTTX* |
| 3903 | 9400 | A | 4183 | 260 | 387 | REVGRVRWLTVPVIPARWEAEVGRS *GQEIKTILANTVKPRLY |
| 3904 | 9401 | A | 4184 | 1212 | 1442 | |
| 3905 | 9402 | A | 4185 | 3844 | 4180 | KYKKCVGCGGRSL*S*LLRRLRQEN RLSPGGGDCSEPRSSHCTPAWVTER /GDSVSKKKKKNLLTWLVNKLCP CRAWWLTPVIPALWEAEAGRSRGQ EIETILANTVKPRLY |
| 3906 | 9403 | A | 4186 | 8 | 385 | |
| 3907 | 9404 | A | 4187 | 2 | 284 | |
| 3908 | 9405 | A | 4188 | 1477 | 1697 | |
| 3909 | 9406 | A | 4189 | 17 | 385 | |
| 3910 | 9407 | A | 4190 | 1 | 837 | GKVVLELERFLPQPFTGEIRGMCDF MNLSLADCLLVNLAYESSVFCTSIV AQDSRGHIYHGRNLDYAFGNVLRK LTVDVQFLKNGQIAFTGTTFIGYVG LWTGQSPHKFTVSGDERDKGWWW ENAI AALFRRHIPVSWLIRATLSESE NFEAAVGKLAKSPLIADVNYIAGG TCPREGVVVTRNRDGPDIGPLNPL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NGAWLRVETDYYHWKPAPKEDDR RTSA\IKALNATGQANLKLEALFQIL TVVPVYNNLTYYTTAMSAGSPYKY MTRIRNPS |
| 3911 | 9408 | A | 4191 | 653 | 727 | |
| 3912 | 9409 | A | 4192 | 26 | 161 | |
| 3913 | 9410 | A | 4193 | 3 | 186 | |
| 3914 | 9411 | A | 4194 | 28 | 186 | |
| 3915 | 9412 | A | 4195 | 356 | 428 | |
| 3916 | 9413 | C | 4196 | 35 | 430 | MKSCRXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXSETNSWEATRKNPFSSNSESASFIS RSQGHKDAKKEFVPLXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXLQSHPLVR* |
| 3917 | 9414 | A | 4197 | 213 | 394 | |
| 3918 | 9415 | A | 4198 | 28 | 123 | |
| 3919 | 9416 | A | 4199 | 1578 | 1835 | SNKSLPHNCIPPQMRNYSRGNLLQY IDYVQLHRNLYAGEIYFHC*RKSAL CNSSWREGAVGCLPMDFPRLHLSL SPSSLHCRNKP |
| 3920 | 9417 | A | 4200 | 213 | 305 | |
| 3921 | 9418 | A | 4201 | 1715 | 1850 | |
| 3922 | 9419 | A | 4202 | 4016 | 4315 | |
| 3923 | 9420 | A | 4203 | 28 | 239 | |
| 3924 | 9421 | A | 4204 | 7 | 216 | |
| 3925 | 9422 | A | 4205 | 1 | 576 | |
| 3926 | 9423 | A | 4206 | 1 | 500 | |
| 3927 | 9424 | A | 4207 | 1 | 1266 | |
| 3928 | 9425 | A | 4208 | 1 | 162 | |
| 3929 | 9426 | A | 4209 | 1 | 229 | |
| 3930 | 9427 | A | 4210 | 197 | 416 | |
| 3931 | 9428 | A | 4211 | 1 | 131 | |
| 3932 | 9429 | A | 4212 | 76 | 274 | |
| 3933 | 9430 | A | 4213 | 295 | 2530 | RPATMAARPLPVSPARALLLAG ALLAPCEARGVSLWNEGRADEVVS ASVRSGDLWIPVKSFDKSNHPEVLN IRLQRESKELIINLERNEGLIASSFTE THYLQDGTDVSLARNYTVILGHICY YHGHVIRGYSDSAVSLSTCSGLRGLI VFENESYVLEPMKSATNRYKLFPA KKLKSVRGSCGSHHNTPNLAANKV FPPPSQTWARRHKRETLKATKYVE LVIVADNREFQRQGDLEKVKQRLLI EIANHVDFKFRPLNIRIVLVGVEVW NDMDKCSVSQDPFTSLHEFLDWRK MKLLPRKSHDNAQLVSGVYFQGT IGMAPIMSMCTADQSGGIVMDHSD NPLGAAVTLAHELGHNFNMHDTL DRGCSCQMAVEKGGCINASTGYP FPMVFSSCSRKDLETSLEKGMGVCL FNLPEVRESFGGQKCGNRFVEEGEE CDCGEPEECMNRCNATTCTLKPD AVCAHGLCCEDCQLKPAGTACRDS SNSCDLPEFCTGASPHCPANVYLHD GHSCQDVGDCYNGICQTHEQQCV TLWGPGAKPAPGICFERVNSAGDPY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GNCCKVSKSSFAKCEMRDAKCGKI QCQGGASRPVIGTNAVSIETNIPLQQ GGRIICRGTHVYLGDDMPDPGLVL AGTKCADGKICLNRCQNISVFGV HECAMQCHGRGVCNNRKNCHCEA HWAPPFCDKFGFGGSTDSGPIRQAG KEARQEAAESNRERGQGV\EP LGSQ EHASTASLTLI |
| 3934 | 9431 | A | 4217 | 2 | 119 | |
| 3935 | 9432 | A | 4218 | 2 | 147 | |
| 3936 | 9433 | A | 4219 | 10 | 216 | |
| 3937 | 9434 | A | 4220 | 245 | 455 | |
| 3938 | 9435 | A | 4221 | 1 | 2867 | MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEESNQTGTSRWDG VSKKAPRHLSVPCTRPREARQEAE DSTSRLSAESGETDQDAGDVGPDI PDSYYGLLGTLPCQEALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTQLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIAK QAERVFPNSVICKTFHSMAYGHGR KYQSKKKLNLFKLTPFMVNSVLAE GKGGFIRAKLVCKTLENFFASADEE LTIDHVPIWCKNSQGQRMVEQSE KLNGVLEASRLWDNMRKLGECTEE AHQMTHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFSGFKRYVTAAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLPLPHFRVESFSE DEWNLLYVAVTRAKKRLIMTKSLE NILTLAGEYFLQAELTSNVLKTGV VRCCVG\QCNNALSPVDTVLTMK KL\PIY*ATGK\ENKGGYLCHSCAE QQHRDPWRFLTASPEQVRAMEPHF GGTSYCPRHEALLFLVF |
| 3939 | 9436 | A | 4222 | 57 | 302 | |
| 3940 | 9437 | A | 4223 | 1 | 550 | DAHIIGRIESYSCKMAGDDKHMFK QFCQEGQPHVLEALSPPQTSGLSPS RLSKSQGGEEGPLSDKCSRKTLFY LIATLNEFRPDYDFSTARSHFSRE PSLKLVLNAVNCSLFSVREDFKD LKPQLWNAVGRGDLPLKCDIYS\Y |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NPDLSDPSREDGSLWSFNFFYNK RLKRNRL |
| 3941 | 9438 | A | 4224 | 11 | 511 | GRTRSIAGEETTQRPGPNCGGNCLC LHTLAINMRICYSQTTPFHPLRLKG QRWPF\FSSLELFPVGFPRALLVQS TLPKPRPERAFTAPSLFPVTLGFCLG RILCQRLLLCPSCLATALSINGYSRT QECQSWKGRDTGLHKGKLLLEALG GTEGFGDRARAKIEDS |
| 3942 | 9439 | A | 4225 | 1 | 279 | |
| 3943 | 9440 | A | 4226 | 1011 | 1322 | |
| 3944 | 9441 | A | 4227 | 3 | 468 | TPLHVYNEVMSVGQKYGIRNAGYY ALRSLRIEKFFAFWGQDINNLT\TPL ECGRESRVKLEKGMDFIGRDALLQ QKQNGVYKRLTMFILDHDSDDL WPWWGEPIYRNGQYVGKTT\SAY SYSLEHVC LGFVHNFS EDTGEEQ VVTADFINRG |
| 3945 | 9442 | A | 4228 | 1 | 1236 | |
| 3946 | 9443 | B | 4229 | 1 | 1742 | MKRDNSGGCLPAPASAWPARPRQQ AEWRALTRGPANHCIIISTLGEPPE TPLIGLRTFQCCRLVTDGRVLAGTV SSEPTDGFRSPAPGPGRRTSAMVLL KLGKTPGEFFPFLGSSSQPPSHELNI GKRLDDTKILPGNMKDNFWEMGD TGPCGPCSEIHYDRIGGRDAAHLVN QDDPNVLEIWNLVFIQYNRFGNCVE LQASAAFNWNNQRCKTRNRYICQF ADLRRNLNIINDDITGRVHKDRKLL TGDSPFAANALGKLAAQEMMAAY AVSLPKLTALLRVFSTVRSIGERFS PIRVRLRLRHTTPNYIYQRLIPYVCV LPTTELSINLNMLTENDIPLFRALFL NNITDADARVLLQKRPREGWLTTD AFLYWAQQDFSGVKPLVAQHW EW MTFSADSVSSVHTLTDDLPLESLAD QPGAGNVHLLIPPEGLLYRSLTLPN AKYKLTAQTLQWLAETLPDNTQD WHWTVVDKQNESVEDCLIPFGKP QGKGCKLEKSVWAAGRPF SYAGDK NRQLTRYSDTRWHEDSVRNRWFSV MVGPSVRVNEWFSAYAMAGMAYS RVSTFSGDYLRVTDNKGS* |
| 3947 | 9444 | A | 4230 | 1 | 638 | |
| 3948 | 9445 | A | 4231 | 1377 | 1746 | |
| 3949 | 9446 | B | 4232 | 1 | 1716 | MSQYYQPQRPEHIELD SHAKFFPH HHLQVADSAAHLAASPLRRTHRAL TWAQALPQEEGSGAPSPPGAPSPTP KSFGR TMSASAVFILDVKGKMESC YVVQDVLNSWSPAIPLLQPPKVSDD SGGHIEECQCLPVYSFLYKTIEVGI LRILQGAGGGEHPDNFVIVYELLDE LMDFASRRPPTARSCRIHHS AEQQA GDGQVTGAPT VTNVSWRSEGIKS MQRQRPSENRNRYHQAQVFLSGMP ELRLGLNDRVSSSSLAAGQFKKSQ WPTVWRYLCLYPAMRLPQIQDQCG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; v=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QRQVCAGRNVVIWSIKSFPGGKEYL MRAHFGLPRWKRKRWRAGPPSGSS LDPLLHRLWDPGPIMKIEKSGYQA LPWVRTSPRVAIPTSYQLEGRRDGG LNTGFLTAPDADFRGRAGEEPAGR AGVSGWGAGTESSAAGCTAAAPRE GCSASARRLLRADSAAGLGRAGGFA GRQCRHAAGGGCAGDRLSGAAAR GDVQECAAFCTGSWCIPSTLQRQD GAAGFIVPPQSPFEGHDVWQHRHR PELLKQGASPNVQDTSQTVQSMTQ PALDSWTP* |
| 3950 | 9447 | A | 4233 | 1 | 372 | |
| 3951 | 9448 | B | 4234 | 48 | 1158 | MSASAVFILDVKGKPLISRNYKGDV AMSKIEHFMPLLVQREEEGALAPLL SHGQVHFLWIKHSNLYLVATTSKN ANASLVYSFLYKTIEVFCEYFKELE EESIRDNVVIVYELLDELMDFGFPQ TTDSKILQEYITQQSNKLETGKSRVP PTVTNAVSWRSEGIKYKKNEVFIDV IESVNLLVNANGSVLLSEIVGTIKLK VFLSGMPELRLGLNDRVLFELTGRS KNKSVELEDVKFHQCVRLSRFDND RTISFIPPDGDFELMSYRLSTHVKPLI WIESVIEKFSHSRVEIMVKAAGQFK KQSVANGVEISVPVPSDADSPRFKT SVGQRQVCAGEKRRYFGVLSLSGG AREYLMRAHFGLPKCEKERX* |
| 3952 | 9449 | B | 4235 | 153 | 458 | KKDLSLEEIQKKLEAAEERRKSHEA EVLKQLAEKREHEKEVLQKAIEEN NNFSKMAEEKLTHKMEANKENRE AQMAAKLERLREKDKHIEEVRKTK NPRPC* |
| 3953 | 9450 | A | 4236 | 3 | 182 | |
| 3954 | 9451 | A | 4237 | 49 | 607 | NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASGQAFELILS PRAKEFVPEFPLSPPKEEGFFPGGKF REN*EAAEERRQSP*SCSS*RQLAE KLRAPRKKCFQKAIEENNNFQ*NGQ KRKLTPHKMEANKETPERPQMAVA KLEPFAEEKDKAH*KKCGKNKESK DPADETEAGLI |
| 3955 | 9452 | A | 4238 | 1 | 356 | TELQQEQLQTVVGTYHGSPDQSHQ VTGNHQPPQNTGFPR/SNQPYYN SRGVSRGGSRGARGLMNGYRG PAN GFRGGYDGYRPSFSNTPNSGYTQSQ FSAPRDYSGYQRDGYQQNFIP |
| 3956 | 9453 | A | 4239 | 1 | 2206 | RLPPAFSSLSLRSEDALGHQPQRERS KSSGPPPPSGSSGSEAAAGAGAAAP ASQHPATGTGAVQTEAMKQILGVI DKKLRNLEKKKGKLDDYQERMNK GERLNQDQLDAVSKYQEV TNNLEF AKELQRSFMALSQDIQKTIKKTARR EQLMREEAEQKRLKTVLELQYVLD KLGDDDEVRTDLKQGLNGVPILSEE LSLLDEFYKLVDPERDMSLRRLNEQY EHASIHLDLLEGKEKPVC GTTYK VLKEIVERVFQSNYFDSTHNHQNGL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | CEEEEADSAPAVEDQVPEAEPEPAE EYTEQSEVESTYVNRQFMAETQFT SGEKEQVDEWTVETVEVVNSLQQQ PQAASPSVPEPHSLTPVAQADPLVR RQRVQDLMAQMGGPDNFIQDSML DFENQTLDPAlVSAQPMNPTQNMD MPQLVCPVHSESRLAQPNQVPVQP EATQVPLVSSTSEGYTASQPLYQPS HATEQRPQKEPIDQIQATISLNTDQT TASSSLPAASQPQVFQAGTSKPLHS SGINVNAAPFQSMQTVFNMNAPVP PVNEPEVTLKQIQNQSQASYNQSFSS \QSPS*QQTELQQ\EQLOTVVGVTY HGS\QDQSHQ\VTGNHQQ\PPQ\QNT GIST*AIRPYNSRGVSRGGSRGAR GLMNGYRGPANGFR\GGYDGLPAP SFLKLPSNGY/SHSPQFQCLPRDYL WPIQRDG/YIQQNFKRGSQSGPRG APRGRG\GPPRPNRGMPQMNTQQV K |
| 3957 | 9454 | A | 4240 | 1 | 151 | |
| 3958 | 9455 | A | 4241 | 5 | 120 | |
| 3959 | 9456 | A | 4242 | 1 | 315 | EQMVSEDVPC/D/HRVHARIIGSR/G KAIRKIMDEFKVDIRFPQSGAPDPN CVTVTGLPENVEEAIDHILNLEEEYL ADVVDSEALQVYMKPPAHEEAWP CPLRTCSTV |
| 3960 | 9457 | A | 4243 | 107 | 4057 | PFCCGFPGLCVGVIRSTMSSVAVLTQ ESFAEHRSGLVPPQIKVATLNSEES DPPTYKDAFPPLPEKAACLESAQEP AGAWGNKIRPIKASVITQVFHVPLE ERKYKDMNQFGEQAKICLEIMQ RTGAHLELSLAKDQGLSIMVSGKL DAVMKARKDIVARLQTQASATVAI PKEHHRFVIGKNGEKLQDLELKTAT KIQIPRPDDPSNQIKITGTKEGIEKAR HEVLLISAEQDKRAVERLEVEKAFH PFIAGPYNRLVGEIMQETGTRINIPPP SVNRTIVFTGEKEQLAQAVARIKK IYEEKKKKTTTIAVEVKKSQHKYVI GPKGNSLQEILERTGVSVEIPSDSIS ETVILRGEPEKLQALTEVYAKANS FTVSSVAAPSWLHRFIIIGKKGQNLA KITQQMPKVHIEFTEGEDKITLEGPT EDVNVAQEIEGMVKDLINRMDYV EINIDHKFHRHLIGKSGANINRIKDQ YKVSVRIPPDSEKSNLIRIEGDPQGV QQAKRELLELASRMENERTKDLIE QRFHRTIIGQKGERIREIRDKFPEVII NFPDPAQKSDIVQLRGPKNEVEKCT KYMQKMVADLVENSYSISVPIFKQF HKNIIGKGGANIKKIREESNTKIDLP AENSNSETIIITGKRANCEAARSRLS IQKDLANIAEVEVSIPAKLHNSLIGT KGRILRSIMEECGGVHIHFPVEGSGS DTVVIRGPSSDVEKAKKQLLHLAEE KQTKSFTVDIRAKPEYHKFLIGKGG GKIRKVRDSTGARVIFPAAEDKDQD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LITIIGKEDAVREAQKELEALIQNLD NVVEDSMLVDPKHHRHFVIRRGQV LREIAEEYGGVMVSFPRSGTQSDKV TLKGAKDCVEAAKKRIQEIIEDLEA QVTLECAIPQKFHRSVMGPKGSRIQ QITRDFSQIKFPDREENAVHSTEPV VQENGDEAGEGREAKDCDPGSPRR CDIIISGRKEKCEAAKEALEALVPV TIEVEVPFDLHRYVIGQKGSIRKM MDEFEVNIHVPAPELQSDIIAITGLA ANLDRAKAGLLERVKELQAEQEDR ALRSFKLSVTVDPKLHSPGLSGRK GASNSQI/RGLKHDVNIQFP\DKD\D ANQHQD\QITFTGYEKNHSSLPGDAI LRIVG\ELE\QMVSE\DVPLNHRVSR PASFGARGKSHPPKIMYEFK\DIRF PNKSGAPKTPNCVNC*RGFP\ENVE ESHSTQHPSILEEE\YL\ADVVDSEA LQ\VYMEPP/AHTEEAKGNFSRG\FD VRDAPL\TA\SSSEKAS\DMSSSEEFP SFWG*RWLPKTL\WGPKTIMIKKE QNPLPAC |
| 3961 | 9458 | A | 4244 | 11 | 323 | |
| 3962 | 9459 | A | 4245 | 3 | 171 | |
| 3963 | 9460 | B | 4246 | 148 | 405 | XKLSVERKDPLAALAREYGGSKRN ALLKWCQKKTQGYAKRNLLAFE AAESVGIKPSLELSEMLYTDRPDWQ SVMQYVAQIYKYFET* |
| 3964 | 9461 | A | 4247 | 2 | 438 | AVGGNGGCPRPSRVTSQSTCRFGPR TASHSASRAGLCTASR*VPGWV*CL HFQPLQMPTRDSSFSPDYSAPGRGC GQAGRCGAEHRRPGHRSSCC*NW* CQCShNLVSSSGTISVEHCAWNHRI PGPRLPEGLFFPH*VCFVVSM |
| 3965 | 9462 | A | 4248 | 3 | 256 | |
| 3966 | 9463 | A | 4249 | 3 | 444 | |
| 3967 | 9464 | A | 4250 | 3 | 828 | VKGVPGVKAERFE*RMTAKHCALS LVGEPIMYPEINRFLKLLHQCKISSF LVTNAQFPAEIRNLEPVTQLYVRVD ASTKDSLKKIDRPLFKDFWQRFLDS VKALAVKQQRVTYRLTLVKAWNV IESLQAYAQLGSLGNPDFIEVKGVT YCRESSASSLTMAHVPWHEEVVQF VRELVDLIPEYEIACEHEHSNCLLIA HRKFKIGGEWWTWIDYNRFQELIQ EYEDSGGSKTFSKDY MARTPHWA LFGASERGFDPKDTRHQRKNKSKAI SGC |
| 3968 | 9465 | A | 4251 | 1 | 384 | |
| 3969 | 9466 | A | 4252 | 3 | 1225 | |
| 3970 | 9467 | A | 4253 | 1 | 864 | |
| 3971 | 9468 | A | 4254 | 1 | 1266 | GNSPPSELKWKAKSEDLRHRGLKA QAEIKGSTQQIGFTTDPRMARSSPYP TDVARVVNAPIFHVNSDDPEAVMY VCKVAAEWRSTFHKDVVVDLV CY RRNGHNEMDEPMFTQPLMYKQIRK QKPV LQKYAELLVSQGVVNQPEYE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | CVSMHGVRNKPSYNSTKSSMDGLI LHPATGLVFVLSKQCEEIHQPVVWT CEQREAENATAEENRVLLAMVNPT VFFDIAVDG\EPLGRVSFEVGRAAA CGNGAQKVGRGRENFRCEPLERK GFGL*GVPCFHRLFPRVLCVQGGEL QQRHNGNWWASPILWGRKFERLK NFHP*KPYGSPGILSPWQNA GPQTQ MVPQFFICTAQDCSGWNGQAMWV FGTSERKAMNIVEAHWSRFG\SRIN GKTQQRSPFADCGQLLISLTCVFIF NHPDHSL |
| 3972 | 9469 | A | 4255 | 3 | 275 | |
| 3973 | 9470 | A | 4256 | 125 | 315 | |
| 3974 | 9471 | A | 4257 | 3 | 292 | |
| 3975 | 9472 | A | 4259 | 1 | 3045 | MDKFLNTYTLPRLKQEEVESLNRPI TGSDIEAII NSLPTKKKSRT RWHSRI LPEVQGGAEKEGILPNSFYEASIIIP KPASDTTKKENFRPISLMNINAKILN KILAKQIRQHIKKLIHHDQVGFIPGM HGLFNICKSVNIIQHINRTNDKNHMI ISIDAEKPFDKIQQHFM LKTLNKL A QNLLKLIGNFSKVSGYKINVQKSQA FLYTNNRQTESQIMNEFPFTIASKRI KYLGIQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCS\WEKTTLKFI W/NQKRAHIAKSIISQKNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWGKDSL FNKWCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLKSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYAAKKHMKK CSSSLVIREIQIKTTMRYHLTPVRMA IHKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS VWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVILLHVFWDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLP CSSAC RRPIVGLQLVMINS GN FQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDPLL TAPL GSTPQAAVCRGPRGRELRAAPADS HLFQRDLWPFNKVIVHGEKGSNQT SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENCGFSD PSDPQNLQKGEGCPSLVRASTAPPQ EKATEQPLLCKTTESPFGMTVGPCT DETLDHGAPSKHVPGT AHNELALL DLRVIKSAGSAAVHHKLKVLHWRS SLSNNKGTGRLYEQVA |
| 3976 | 9473 | A | 4260 | 1 | 2526 | |
| 3977 | 9474 | A | 4261 | 1 | 3111 | |

MISSING AT THE TIME OF PUBLICATION

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VDTIAADESFSQVDFGGRLMKDYG ACMSLLSVRVFFKKCPSIVQNFAVF PETMTGAESTSLVIARGTCIPNAEEV DVPIKLYCNGDGEWMVPIGRCTCK PGYEPENSVACKGPVNNTEKAKSG EMWFSPEEYGWYAAFLALRKCSQ CPEDAVAASGAVALENLMEHGHIR LDKASKDSESSTPHDPTLLFHSGPQP NFRHFQGWNTVTSEGLIHLPKSKT QSQCPGLFGGSLDSRIDIGGAWYFC HTHTASSASTPSEEAGSLADPSNETE SLLFACTALCSPWECQLLDLASLFQ GIMLMPRAVQFFKCWDKVTVRNQ WRMHSHGPSCLGVSFQKGLCQEM VYISTRGSSSLRPLVLSLHGWAVD TAIHTCIPFPTDIIWIQDLIAGLKDEW FDTHPGRRIGRPAQLCSSRSGVH |
| 3980 | 9477 | A | 4264 | 1 | 2653 | MGDFTPLSTLDRSMRQKVNKDIQ ELNSALHQADLIDIYRNHPESTEYT FFSAPHHTYSKIDHILGSKAPLSKYR RSEIKINCLSDHSAIKLELRIKKLTQ NRSTTWKLNNLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLWDTL KAVCRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTTHSKASRRQEIS KIRGELKEIETQKTLOKINESRGWFF EKINKIDRLLARLIKKKREKNQIHAI KNDKGDMSTNHTEIQTIREYYKHL YANKLENLKEIDKFLETYSLPRLNQ EEVESLNRPIGTSEIEAIIINSIPNKR S PGPDGFTAKFYQRYKEELLISNFSK VSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMKYLGIQPTRD MKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKNWKKT TLKFIWNQKRARIAKSILSQKNKAG GIMLPDFKLYYKATITKTAWYWYQ NRDIDQWNRTEPSEIMPHIYNHLIFD KPDKNKKWGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVPRPKTIKLEENPGNTIQDIGMG EDFMSKTPEAMATKAKIDKWDLIK LKSFCTAKETTIRLNRPPTWEKIFA IYSSDKGLISRIYNELQQIYEKKTNN PIKKWAKDMNRHLSKEDIYAAKRH MKKCASSLAIREIQIKTTMRYHLTP VRMAIKKSGNNRCWRGCGEIGTLL HCWWDCCLVQPLWKS VWRFLRDL ELEIPFDPAIPLLG IYPKDYKSCCYE DTCTHMFIVALFTIAKTWNQPKCPT MIDWIKKMWHIYTM EYYADIKKDE FMSFVRTRMKLETILSKISQVEKKT KHRMFSLIGGN |
| 3981 | 9478 | A | 4265 | 1 | 2988 | |
| 3982 | 9479 | A | 4266 | 1 | 2515 | MGDFTPLSTLDRSTRQKVNKDTQ ELNSAPHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHILGSKALLSEC KRTEIITNYLSDDSAIKLELRIKNLT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QNRSTTWKLNLLDDYWVHNEM KAEIKMFFETNENKDDTYQNLWDA FKAVCRGKFVALNAHKRKQGRSKI DTLTSQLELEKQEQTTHSKASRRQE ITKIRAELEKEIETQKTQKINESRSW FFERINKIDRQLARLIKKKREKNLID AIKNDKGDITTDPTETIQTIREYYKH LYANKLENLEEMDKFLDTYTLPR NQEEVESLNRPTGSEIVAINSLTTK KSPGPDGFTAIFYQRAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLENPIV SAQKLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASKRIK YLGILTRDVKDLFKENYKPLLKEI KEDTNKWKNIPCSWVGRINIVKMAI LPKVIYRFNAIPIKLPMTFFTELKKT TLNFIWNQKRAHIAKS/VLSQKNKA GGITLPDFKLYYKATVTKTAWYWY QNRDIDQWNRTEPSEIMPRIYNYLI FDKPEKNKQWGKDSL FNKWCWKN WLAICRKLKLDPFLTPYTKINSRWI KDLNIRPKTIKTLEENLGITIQDIGM GKDFMSKTPKAMATKAKIDKWDLI KLKSFCTAKETTNRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSSLAIREMOIKTTMRYH LTLVRMAIIKSGNNRCWRGRGEIG TLLHCWWDCCLVQSLWKS VWQFL RDLELEIPFDPAIPLL |
| 3983 | 9480 | B | 4267 | 1 | 2634 | MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQGDLIDIYRTLHPKSTEYI FFSAPHHTYSKIDHILGSKALLSKCK RTEIITNDLSDHSAIKLELRIKNLTQ NCATTQKLNNLLNDYWVHNEMK AEIKMFFETNENKDDTYQNLWDAF KAVCRGKFIALHAHKRKQERSKIDT LTSQLELEKQEQTTHSKASRRQEIT KIRAELEKEIETQKTQKINESRSWFF ERINKIDRLLARLIKKKREKNQIDAI KNDKGDITTDPTETIRTTVREYYKHL YANKLENLEEMDTFLDTYTLPRLN QEEVESLNRPTGAEIVAINSLPTKK SPGPDGFTAIFYQRFKGLRQNSTT FMPKTLNKLIGDGYLKIRAIYDKP TANIILNGQKLEAFPLKTGTRQGW LSPLLFNIVLEVLAIRQEKEIKGIQ LGKEEVKLSLFADDMIVYLENPIVS AQNLLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIASKR IKYLGILTRDVKDLFKENYKPLLK KIKEDTNKWKNIPCSWVGRINIVKM AILPKVIYRFHA IPIKLPMTFFTELEK TTLKFIWNQKRACIAKSILNQKNKA GGITLPDFKLYYKAIVTKTAWYWY QNRDIDQWIRTEPSETLHIYKYLIF DKPEKNKQWGKDSL FNK WY WEN WLAICRKLKLDPFLTPYTKINSRWI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KDLNIRPKTIKLEENLGFTIQDIGM GKNFMSKTPKAMATEAKIDKWDLI KLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPLKKWAKDMNRHFSKEDIYAA KKHMKKCSPLAIREMQIKTTMRY HLPVRMTIISQETTGADEDVEK* |
| 3984 | 9481 | A | 4268 | 1 | 2429 | |
| 3985 | 9482 | A | 4269 | 1 | 2745 | |
| 3986 | 9483 | A | 4270 | 1 | 3210 | MVKGSIQQEELTILNIYAPNTGALRF IKQVLRDLQRDLDSHTIUMGDFHTP LSTLDRSTRQKVNKDIQELNSALHQ EDLIDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEITNC LSDHSAIKLELRIKNLTQNRSTTWK LNNLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTFKA VCRGKF IALNAHKRKQERSKIDTLTSQKEL EKQEQTTHSKASRRQEITKIRAEKEI ETQKTLQNINESRSWFFERINKIDRP LARLIKKKREKNQIDAIKNDKGDIT TDPTEIQTIREYYKHL YANKLENL EEMDKFLNTYTLPTLNQEEVESLNR PITGAEIVAIINSLPTKKSPGPDGFTA EFYQRYKEELVPFLLKPFQSIEKEGI LPNSFYEASIIIPKPGRDTTKKENFR PISLMNIDAKILNKILAKRIQQHIKN LIHHDQVGFIPGMQGWFNIRKSINVI QHINRAKDKNHMIIISIDAEKAFDKI QQPFMLKTLNKLDDMIVYLENPIVS AQNLLKLISNFSKVSGYKINIQKSQA FLYTNNRQTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKV ENHKPLL EIKEDTNKWKNIPCSWVGRINIVKM AILPKVIYR/FNAIPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSERTPHIYNYL IFDKREKNKQWGKDSL FNKWCWE NWLAI CRKLKLDPFLTPYTKINSRW IKDLNVRPKTIKLEENLGFTIQDIG MGKDFISKTPKAMATKAKIDKWDL IKLKSFC TAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSPLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGCGEIG TLLHCWWDCKLVQPLWKAVWRFL RDLELEIPFDPAIPLLG IYPKDYKSC CYKDTCTRRKQLDCAEPVEPRKVG DGEWSLTKWTRPGSRALPWPPEQA KPYPPTLPTLAQDF |
| 3987 | 9484 | A | 4271 | 3 | 3655 | |
| 3988 | 9485 | A | 4272 | 1 | 3615 | |
| 3989 | 9486 | A | 4273 | 1 | 4038 | |
| 3990 | 9487 | A | 4274 | 1 | 3317 | MGDFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLQPKSTEYT FFSAPHHTYSKIDHIVGSKALLSKCK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RTEIITNYLSDHSAIKLELRIKNLTQS RSTTWKLNNLLNDYWVHNEMKA EIKMFFETNENKDDTTYQNLWDAFK AVCRGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTTHSKASRRQEITKI RAELKEIETQKTLOKINESRSWFFER INKIDRPLARLIKKKREKNQIDTIKN DKGDITTDPTIEIQTIREYYKHLA NKLENLDEMDFLHTYTLPRLNQE EVESLNGPITGAEIVAIIDSLPTKKSP GPDGFTAIFYQRYKEELVPFLKLF QSIEKEGILPNSFYEASIIIPKLGRDT TKKENFRPLSLMNIDAKILNKILAK RIQQHIKKLIHHDQVGFIPGMQGWFF NIRKSINVIQHINRGKDKNHMISID AEKAFDKIQPFMLKTLNKLIGDGT YFKIIRAIYDKPTANIILNGQKLEAFP LKTGTROGCPLSPLLFNIVLEVLAR AIRQEKEIKAQNLLKLISNFRKVSFY KINVQKSQAFLYTNNRQTESQIMRE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPCSWI GRINIVKMAILPKVIYRFNAIPIKLPT TFFTELEKTILKFIWNQKRAHIAKTI LSQKNKAGGIMLPDFKLYYKATVT KTAWYWYQKRDIDQWNRIELSEIIP HIYNHLIFDKPDKNKKWKGKDSVFN KRCWENWLAICRKLKLDFTLTPYT KINSRWIKDLHVRPKAIKTLEENLGI TIQDIGMGKDFTSKTPKAMATKAKI DKWDLIKLSFCTAKETTIRVNRQP TKWEKIFAIYSSDKGLISRIYKELKQ IYKKKTNNPIKKWAKDMNRHFSKE DIYAANRHMKKCSSSLAIREMQIKT TMRYHLTPVRKAIKKSGNNRCWR GCGEIGTLLHCWWDCCLVQPLWK TVWQFLRDLELEIPFYPAIPLGIYP KDYKSCCYKDTCTRMFIAALFTIAK TWNQPKCPTMIDWIKKMWHIYTM EYYAAIKNDEFMSFVGTWMKLEIII LSKLSQEQTCKHGFSLIGGN |
| 3991 | 9488 | A | 4275 | 959 | 2955 | |
| 3992 | 9489 | A | 4276 | 1 | 2870 | MKAIEIKMFFDTSSENKDDTTYWNLW DAFKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTTHSKASRR QEITKIRAELEIETQKTLOKINESRS WFFERINKIDRPLARLIKKKREKNQI DAIKNDKGDITTDPTIEIQTIREYYK HLYANKLENLEEMDFLDTYTLPR LNQEEVESLNRPTGSEIVAIINSLPT KKSPGPDGFTAIFYQSWAETQPKK ENFRPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFFNIRK SINVTQHINRAKDKNHMISIDAEKA FDKIQPFMLKTLNKLIGDGTYFKII RAIYDNPTANIILNGQKLEAFPLKTG TROGCPLSPLLFNIVLEVLARAIRQE KEIKGIQLGKEEVKLSLFADNMIVY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LENPIVSAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSQLP FTIASKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSGVEG RINIVKMAILPKNWKKTTLKFIWNQ KRARIAKSILSQKNKAGGITLPDFKL YYKATATKTAWYQNRDLQW NRTEPSEITPHIYNLIFDKPDKNKQ WGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNIRPKTI KTLEENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKQESFCTAK ETTIRVNRQPTKWEKIFATYSSDKG LISRIYSELKQIYKKKTNNPIKKWAK DMNRHFSKEDIYAAKKHMKKCPSS LAIREMQIKTTMRYHLTPVRMAIHK KSGNNRCWRGCGEIGTLLHCWWD CKLVQPLWKS VWRFLRDLELEIPFD PAIPLLG IHPKDYKSCCYNDTCTRM FIAALFTIAKTWNQPKCPTIIDWIKK MWHIYTMEYYAAIKNDEFVSFVGT WMKLEIILSKLSQEQTTHRIFSLIG GN |
| 3993 | 9490 | A | 4277 | 1 | 2982 | |
| 3994 | 9491 | A | 4278 | 1614 | 4577 | TEPKTKTT*LSQ*MQKKPLTKFSNPS C*KLSIN/IVLEVLARAIHQEKEIKGI QLGKEEVKLSL FADDMIVYLENPIV SAQNLLKLISNFSKVSGYKIN VQKS QAFLYTNNRQTESQIMSELPFTTAS KRIKYLGIQLTRDVKDLFKENYKQL LKEIKEDTSKWKNIPCSWVGRINIV KMAILPKVIYRFNAIPIKLPMPFFTE LEKTTLKFIWNQKRACIAKSILSQK NKAGGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPHIYN YLIFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLD PFLTPYTKINS RWIKDLNVRPKTIKTLEENLGIIQDI GMGKDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPRKW EKIFATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKEDIY AAKKHMKKCSPSLAIREMQIKTTM RYHLTPVRMAIHKSGNNRCWRGC GEIGTLLHCWWDCKLVQPLWNSV WRFLRDLELEIPFDPAIPLLG IYPND YKSCCYKDTCTRM TITSVEEKSQSE KLSYIFLKEKICLMYVGLLNILVSL GKVPFWLYLGSRLATPPTSSQLFFIG GKERSPDEQGV DILIVLIFRYPSTDS AEQIKKKIEKALYQSLKTKQLSLTN KPSFRLTRCGIRMTSSNMPLPASSST QRIVQGRETAMEGEWPWQASLQLI GSGHQCGASLISNTWLLTAAHCFW KNKDPTQWLATFGATITPPAVKRN RKIILHENYHRETNENDIALVQLSTG VEFSNIVQRVCLPDSSIKLPKTSVF VTGFGSIVDDGPIQNTLRQARVETIS |

MISSING AT THE TIME OF PUBLICATION

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LPCLMIPSQMLLENFSAAPGHRCW THMLDNGSAVSTNMTPKALLTISIP PGPNQGP HQCRRFRQPQWQLDPN ATATSWSEADTEPCVDGWVYDRSV FTSTIVAKWDLVCSSQGLKPLSQSIF MSGILVGSFTWGLLSYRFGKPMLS WCCLQLAVAGTSTIFAPTFVIYCGL RFVAAF GMAGIFLSSLTLMVEWTTT SRRAVTMTVVGCASFAGQAALGGL AFALRDWRTLQLAASVPFFAISLIS WWLPESARWLIK GKPDQALQELR KVARINGHKEAKNLTETPPPPPIPI PSPTAPPLSTPTITFTAITPSPAPPIS LTPQPPSLQNISTTFTTIVTIGNSTIIN STHTVTSITHHLHLHVARTHLMGVL DVSGETECVYLKVLMSVKEEVAS AKEPRSVLDLFCVPVLRWRSCAML VVKYAVLGRDLTSSLARSFSLISY YGLVFDLQSLGRDIFLLQALFGAVD FLGRATTALLSFLGRRTIQAGSQA MAGLAILANMLVPQDLQTLRVVFA VLGKGCFGISLTCLTIYKAELFTPV RMTADGILHTVGR LGAMMGPLILM SRQALPLLPLLYGVISIASSLVVLF LPET\QGLPLPDTIQDLESQKSTAAQ GNRQEAVTVESTSL |
| 4009 | 9506 | A | 4293 | 3672 | 3967 | LQPPPHGRRGLLHHLSPGHGPHHPP VTPQTRSPAQP/PGQMGPRAPLGCC LPPPPRPPTCRREK*TTETRFSPCWR TRPWGPGPPRPLSRGGPLPCAPA |
| 4010 | 9507 | A | 4294 | 1773 | 2213 | AHWLHLPRLP HHRAQWAAALQPG PAGWGWSWQPQLCSAGRLLCHGAI GRP/LSIFCWTWDLGASSCGHPAAR SMMASGV TWTSRGMGEKRV SSTPF PIFFPAASPPPSRLPNC PFCHRTLAE RAQHLASVRPGLHLSSPTCCMKCSC |
| 4011 | 9508 | A | 4295 | 1 | 616 | |
| 4012 | 9509 | A | 4296 | 93 | 502 | EERKRPHLGAWWENRKCFFSFQPD FKAAECRETVARPSLSIPQDCLSVSL ADTNQLCLEVRLARGVCRRRAHLS PPVCIQSPLSQGH*LLCSK*SASIIGA GLANFQGTDSLVAEHPVSWIHN SN FVFHPGYFRL |
| 4013 | 9510 | A | 4297 | 1537 | 2360 | TCCTNVVWGAPPHRDSRVSDRVHS QKSRRACYGQRNKRPGG*G*ILISA KKQLLSPRR*LKVWPMRSASLQSM PLASPSVCP PGLLFLWP*QALLPS DCG/PLSLTRL SR*GG\PPRPHWCSR FRWLCARVLL |
| 4014 | 9511 | A | 4298 | 1 | 493 | MEAPAE LLAALPALATALALLAW LLVRRGAAASPEPARAPPEPAPPAE ATGAPAPSRPCAPEPAASPAGPEEP GEPAGLGELGEPAGPGEPEGP GDPA AAPAEAE/PGGGGEAGTHRGRGP LPTPGAPAAAAVPRRARERGRGLQ PRLPPGSAEPAARRKCR |
| 4015 | 9512 | A | 4299 | 2 | 418 | |
| 4016 | 9513 | A | 4300 | 8808 | 9100 | RKVLFFFFFEMKSRSA\RLGCSGTI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SAHCNLCCLPGSSDSPASASRVAGMT GAHNHIQLIFVFLVGMGFHHVGQA GLELLT*VIHPPQSPKVLGLQV |
| 4017 | 9514 | A | 4301 | 3 | 101 | |
| 4018 | 9515 | C | 4302 | 5673 | 5894 | MWQLTPAILALGEIEAGGLFEPRRV KLA WPAQEELVSTKNTKISWVWW RAPVVPATQEA EVGGSLELERSRLQ * |
| 4019 | 9516 | A | 4303 | 1 | 241 | |
| 4020 | 9517 | A | 4304 | 58 | 180 | |
| 4021 | 9518 | A | 4305 | 2 | 325 | FFFFFFFFFETESLSVTQAGEPGHD LGSLEPPPPRFKQFSCLSLPSS\WIYR HVPPCPANFFFFLVETGFHHVGQAG LKLLTSNDPPASASQSSGIRGVSHLT RLVS |
| 4022 | 9519 | A | 4306 | 206 | 386 | |
| 4023 | 9520 | A | 4307 | 2 | 260 | |
| 4024 | 9521 | A | 4308 | 5 | 227 | |
| 4025 | 9522 | A | 4309 | 676 | 1076 | FLLCFPPCLSPKFFLFLGKIYSQSN WCVIVNWRIELGWMFNKICDSKIIF SLGSFLCKIKAHWGLWKSPTTSFQE RSPFFSSLFRAMRAKPSRSM/RLFF ELLVKSLPVASPV EPLSVIAEQSSQI CPCHGI |
| 4026 | 9523 | A | 4310 | 3 | 205 | |
| 4027 | 9524 | A | 4311 | 3 | 345 | |
| 4028 | 9525 | A | 4312 | 118 | 7473 | |
| 4029 | 9526 | A | 4313 | 1 | 297 | |
| 4030 | 9527 | A | 4314 | 366 | 504 | |
| 4031 | 9528 | A | 4315 | 1 | 2899 | MDAPKAGYAFEYLIETLNDSSHKKF FDVSKLGTKYDVL PYSIRVLEAAV RNCDFGLMKKEDVMNILDWKTQ SNVEVPFFPARVLLQDFTGIPAMVD FAAMREAVKTLGGDPEKVHPACPT DLTVDSLQIDFSKCAIQNAPNPGG GDLQKAGKLSPLKVQPKKLPCRQ TTCRGSCDSGELGRNSGTFSSQIENT PILCPFHLQPVPEPETVLKNQEV EFG RNRERLQFFKWSSRVLKNVAVIPPG TGMAHQINLEYLSRVVFEEKDLLFP DSVVGTD SHITMVNGLGILGWGVG GIETEAVMLGLPVSLTLPEVVGCEL TGSSNPVTSIDVVLGITKHLRQVG VAGKFVEFFGSGVSQLSIVDRTTIA NMCPEYGAILSFFPVDNVT LKHLEH TGFSKAKLESMETYLKAVKLFRND QNSSGEPEYSQVIQINLNSIVPSVSG PKRPQDRVAVTDMKSDFQACLNEK VGFKGFQIAAEKQKDIVSIHYEGSE YKLSHGSVVIAAVISCTNNCNPSVM LAAGLLAKKAVEAGLRVKPYIRTSL SPGSGMVTHYLSSSGVLPYLSKLG EIVGYGCSTCVGNTAPLSDAVLNA VKQGD LVTCGNFIWKKNFEGRLC DCVRANYLASPPLVVAYAIAGTVNI DFQTEPLGTDPTGKNIYLHDIWPSR EEVHRVEEEHVILSMFKALKDKIEM |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GNKRWNSLEAPDSVLPWDLKSTY IRCPSFFDKLTKEPIALQAIENAHVL LYLGDSVTTDHISPAGSIARNSAAA KYL TNRGLTPREFNSYGARRGND VMTRGTFANIKLFNKF IGKPAPKTIH FPSGQTL DVFEAAELYQKEGIPLIL AGKKY GSGNSRDWAAKGPYLLGV KAVLAESYEKIHKDH LIGIGIAPLQF LPGENADSLGLSGRETFSLTFPEELS PGUTLNIQTSTGKVFSVIASFEDDV EITL\YKHG\GLLN FV\ARKFS |
| 4032 | 9529 | A | 4316 | 1 | 178 | |
| 4033 | 9530 | A | 4317 | 165 | 403 | PSSRSRAPSPPTLTCGASCCPTCPAC FPAPSR RAGAAGGAG*RPRGGPTST TCYGPTETWLYQLQTVGSRNTTRT PKST |
| 4034 | 9531 | A | 4318 | 3 | 404 | |
| 4035 | 9532 | A | 4319 | 3 | 217 | |
| 4036 | 9533 | A | 4320 | 3 | 423 | SFFIHRTKGKGPLMSSSFKKLYFSLT TEALSFAKTPS/CQGQGC DKTRSRV TLQEWNDPLDHDLEAQLIYRHLLG VEAMLWERHRELSGGAEAGTMPTS PGKVPEDSLARLLRVLQDLREAHSS SPAGSPSEPNCLELQ |
| 4037 | 9534 | A | 4321 | 2 | 3040 | DPGVWLPPSRDPAMAKRSSLYIRIV EGKNLPAKDITGSSDPYCIVKVDNE PIIRTATVWKTLC PFWGEEYQVHLP PTFHAVAFYVMDEDALSRDDVIGK VCLTRDTIASHPKGFSGW AHLTEVD PDEEVQGEIHLRLEVWPGARACRL RCSVLEARDLAPKDRNGTSDPFVR VRYKGR TRET SIVKKSCYPRWNETF EFELQEGAMEALCVEAWDWDLV RNDFLGKVVIDVQRLRVVQ QEEGW FRLQPDQSKSRRHDEGNLGS LQLEV RLRDET VLPSSYYQPLVHLLCHEVK LGMQGP GQLIPLIEETTSTECRQDV ATNLLKLFLGQGLAKDFLDLLFQLE LSRTSETNTLFRSNSLASKSMESFLK VAGMQYLHGV LGPIINKVFEEKKY VELDPSKVEVKDVGCSGLHRPQTE AEVLEQSAQTLRAHLGALLSALSRS VRACPAVV RATFRQLFRRVRERFPG AQHENVPFIAVTSFLCLRFFSPAIMS PKLFHLRERHADARTSRTLLLLAKA VQNVGNMDTPASRAKEAWMEPLQ PTVRQGV AQLKDFITKLVDIEEKDE LDLQRTL SL*APPVKEGPLFIHRTKG KGPLMSSSFKKLYFSLTTEALSFAK MPSSKKSALIKLANIRAAEKVEEKS FGGSHVMQVIYTDDAGR PQTAYLQ C/KGV PFCVRVQSHWEK**YQGHQI YLAGSGIPTSVAKGPAAAEIQTPAS WAPTIPVPSVGTSGAAATKKTRQC VNELNQWLSALRKVSINNTGLLGS YHPGVFRGDKWSCCHQKEKTD TDF RSVPQTGVQWRDLGSLQSPPRVK QFSCNLNPSSWDDRHSPPSLANFFV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | F*LEMGFHHVSQAALVLLLLLLLLL FDTESRSIIQAGVQWCNLGSLQSPFP RLG*FSCLSLPSTTGASHCTQLSQGC DKTRSRVTLQEWNDPLDHDLEAQL TYRHLLGVEAMLWERHRELSSGGTE AGTVPTSPGKVPEDSLARLLRVLQD LREAHSSSPAGSPSEPNCLELQT |
| 4038 | 9535 | A | 4322 | 308 | 658 | |
| 4039 | 9536 | A | 4323 | 1 | 2662 | MAKRSSLYIRIVEGKNLPAKDITGSS DPYCIKVDNEPIIRYRPHQDRGA LSLSSARALPAKGATVWKTLCPF WGEEYQVHLPPTFHAVAFYVMDE DALSRDDVIGKVCLTRDTIASHPKG FSGWAHLTEVDPDEEVQGEIHLRLE VWPGARACRLRCVLEARDLAPKD RNGTSDPFVRVRYKGRTRETSIVKK SCYPRWNETFEFELQEGAMEALCV EAWDWDLVSRNDFLGKVVIDVQR LRVVQQUEEGWFRLQPDQSKSRRHD EGNLGSLQLEVRLRDETLPSSYYQ PLVHLLCHEVKLGMOGPGQLIPLIE ETTSTECRQDVATNLLKLFLGQGLA KDFLDLLFQLELSRTSETNTLFRSNS LASKSMESFLKFALHVYLAPSWAD TAGKRCKGGCREKVGSWSGTGGD RINVTCGGPQVAGMQYLHGVLGPII NKVFEEKKYVELDPSKVEVKDVGC SGLHRPQTEAEVLEQSAQTLRAHLG ALLSALSRSVRACPAVVRATFRQLF RRVRERFPGAQHENVPFIAVTSFLC LRFFSPAIMSPKLFHLRERHADARTS RTLALLAKAVQNVGNMDTPASRAK EAWMEPLQPTVRQGV AQLKDFITK LVDIEEKDELDLQRTLSLQAPPVKE GPLFIHRTKKGKPLMSSSFKKLYFSL TTEALSFAKTPSSKKSALIKLANIRA AEKVEEKSFGGSHVMQVIYTDAG RPQTAYLQCKCVNELNQWLSALRK VSINNTGLLGSYHPGVFRGDKWSC CHQI*ITGQG\CDKTRVTG*PCREW NDLLDRDLESQLIYRHLLGVEAML WERHRELSSGGAAGTVPTKPLAKV PEDSLARLAPGCLQDLREAHSSSPA GSPSEPNLASLEAADVRPALRSPC |
| 4040 | 9537 | A | 4324 | 69 | 194 | |
| 4041 | 9538 | A | 4325 | 1350 | 2203 | TWRLDPQIISSPKPQPGGTYTLEV KSSKSKKVLSPHP*WPPLRLWQR\G GSPEGGTQAPDGLPPPPRPKSERV GSPKLSGGKR/EGSHPGGPPHITHP/ DGEEKAKSSWFGLREAKDPTQKPS PHPVKPLSAAPVEGSPDRKQSRSSL SIALSSGLEKLKTVTSGSIQPVTAQAP QAGQMVDTKRLKDSAVLDQSAKY YHLTHDELISLLLQRERELSQRDEH VQELESYIDRLLVIMETSPTLLQIPP GPPK |
| 4042 | 9539 | A | 4326 | 2 | 761 | |
| 4043 | 9540 | A | 4327 | 2 | 410 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4044 | 9541 | A | 4328 | 295 | 780 | |
| 4045 | 9542 | A | 4329 | 1 | 2203 | |
| 4046 | 9543 | A | 4330 | 1 | 190 | RFIMLVRLVFNS*PQ/CDPPASASQS AGITGMSHRARPELSVLTQGFRNW AFRLLLQCHSPDFF |
| 4047 | 9544 | A | 4331 | 2 | 269 | |
| 4048 | 9545 | A | 4332 | 3 | 223 | DFEPSLQHCSSKLCRNILRASSCHSS WGRM*FPGSV*PTWKI*REESCEWS RTAINPKYKILLHGFVVRTVWR |
| 4049 | 9546 | A | 4333 | 2 | 366 | PCSEPPTRRSGATPSHPGGCGAKL CRNILRASSCHSSWGRM*FPGSV*P TWKI*REESCEWSCTAINPSTRSCCT VCGTNCLEETPTTCPSTRGLQCGRG LTRATGNCPRNDGLTLLSLN |
| 4050 | 9547 | A | 4334 | 3 | 131 | |
| 4051 | 9548 | A | 4335 | 923 | 1442 | GGPCLCRPSWPAVLQVRSGLPTSIPS PWPLFCLPQSILLGPLEMPG*RPLLQ RPFYRMSLRTCQRRVRCWTWSVRC RTAWHTRVFLKLPDTFTNDSSTTGF *AKPSALLSTGWS*WATA/CGGGA AALLATMLRAAYPAGQVLRLLPSP PAPGAKLCRNILRASSCHSSWGRM |
| 4052 | 9549 | A | 4336 | 1 | 137 | |
| 4053 | 9550 | A | 4337 | 876 | 1012 | |
| 4054 | 9551 | A | 4338 | 148 | 278 | |
| 4055 | 9552 | B | 4339 | 7 | 673 | MVEVTILMIMGLYRIYGFAVAVVS MILSYNVCSEGEVVSVMFSFVVTSS SCGMHRSTLLSSVYSHLIFDSA YVIN NVADALSRGFSMHCMHCDNLKTC HTSHGSVMAETA VINHKKRKNPRI VQSNDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHVAKY AEIFGLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPWFIKX * |
| 4056 | 9553 | A | 4340 | 786 | 1088 | |
| 4057 | 9554 | A | 4342 | 1 | 66 | |
| 4058 | 9555 | A | 4343 | 2 | 80 | |
| 4059 | 9556 | A | 4344 | 8 | 258 | |
| 4060 | 9557 | A | 4345 | 5 | 383 | |
| 4061 | 9558 | A | 4346 | 99 | 634 | TTTMSSKRTKTKTKKRPQRATSN VFAMFDQSQIQEFKEAFNMIDQNR DGFIDKEDLHDMLASLGK\NPTDAY LDAMMNEAPGPINFMTFLTMFGEK LNGTDPEDVIRNAFACFDEEAVGTI QEDYLRELLTTMGDRFTDEEVDEL YREAPY*QKGGISNYIEFTRILTGRP PKHKDD |
| 4062 | 9559 | A | 4347 | 1 | 966 | |
| 4063 | 9560 | A | 4348 | 3 | 215 | |
| 4064 | 9561 | A | 4349 | 1 | 1416 | NSGGSGGGTSGSGSSSGQGKMGQS QSGGHGPGGGKKDDEDKKKKYEPP VPTRVGKKKKKTKGPDAASKLPLV TPHTQCRLKLLKLERIKDYLLMEEE FIRNQEOMKPLEEKQEEERSKVDDL RGTPMSVGTLEEIIDDNHAIVSTSVG SEHYVSILSFVDKDLLEPGCSVLLN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HKVHAVIGVLMDDTDPLVTVMKV EKAPQETYADIGGLDNQIQEIKESV ELPLTHPEYYEEMGIKPPKGVHPFG PTWPRVKTLAKAVANQTSASFLR WVGVELIQKYLGDGPKLVRELFV A\EEHAPSIVFIDEIDAIGTKRY\DSN SGGE\REFHRTNVGN*LEPVGMGFD SRG\DV\KVFPWATNR\ETLADPAL\N RPGRI\DR\KNEFPLPDEKTKKRIFI HTSRMTLADDVTLADDLIHGLKIDLS GAD\KAIC\TEAGL\MGL*GERRMK VTNEDFKKSKENVLYKKQEGTPEG LYL |
| 4065 | 9562 | A | 4350 | 2 | 70 | |
| 4066 | 9563 | A | 4351 | 1 | 1605 | |
| 4067 | 9564 | A | 4352 | 3 | 193 | |
| 4068 | 9565 | A | 4353 | 3 | 127 | LFHPCQDSQQHH*CVCCRLTGHGA A*VHGPCQAVQTYRASH |
| 4069 | 9566 | A | 4354 | 2 | 323 | |
| 4070 | 9567 | A | 4355 | 3 | 85 | |
| 4071 | 9568 | A | 4356 | 49 | 413 | |
| 4072 | 9569 | A | 4357 | 3 | 338 | |
| 4073 | 9570 | A | 4358 | 1 | 3735 | |
| 4074 | 9571 | A | 4359 | 2 | 317 | |
| 4075 | 9572 | B | 4360 | 2576 | 2685 | MDGKNSSGSKRYNRKRELSYPKNE SFNNQSRSSSQSKTFNKMPQRG GGSSKLFSSSFNGGRRDEVAEAQRA EFSPAQFSGPKKINLNHLLNFTFEPR GQTGHFEGSGHGSWGKRKNWGHK PFNKELFLQANCQFVVSSEDQDYTA HFADPDTLVNWDVFEQVRICSHEV PSCPICLYPPTAAKITRCGHIFCWAC ILHYLSLSEKTWSKCPICYSSVHKK DLKSVVATESHQYVVGDTITMQLM KREKGV LVALPKSKWMNVDHPIHL GDEQHSQYSKLLLASKEQVLHRVV LEEKVALEQQLAEKHTPESCFIEA AIQELKTREEALSGLAGSRREVTGV VAALEQLVLMAPLAKESVFQPRKG VLEYLSAFDEETTEVCSLDTPSRPLA LPLVEEEEAVSEPEPEGLPEACDDLE LADDNLKEGTICTESSQQEPITKSGF TRLSSSPCYFYFYQAEDGQHMFLHP VNVRCLVREYGSLEERSPEKISATVV ELAGYSMSEDVRQRHRYLSHLPLTC EFSICELALQPPVVSKEITLMEFSDDI EKRRQRQRQKKAREERRRERRRIEIE NKKQGKCPEVHIPLNLQQFPFAFKF LYLLLFEKPRKETGKNVAMKAENR CRRRPPPALNAMSLGPRRARSAPTA VAAEAPVDAAELPQRRRHRLRHGQ EQRLQQLLRLFGQQQRATAAPLRL GGASRRV* |
| 4076 | 9573 | A | 4361 | 3 | 93 | |
| 4077 | 9574 | A | 4362 | 1 | 289 | VGNPQQEVQNIFKAKHPMDTEVTK AKIIGFGSALLEEVDPNPANFVGAGI IHTKTTQIGCLVRLEPNLQAQMYRL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | T/LRTSKEAVSQRLCELLSAQF |
| 4078 | 9575 | A | 4363 | 1 | 275 | |
| 4079 | 9576 | A | 4364 | 2 | 2803 | RGLAVFISDIRNCKSKEAEIKRINKE LANIRSKFKGDKALDGYSKKKYVC KLLFIFLLGHDIDFGHMEAVNLLSS NRYTEKQIGYLFISVLVNSNSELIRLI NNAIKNDLASRNPTFMGLALHCIA VGSREMAEAFAGEIPKVLVAGDTM DSVKQSAALCLRLRYRTSPDLVPM GDWTSRVVHLLNDQHLGVVTAAT SLITTLAQKNPEEFKTSVSLAVSRLS RIVTSASTDLQDYTYFVPAPWLSV KLLRLLQCYPPDPAPVRGRLTECLE TILNKAQEPPKSKKVQHSNAKNAV LFEAISLIHHHDSEPNLLVRACNQLG QFLQHRETNLRYLALESMTLASSE FSHEAVKTHIETVINALKTERDVS RQRAVDLLYAMCDRSNAPQIVAEM LSYLETADYSIREEIVLKVAILAEKY AVDYTWYVDLILNLIRIAGDYVSEE VWYRVIQIVINRDDVQGYAAKTVF EALQAPACHENLVKVGGYLGEFG NLIAGDPRSSPLIQFHLHLSKFHLCS VPTRALLSTYIKFVNLFPVKPTIQ DVLRSDSQLRNADVELQQRAVEYL RLSTVASTDILATVLEEMPPFERES SILAKLKKKKGPSTVTDLEDTKRDR SVDVNGGPEPAPASTSAVSTPSPSA DLLGLGAAPPAPAGPPPSSGGSGLL VDVFSDSASVVAPLAPGSEDNFARF VCKNNGVLFENQLLQIGLKSEFRQN LGRMFIFYGNKTSTQFLNFTPTLICS DDLQPNLNLQTKPVDPTVEGGAQV QQVVNIECVSDFTEAPVLNIQVHGS GGTFQNVSLQLPITLNKFFQPTVEK FCQDFFQRWKQTSNPQQEVHNIFK AKHPMDTEFTK\AKIIGFGSELLAE VDPNPANFVGAG\IHTKTTQ\GCP LRL*PNLQAQMY\RLTLRTSKEAVS\ Q\RLCELLSAQF |
| 4080 | 9577 | A | 4365 | 2 | 231 | |
| 4081 | 9578 | A | 4366 | 1 | 224 | |
| 4082 | 9579 | A | 4373 | 131 | 381 | |
| 4083 | 9580 | A | 4374 | 93 | 449 | |
| 4084 | 9581 | A | 4375 | 11 | 594 | |
| 4085 | 9582 | A | 4376 | 1 | 1410 | |
| 4086 | 9583 | A | 4377 | 1 | 66 | |
| 4087 | 9584 | A | 4378 | 1 | 553 | RRGPLSQNGSFGPSVSGGECSPPLT VEPPVRPLSATLNRDMRSEFGSV DGPLPHPRWSAEASGKPSPSDPGSG TATMMNS\SS*GSSPTRVLDEGMQT VLQEPEVPSVPSITSLAERPVAVNM APKGPPFPFPGVPLMSTPMGGPVPPPI RYGPPPQLCGPFGPRALPPFPGPM RPPLCLRE |
| 4088 | 9585 | A | 4379 | 1 | 3589 | AFLSKVEEDDYPSEELLEDENAINA KRSKEKNPGNQGRQFDVNLQVPDR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AVLGTIHPDPEIEESKQETSMILDSE KTSETAAKGVNTGGREPNTMVEKE RPLADKKAQRPFERSDFSISIKIQT ELGEVFQNKDSYDLKNDNPEEHLK TSGLAGEPGELSKEDEHGNTKYM GTESQGSAAAEPEDDSFHWTPHTSV EPGHSDKREDLLISSFFKEQQSLQR FQKYFNVHELEALLQEMSSKLKSA QQESLPYNMEKVLDKVFRASESQIL SIAEKMLDTRVAENRDLGMNENNI FEEAAVLDDIQDLIFVRYKHSTAE ETATLVMAPPLEEGLGGAMEEMQP LHEDNFSREKTAELNVQVPEEPHL DQRVIGDTHASEVSQKPNTKDLDP GPVTTEDTPMDAIDANKQPETAEE PASVTPLNAILLIYSFMFYLTSLV ATLPDDVQPGPDFYGLPWKPVFITA FLGIASFALWRTVLVVKDRVYQV TEQQISEKLKTKMKNTELQKLSN YEQKIKESKKHVQETRKQNMILSDE AIKYKDKIKTLEKNQEILDDTAKNL RVMLESEREQNVKNQDLISENKKSI EKLKDVISMNASEFSEVQIALNEAK LSEKVKSECHRVQEEENARLKKKK EQLQOEIEDWSKLHAELSEQIKSFE KSQKDLEVALTHKDDNINALTNCIT QLNLECESESEGQNKGGNDSDEL ANGEVGGDRNEKMKNQIKQMMDV SRTQTAISVVEEDLKLQLKLRSV STKCNLEDQVKLEDDRNSLQAAK AGLEDECKTLRQKVEILNELYQQKE MALQKKLSQEEYERQEREHRLSAA DEKAVSAAEEVKTYKRRIEMEDE LQKTERSFKNQIATHEKKAHENWL KARAAERAIAEEKREAANLRHKLL ELTQKMAMLQEEPVIVKPMMPGKPN TQNPPRRGPLSQNGSFGSPVSGGE CSPPLTVEPPVRPLSATLNRRDMPR SEFGSVDGPLPHPRWSAEASGKPSP SDPGSGTATMMNSSSRGSSPTRVL DEGK\VNMGPKGAPSPKEFPLMS TPMGGPVPPPIRYGPPQLCGPFGP RHLPPPFPGMRPPLGLREFAPGVP PGRDPLPHPRGFLPGHAPFRPLGS LGPREFYFIPGTRLPPPTHGPQEYPPP PAVRDLLPSGSRDEPPPASQSTSQD CSQALKQSP |
| 4089 | 9586 | A | 4380 | 3 | 148 | |
| 4090 | 9587 | A | 4381 | 1885 | 2826 | CLQEAIMDGTETIAVSPRSLHSELMC PICLDMLKNTIGSA*ASVPLTDHSG L PFSYPRNKECPTCRKKLVSKRSLRP DPNFDALISKIYPSREEYEAHQDRV LIRLSRLDRGGTLGGGTGPPSPPGA PSPPEPGDPYLQSSSEALWL*ACPP SHSRVYVKTGNATVDHLSKYLALRI ALERRQQQEAGEPGGPGGGASDTG GPDGCGGEGGGAGGGDGPEEPALP SLFHLLQLSSLFSPLSLLPPPQTLNGS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LTLELVNSPRRPLPRQGLTLRALSLP GSPQHPGKLLTGGCALGFSTPATLH TGKQPYVCAT |
| 4091 | 9588 | A | 4382 | 2 | 456 | DRGGTLGGGTLGPPSPPGAPSPPEP GGDPYLQSSSEALWL*ACPPSHSRY VKTTGNATVDHLSKYLALRIALERR QQQEAGEPGGPGGGASDTGGPDGC GGEGGGAGGGDGPEEPALPSLFHLL QLSSLFSPLSLLPPPQTLNGSLTLEL V |
| 4092 | 9589 | A | 4383 | 58 | 1262 | CLQEAIMDGTEIAVSPRSLHSELMC PICLDMLKNTMTTKECLHRFCSDCI VTALRSGNKECPTCRKKLVSKRSLR PDPNFDALISKIYPSREEYEAHQDRV LIRLSRLHNQQALSSSIEEGLRMQA MHRAQRVRRPIPGSDQTTMSGGE GEPGEGEGDGEDVSSDSAPDSAPGP APKRPRGGGAGGSSVGTGGGGTGG VGGGAGSEDSGDRGGTLGGGTLP PSPPGAPSPPEPGGEIELVFRPHLLV EKGEYCQTRYVKTTGNATVDHLSK YLALRIALERRQQQEAGEPGGPGG GASNTEELNVCGGEGGGAGGGDG\ PKEPALPSLEGVSEKQYTTYIAPGG GAFTTL\NGSLTLELVNEKFWKVS RPLELCYAPHPRIQSDPHPGDKPEE RGPLG |
| 4093 | 9590 | A | 4384 | 3 | 221 | |
| 4094 | 9591 | A | 4386 | 2 | 271 | |
| 4095 | 9592 | A | 4387 | 54 | 990 | HSIMMKIPWGSIPVLMLLLLGLIDI SQAQLSCTGPPAIPGIPGTPGPDG QPGTPGIKGEKGLPGLAGDHGEFGE KGDWPWPGNPGKVGPKGPMGPKGG PGAPG\APGPKG\DSGDYKATQKIAF SATRTINVP/LLRRSQTNIRFRPCITN MNTNYE\PRSGKFTLQGCPLY*FN LSTPSSRG\NLCVNLMRGRERAQE/ VWVTFCDYCLTNTPGSPQGGNGP QLKKAPKGGGGGEKKTVPAGPPN KNFTYWGMGGCPTAIFSGFLAFFQI WGLTCGLASHPTPAPPAQQRSLYP QQQPYDQAKCTQ |
| 4096 | 9593 | A | 4388 | 3 | 493 | |
| 4097 | 9594 | B | 4389 | 272 | 2158 | MGPLMVLFCLFLYPGLADSAPSCP QNVNISGGTFTLSHGWAPGSLLTYS CPQGLYPSPASRLCKSSGQWQTPGA TRSLSKAVCKPVRCPAPVSFENGIY TPRLGSYPVGGNVSFECEDGFILRG SPVRQCRPNGMWDGETAVCDNGA GHCPNPGISLGAVRTGFRFGHGDV RYRCSSNLVLTGSSERECQNGVW SGTEPICRQPYSYDFPEDVAPALGTS FSHMLGATNPTQKTKEGLGRKIQI RSGHLNLYLLDCSQSVSENDFLIF KESASLMVDRIFSFEINVSVAITFAS EPKVLMSVLNDNSRDMTEVISSLEN ANYKDHENGTTGTNTYAALNSVYL MMNNQMRLLGMEITMAWQEIRHAI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ILLTDGKSNMGGSPKTAVDHIREIL NINQKRNDYLDIYAIGVGKLDVDW RELNELGSKKDGERHAFILQDTKAL HQVFEHMLDVSKLTDTCGVGNMS ANASDQERTPWHVTIKPKSQETCR GALISDQWVLTAAHCFRDGNDHSL WRVNVGDPKSQWGKEFLIEKAAS PGFDVFAKKNQGILEFYGDDIALLK LAQKVKMSTHARPICLPCTMEANL ALRRPQGSTCRDHENELLNKQSVL CTFWSPLNKSKPKI* |
| 4098 | 9595 | A | 4390 | 2 | 201 | |
| 4099 | 9596 | A | 4391 | 1 | 130 | |
| 4100 | 9597 | A | 4392 | 2 | 215 | |
| 4101 | 9598 | A | 4393 | 3 | 300 | |
| 4102 | 9599 | A | 4394 | 3 | 310 | |
| 4103 | 9600 | A | 4395 | 2 | 228 | |
| 4104 | 9601 | A | 4396 | 2 | 448 | PRVRKDAVRDGLRAVKNAIDDGCV V/PGAGAVEVAMAEALNKYKLSVK GKAQLGVQAFADALLVIPKVLAQN SGFDLQETLVKI*AEHSESGQLVGV DLNTGEPVVAEAGIWDNDCVKK QLLHSCTVIATNILLVDEIMRAGMS SLKG |
| 4105 | 9602 | A | 4397 | 2 | 100 | |
| 4106 | 9603 | A | 4398 | 3 | 174 | |
| 4107 | 9604 | A | 4399 | 1 | 147 | |
| 4108 | 9605 | A | 4400 | 1 | 104 | |
| 4109 | 9606 | A | 4401 | 153 | 480 | TTLKQQFSFMSYKAVKLKVFLIMSC YPRNPSHFP*CGA/WVMCPLRVGSE RRLCPFMATS/QSLSNKFHNRKIFMS REIKFRNLLKKNETQLMYLQIFRW YTKQRLFLF |
| 4110 | 9607 | A | 4402 | 1 | 186 | |
| 4111 | 9608 | A | 4403 | 3 | 478 | |
| 4112 | 9609 | B | 4404 | 56 | 390 | XAAVYVQPFLDKSGLEKYLYPASAA APFPLLYPGIPAAAAAFPCLSVLSP PPEKAGAAAATLLPHEVAPLGAPHP QHPHGRTHLPFAGPREPGNPESQAQ EDPSQPGKEAP* |
| 4113 | 9610 | A | 4405 | 2 | 485 | |
| 4114 | 9611 | A | 4406 | 105 | 183 | |
| 4115 | 9612 | A | 4407 | 1 | 1560 | MLRKKEKANYRLLAERTRKRPRKA SAELQRKHYPMLRGHLRLFLPGRL RPLPSNPRLAFPAERGGGHCGPMR HFPVSTQERGTADPVHPASPLPPNQ APNAGHSPTPRSPNTSSPRRRRRR PESGWGRPGGGFTSILRPDSPLPTRV QYGTERKRRGQSSRDAFSARRQSV GGGANWEGGGAKRARRGTGPAG WRAEGGGAACRG SARASPAFRGRG PLPPFASGRVPGRQCGLRQWLQEK LLGPSDHLSCFQMPGTSVCDCAACL RACTEKPCDSNMWDSQAPWTGLK TRLTYRIFTINDLRQDWRDYFEK YGKIETIEVMEDRQSGKKRGFAFVT FDDHDTVVDKIVGRGGGSGNFMGRG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; * =Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GNFGGGGGNFGRRGGNFGGRGGYG GGGGGSRGSYGGGDGGYNGFGGD GGNYGGGPGYSSRGGYGGGGPGY GNQGGGYGG/G/GGGYDGYNEGNN FGGGNYGGGGNYNDFGNYSGLQQ QS\NYGPMKGGSLGG\RSSGSPYGG GYGSG\G\GSGGYGSRRF |
| 4116 | 9613 | A | 4408 | 2 | 370 | |
| 4117 | 9614 | A | 4409 | 1 | 159 | |
| 4118 | 9615 | A | 4410 | 3 | 261 | |
| 4119 | 9616 | A | 4411 | 1 | 8748 | |
| 4120 | 9617 | A | 4412 | 1 | 2176 | |
| 4121 | 9618 | A | 4413 | 37 | 441 | |
| 4122 | 9619 | A | 4414 | 1 | 1940 | PVLRHAVWLKSEGKSSFGLCAPLR KGSFLQKSWIFRPVMADKLTRIAI VNHDKCKPKKCRQECKKSCPVVR MGKLCIEVTPQSKIAWISETLCIGCG ICIKKCPFGALSIVNLPSNLEKETTH RYCANAFKLHRLPIPRPGEVLGLVG TNGIGKSAALKILAGKQKPNLGKY DDPPDWQEILTYFRGSELQNYFTKI LEDDLKAIKPQYVDQIPKAAKGT GSILDRKDETKTQAIVCQQLDLTHL KERNVEDLSGGELQRFACAVVCIQ KADIFMFDEPSSYLDVKQRLKAAITI RSLINPDRYIIVVEHDLVLDYLSDFI CCLYGVPSAYGVVTMPFSVREGINI FLDGYVPTENLFRDASLVFKVAET ANEEEVKKMCMYKYPGMKKKMG EFELAIVAGEFTDSEIMVMMLGENG MGKTTFIRMLAGRLEPDEEGEVPVL NVSYKLQKISPKSTGSRVQLLREKIR DAYTHPQFVTNVMKPLQIENIIDQE VQTLSSGGELQRVTLAL*LGQNLDP VYL\DEPPA\YLDSEQLMAARVV KRFIPHAKKTA\FVVGWTWTFIMATY LADRIVVFD\GVPSTKNTVANSPQT LLAGMKNKFLSQLEITFRDPNNYRP RINKLNSIKDVEQKKSGN\YFFLDD |
| 4123 | 9620 | A | 4415 | 1 | 122 | |
| 4124 | 9621 | A | 4416 | 2 | 1382 | |
| 4125 | 9622 | A | 4417 | 135 | 282 | |
| 4126 | 9623 | A | 4418 | 2 | 1652 | |
| 4127 | 9624 | A | 4419 | 3 | 279 | |
| 4128 | 9625 | A | 4420 | 8 | 353 | |
| 4129 | 9626 | A | 4421 | 1 | 1542 | |
| 4130 | 9627 | A | 4422 | 1 | 496 | |
| 4131 | 9628 | A | 4423 | 70 | 365 | |
| 4132 | 9629 | A | 4424 | 1 | 3771 | |
| 4133 | 9630 | A | 4425 | 2 | 285 | |
| 4134 | 9631 | A | 4426 | 1 | 724 | |
| 4135 | 9632 | A | 4427 | 58 | 197 | |
| 4136 | 9633 | A | 4428 | 640 | 813 | |
| 4137 | 9634 | A | 4429 | 3 | 268 | |
| 4138 | 9635 | A | 4430 | 1 | 1512 | |
| 4139 | 9636 | A | 4431 | 3 | 1625 | |
| 4140 | 9637 | A | 4432 | 1 | 330 | GKTITLEVEPSDTIENVKAKIQDKEG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | IPPDQQRLIFAGKQLEDGRTLSDYNI QKESTLHLVLRLRGGIKYNCDKMI CRKCYARLHPRAVNCRKKKCGHT NNLRPKKKVK |
| 4141 | 9638 | A | 4433 | 2 | 544 | DPRLLQFFFFLSSLLQRGDRAGWW RRFFGTQTCRVFVKTLTGKNLHPL RYETQ*HPLKNVQKPKISRTKEGIP PDQAAS**FAGK\QLEDGRTLSDY NIQKESTRAPWLLRLR\GGIIEPFSPP GLPKKYN\CDKMI\CRKCYAR/LFHP RCLSTCRK\KKCGSHQTTLRPQRRR SNKGGFFP |
| 4142 | 9639 | A | 4434 | 385 | 499 | |
| 4143 | 9640 | A | 4435 | 2 | 127 | |
| 4144 | 9641 | A | 4436 | 3 | 424 | |
| 4145 | 9642 | A | 4437 | 1 | 110 | |
| 4146 | 9643 | A | 4438 | 1 | 110 | |
| 4147 | 9644 | A | 4439 | 1 | 110 | |
| 4148 | 9645 | A | 4440 | 1 | 110 | |
| 4149 | 9646 | A | 4441 | 1 | 108 | |
| 4150 | 9647 | A | 4442 | 3429 | 7466 | |
| 4151 | 9648 | A | 4443 | 4048 | 4181 | |
| 4152 | 9649 | A | 4444 | 682 | 829 | |
| 4153 | 9650 | A | 4445 | 163 | 320 | EFEGFNPLKLGEAGWARWLTPVIPAL *ETEAGGSRGQEIETILANTVKPHLY |
| 4154 | 9651 | A | 4446 | 1122 | 1446 | |
| 4155 | 9652 | B | 4447 | 124 | 27844 | XRSTVPPRISAYERPVPWPGEWNDP RGPGRRASAVVSPREGNWGVLRDP RLQARKPRMVRSRQMCNTNMSVP TDGAVTTSQIPASEQETLVRPKPLL KLLKSVGAQKDTYTMKEVLFYLGQ YIMTKRLYDEKQOHIVYCSNDLLG DLFGVPSFSVKEHRKIYTMIRNLV VVNQESSDSGTSVSENCHLEGGS DQKDLVQELQEEKPSSSHLVSRPST SSRRRAISETTEENSDELSEGERQKRH KSDSISLSFDESLALCVIREICCERSS SSESTGTPSNPDLDAGVSEHSGDWL DQDSVSDQFSVEFEVESLDESDYSL SEEGQELSDDEDDEVYQVTYQAGE SDTDSFEEDPEISLADYWKCTSCNE MNPPLPSHCNRCWALRENWLPEDK GKDKGEISEKAKLENSTQAEFGDV PDCKKTIVNDSRESCVEENDDKITQ ASQSQESDYSPSTSSSIYSSQEDV KEFEREETQDKEESVESSLPLNAIEP CVICQGRPKNGCIVHGKTGHLMAC FTCAKKLKKRNKPCPVLTGHIRTEQ PIILPKKHKKKKERKSLPEEDVAVS SNVFDFTLTKKKVYLNKLERKSV FKGFQGMGQHWTFINLDKPSNPS SHEVVAWIRRLRVEKTGHSGTLDP KVTGCLIVCIERATRLVKSQQSAGK EYVGIVRLHNAIEGGTQLSRALET TGALFQRPPLIAAVKRQLRVRTIYES KMIEYDPERRLGIFWVSCEADTYSR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TLCVHLGLLLGVGGMQELRRVRS GVMSEKDHMTMHDVLDLDAQWLY DNHKDESYLRRVVYPLEKLLTSHK RLVMKDSAVNAICYGAKIMLPGLVI RYEDGIEVNQEIVVITTKGEAICMV EHDKEFFHPRYHHREFRFDLSKIPE GEAVTAAEFRIYKDYIRERFDNETF RISVYQGIGSLPARQPYLWASEEGW LVFDITATSNHWVNNPRHNLGLQL SVETLDGQTNPKLGLGRHGPQN KQPFMVAFFKATEVHFRSIRSTGSK QRSQNRSKTPKNQEALGWPTMCTD ELSFGLDVLTLQSLFEKRTAAGTRG RPCCKKHELTVSFRDLGWQDWIAP GYARYYCEGECAPPLNSYMNATNH AIVQTLVHFNPETVPKPCCAPTQLN AISVLYFDDSSNVILKKYRNMVVRA CGCH* |
| 4156 | 9653 | A | 4448 | 2 | 129 | |
| 4157 | 9654 | B | 4449 | 1 | 462 | MSQQYYVRLCQIQSPSRVSGREN LVVGDFPDPTLKRVRKGRGCAHCG LTDLPEPTAQVLVEQGQDEALWFH NVISEEFGVGVNIFWKHLPSECYDK TDTYGNKDPTAASRAAQILDRAK TLAELPEEYRDFYARRMVLHIQDK AYSKNSE* |
| 4158 | 9655 | A | 4450 | 3 | 366 | |
| 4159 | 9656 | A | 4451 | 1 | 167 | |
| 4160 | 9657 | A | 4452 | 2 | 382 | TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPFHDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKLVRDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR |
| 4161 | 9658 | A | 4453 | 2 | 252 | |
| 4162 | 9659 | B | 4454 | 31 | 449 | MVLSPADKTNVKAAWGKTYFPFH DLSPGSAQVKGHGKKVADALTNA VAHVDDNAQRAVRPKRPCTRSTFG WTRSNFKLLSHCLLVTLAAHLPAEF NPCGARLPGQVPGFCYAPC* |
| 4163 | 9660 | A | 4455 | 2 | 81 | |
| 4164 | 9661 | A | 4456 | 2 | 81 | |
| 4165 | 9662 | A | 4457 | 3 | 452 | |
| 4166 | 9663 | A | 4458 | 1 | 493 | RPRIRHEHRLRENPPWFLFPAAKTN VKAGLG*G*GSHPPSNVAKTLERIM FLSFPTTKTYFPQLRTLSHGFSQV* GPRSRRLPDALTKRPWRHVDDHAQ TRCPALSDLHAHKLVRDPVNFKLL SHCLLVTLAAHLPAEFTPAVHAYL DKFLASVSTVLTSKYR |
| 4167 | 9664 | B | 4459 | 208 | 420 | MGNPKVKAHGKKVLTSLGDAIKHL DDLKGTFAQLSELHCDKLHVDPEN FKLLGNVLVTSLAIHFGIEFTPE* |
| 4168 | 9665 | A | 4460 | 40 | 534 | SRRHGSVSHREAKATIASLWGKVN VEDAGGETMIRLLLVVYPWPQRSF ASFSSLFSAIMGNPKVKAHGGK VLTSLGDAIKHLDDLKGTFAQLSEL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; V=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HCDKLHVDPENFKLLGNVLVTVLA IHFGKEFTPEVQA\SWQKMVTIGV ANA\SSTYHLNSLPMMQNf |
| 4169 | 9666 | A | 4461 | 2 | 171 | |
| 4170 | 9667 | B | 4462 | 10 | 351 | MAPRTLVL LLSGALALTQTWAGSH SMRYFYTSVSRPGRGEPRFLAVGYV DDTQFVRFDSDAASQRMEPRAPWI EQEGPEYWDRNTRNVKAHSQTDR VDLGTLRGYRVCVSHSL* |
| 4171 | 9668 | A | 4463 | 1 | 986 | |
| 4172 | 9669 | A | 4464 | 3 | 1282 | |
| 4173 | 9670 | A | 4465 | 1 | 1004 | MAVMAPRTLLLLLLLGALALTQTWA GSHSMRYFTTSVSRPGRGEPRFLAV GYVDDTQFVRFDSDAASQRMEPRA PWIEQEGPEYWDRNTRNVKAHSQI DRV DLT LR GYYNQSEAGSHTIQM MYGCDVGSDGRFLRGYQQDAYDG KDYIALNEDLRSWTAADMAAQITQ RKWEAARVAEQLRAYLEGTCVEW LRRHLENGKETLQRTDPPRTHMT HAVSDHEATLRCWALSFP AEITLT WQRDGEDQTH TCHVQHEGLPKPL TLRWEPSSQPTIPVGIAGLVLF GAV ITGA VVA VMWR RKSS DRKGGSYS QAASSDSAQGSDVSLTACKV |
| 4174 | 9671 | A | 4466 | 1090 | 2175 | |
| 4175 | 9672 | A | 4467 | 1 | 780 | |
| 4176 | 9673 | A | 4468 | 59 | 169 | |
| 4177 | 9674 | A | 4469 | 89 | 134 | |
| 4178 | 9675 | A | 4470 | 864 | 1885 | |
| 4179 | 9676 | A | 4471 | 89 | 176 | |
| 4180 | 9677 | A | 4472 | 1 | 1127 | |
| 4181 | 9678 | A | 4473 | 1 | 405 | |
| 4182 | 9679 | A | 4474 | 3 | 199 | |
| 4183 | 9680 | A | 4475 | 3 | 607 | |
| 4184 | 9681 | A | 4476 | 1017 | 2029 | |
| 4185 | 9682 | A | 4477 | 844 | 1572 | |
| 4186 | 9683 | A | 4478 | 1 | 846 | |
| 4187 | 9684 | A | 4479 | 452 | 1220 | |
| 4188 | 9685 | A | 4480 | 1 | 1254 | |
| 4189 | 9686 | A | 4481 | 1 | 1383 | |
| 4190 | 9687 | A | 4482 | 1 | 1290 | |
| 4191 | 9688 | A | 4483 | 666 | 1606 | |
| 4192 | 9689 | A | 4484 | 1 | 1236 | |
| 4193 | 9690 | A | 4485 | 1 | 1269 | |
| 4194 | 9691 | A | 4486 | 719 | 1175 | |
| 4195 | 9692 | A | 4487 | 1 | 1182 | |
| 4196 | 9693 | A | 4488 | 1 | 1377 | |
| 4197 | 9694 | A | 4489 | 1 | 1335 | |
| 4198 | 9695 | A | 4490 | 1 | 2456 | |
| 4199 | 9696 | A | 4491 | 1 | 1827 | |
| 4200 | 9697 | A | 4492 | 1 | 1011 | |
| 4201 | 9698 | A | 4493 | 452 | 950 | |
| 4202 | 9699 | A | 4494 | 1 | 1433 | |
| 4203 | 9700 | A | 4495 | 1 | 1933 | |
| 4204 | 9701 | A | 4496 | 641 | 2107 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4205 | 9702 | A | 4497 | 1 | 2582 | |
| 4206 | 9703 | A | 4498 | 1 | 1095 | |
| 4207 | 9704 | A | 4499 | 1544 | 525 | |
| 4208 | 9705 | A | 4500 | 2 | 161 | |
| 4209 | 9706 | A | 4501 | 3 | 452 | |
| 4210 | 9707 | A | 4502 | 25 | 622 | EFHRLRENPPWFLFPAAKTNVRAVA WG*RS GAHAG EYGA EALER\ MVLFP PPTPKPYFPELRT*AHGFCPKVKGP TAKKVAERA*PNAVAHV DGHAPN GAVPP*ADLQRRTSFRVDPVNFQAP *ATCLLVTLAAHLPAEFTPAV\HA SLGQVPGLSVSTVLTSKIPVKLEPSV GHAFLPLWAFPPAPPPLSCTRTPVGL |
| 4211 | 9708 | A | 4505 | 2 | 213 | |
| 4212 | 9709 | A | 4506 | 2 | 382 | TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNVAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLVTL LAAHLPAEFTPAVHASLDKFLASV TVLTSKYR |
| 4213 | 9710 | A | 4507 | 2 | 252 | |
| 4214 | 9711 | A | 4508 | 1 | 466 | WSPQTQREPTMVLSPADKTNVKAA WGKVG AHAGEYGA EALGR\ FLSP PTKTYFPHFDLSPGSAQVKGHGKK VADALTNAGAHVDD\ MPNALSSPE ATLHAHKLRVDPI\ NFKLLSHCLLVTL LAAHLPAEFTPAVHASLDKFLASV STVLTSKYR |
| 4215 | 9712 | A | 4509 | 256 | 391 | NELHAENLKNEDD VDTGLLGFWTL LIISLTAGFSCCSFSWTVTYFDSFEP GMFPPTPLSPARFKK*R*CRHWTIRI LDSTYNIPNCWILLQLFLDSDLL |
| 4216 | 9713 | A | 4510 | 2 | 490 | |
| 4217 | 9714 | A | 4511 | 1 | 160 | |
| 4218 | 9715 | A | 4512 | 1 | 150 | |
| 4219 | 9716 | A | 4513 | 1 | 73 | |
| 4220 | 9717 | A | 4514 | 2 | 213 | ISPFYHLCQMLKTADVLR RMALWR CRDALLS*GGSSIEIPLFLLYGSRELGL GFCFTGMNHCAQSIYNRF |
| 4221 | 9718 | C | 4515 | 186 | 365 | MFQLLYDSLXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXIYNRF* |
| 4222 | 9719 | A | 4516 | 251 | 454 | GGSSIEIPLFLLYGSRTWILF*EM AAGRVQWLTSVIPALWEAEAGGSR GQEFKTS LAKRVKPHLY |
| 4223 | 9720 | A | 4517 | 3 | 192 | |
| 4224 | 9721 | A | 4518 | 1 | 129 | |
| 4225 | 9722 | A | 4519 | 23 | 115 | |
| 4226 | 9723 | A | 4520 | 1 | 1582 | GRGWRAVLGWSRRRSGLEPATVGS SMALLFLLPLVMHGVSR AEMGTAD LGPSSVPTPTNVTIESYMNPIVYW EYQIMPQVPVFTVEVKNYGVKNSE WIDACINISHHYCNISDHVGDPSNSL WVRVKARVGQKESAYAKSEFAV CRDGKIGPPKLDIRKEEKQIMIDIFH PSVFNVDGEQVDYDPETTCYIRVY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NVYVRMNGSEIQYKILTQKEDDCD EIQCQLAIPVSSLNSQYCVSAEGVL HVWGVTTTEKSKEVCITIFNSSIKGSL WIPVVAALLFLVLSLVFICFYIKKI NPLKEKSILPKSLISVVR SATLET KP ESKYVSLITSYQPFSLEKEVVCEEPL SPATVPGMHTEDNPGKVEHTEELSS ITEVVTTEENIPDVVPGSHLTPIERE SSSPLSSNQSEPGSIALNSYHSRNC ESDHSRNGFDTDSSCLESHSSLSLSDSE FPPNNKGEEKTEGQELITVIKSPPPSF CYDKPAHVLVDLLVDDSGKESLAIG YRPTEDSQRFHEISLSCTQL |
| 4227 | 9724 | A | 4521 | 1 | 408 | |
| 4228 | 9725 | A | 4522 | 2 | 377 | |
| 4229 | 9726 | A | 4523 | 50 | 326 | |
| 4230 | 9727 | A | 4524 | 3 | 1948 | AAAAAAVPASFGLCSRDPAPPQP ASMSGIKKQKTENQQKSTNVVYQA HHVSRNKRQVVGTRGGFRGCTV WLTGLSGAGKTTISFALEEYLVSHA IPCYSLDGDNVRHGLNRNLGFSPGD REENIRRIAEVAKLFADAGLVCITSF ISPFADRENARKIHESAGLPFFEIV DAPLNICESRDVKGLYKRARAGEIK GFTGIDSDYEKPETPERVLKTNLST VSDCVHQVVELLQEQNIVPYTIKDI HELFPENKLDHVRAEAETLPSLSIT KLDLQWVQVLSEGWATPLKGFMR EKEYLQVMHFDTLDDGMALPDGVI NMSIPIVLPVSAEDKTRLEGCSKFVL AHGGRRVAYLTETAEF/HTEHRKE ERCS/RVFWGTTCTKHPHIK/MVME SGDWLVGGDLQVLEKIRWNDGLD QYRLTPLELKQKCKEMNADAVFAF QLRNPVHNGHALLMQDTRRRLLER GYKHPVLLLHPLGGWTKDDDVPLD WRMKQHAAVLEEGVLDPKSTIVAI FPSPMLYAGPTEVQWHCRSRMIAG ANFYTVGRDPAGMPHPETKKDLYE PTHGGKVLSMAPGLTSVEIIPFRVA AYNKAKKAMDFYDLARHNEFD FIS GTRMRKLAREGENPPDGFMAPKA WKVLTDYYRSLEKN |
| 4231 | 9728 | A | 4525 | 1 | 626 | |
| 4232 | 9729 | A | 4526 | 66 | 409 | LGLLQVTTTNPPSPPPNTYLLKMLFK LRTPPFISHHSFILKNYDIQYFSMRDI DRLGIQKVMERTFDLLIGKRQRPIH LSFDIDAFDPTLA PATG\TPVVGGLT YREGMYIAEEIH |
| 4233 | 9730 | A | 4527 | 1 | 1257 | |
| 4234 | 9731 | A | 4528 | 3 | 1086 | FSVLRIMSLRGSLSRLLQTRVHSILK KSVHSVA VIGAPFSQGQKRKGVEH GPAAIREAGLMKRLSSLGCHLKDFG DLSFTVPKDDL YNNLIVNPRSVGL ANQELAEVVSRAVSDGYSCVT LGG DHSLAIGTISGHARHCPDLCVWV DAHADINTPLTTSSGNLHGQPV SFL LRELQDKVPQLPGFSWIKPCISSASI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VYIGLRDVPPEHFILKNYDIQ\YFP MKDIDRLGIQKVMERTFDLLIGKRQ RPIHLSFDIDAFDPTLAPATGTPVVG GLTYREGMYIAEEIHNTGLLSALDL VEVNTQLATSNEEAKTTADLAVDV IASSFGQTREGGHIVYDQLPTPSSPD ESENQARVRI |
| 4235 | 9732 | A | 4529 | 1 | 128 | |
| 4236 | 9733 | A | 4530 | 3 | 126 | |
| 4237 | 9734 | A | 4531 | 1 | 79 | |
| 4238 | 9735 | B | 4532 | 214 | 268 | XELEKLVQVVRQLEAEPGLPPVQPV FITVDPERDDVEAMARYVQDFHPR LLGLTGSTKQDEDQDYIVDHSIAFY LLNSDGLFTDYYGRSRSAEQISDSV RRHMAAFRSVLS* |
| 4239 | 9736 | A | 4533 | 23 | 257 | AYLIDDTEAQSRRGSQAKATPLEGLR TQPSSRPLGGIKLV*YEVLCCLMTA LKA\TQIQLPATSHSAARLRGVLP AIR |
| 4240 | 9737 | A | 4534 | 3 | 229 | |
| 4241 | 9738 | A | 4535 | 1 | 297 | |
| 4242 | 9739 | A | 4536 | 67 | 552 | GPWRFCFSEAVSEPTTVAFDVRPGG VVHSFSHNVGPGDKYTCMFTYASQ GGTNEQWQMSLGTSEDHQHFTCT IWRPPRGKSYL\YFTQFKAEVAGRL RFEYRHGLTFKARILKGESDVPLEN LRNFEV\TKTAVGSQGPAGFPKLT PKLV\IVAKAS\RTCL |
| 4243 | 9740 | A | 4537 | 2 | 232 | RDGTVHARAANKNRVISVLLPSDLV H*LWEP*PDED*DA*SETGDIDHRV TEESHE*PAFHNFMQESMAQYWKR NNK |
| 4244 | 9741 | A | 4538 | 2 | 1094 | RHPVCLLVLMAGSGKTTFVQRLT GHLHAQGTPPYVINLDPVHEVPFP ANIDIRDTVKEYEVMKQYGLGPNG GIVTSLNLFATRFDQVMKFIEKAQN MSKYVLIDTPGQIEVFTWSASGTIT EALASSFPTVVIYVMDTSRSTNPVT FMSNMLYACSLYKTKLPFIVVMNK TDIHDHSFAVEWMQDFEAFQDALN QETTYVSNLTRMSLVLEFYSSLR VVGVS AVLGTGLDEL FVQVTSAAE EYEREYRPEYERLKKSLANAES\QQ EREQLERLRKDMGSVALDAGTAKG VFTVDSLSPVLHPSDLILTRGTLDEE DEEADSDTDDIDHRVTEESHEEPAF QNFMQESMAQYWKRNNK |
| 4245 | 9742 | A | 4539 | 710 | 1053 | |
| 4246 | 9743 | A | 4540 | 3 | 281 | |
| 4247 | 9744 | A | 4541 | 30 | 320 | |
| 4248 | 9745 | A | 4542 | 3 | 115 | |
| 4249 | 9746 | A | 4543 | 1 | 137 | |
| 4250 | 9747 | A | 4544 | 3 | 32 | |
| 4251 | 9748 | A | 4545 | 1 | 135 | |
| 4252 | 9749 | A | 4546 | 1 | 2694 | |
| 4253 | 9750 | A | 4547 | 3 | 544 | |
| 4254 | 9751 | A | 4548 | 2 | 323 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *~Stop codon; /~possible nucleotide deletion; ~possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4255 | 9752 | A | 4549 | 1 | 384 | |
| 4256 | 9753 | A | 4550 | 1 | 1299 | MASPVAQAQAGKLLRALALRPRFLA AGSQAVQLTSRRWLNLOEYQSKKL MSDNGVRVQRFFVADTANEALEAA KRLNAKEIVLKAQILAGGRGKGVF NSGLKGGVHLTKDPNVVGQLAKQ MIGYNLATKQTPKEGVKVNKVMV AEALDISRETYLAILMDRSCNGPVL VGQPQGGVDIEEVAASNPELIFKEQI DIFEGIKDSQAQRMAENLGFVGPLK SQAADQITKLYNLFLKIDATQVEVN PFGETPEGQVVCFDAKINFDDNAEF RQKDIFAMDDKSENEPIENEAAKYD LKYIGLDGNIACFVNGAGLAMATC DIIFLNGGKPANFLDLGGGVKEAQV YQAFKLLTADPKVEAILVNIFGGIV NCAIANGITKACRELELKVPLVVR EGANVQEAQKILNNSGLPITSAIDL EDAAKKAVASVAMK |
| 4257 | 9754 | A | 4551 | 1 | 590 | RVRTKDPNVVGQLAKQMIGYNLAT KQTPKEGVKVNKVMVAEALDISRE TYLAILMDRSCNGPVLVGSPQGGV DIEEVAASNPELIFKEQIDIFEGIKDS QAQRMAENLGFVGPLKSQVEAILV NIFGGIVNCAIANGIPKACRELELK VPLVVRLEGTNVQEAQKILNNSGLP ITSAIDLEDA\AKKAVA\SVAKK |
| 4258 | 9755 | A | 4552 | 3 | 168 | |
| 4259 | 9756 | A | 4553 | 3 | 95 | |
| 4260 | 9757 | A | 4554 | 3 | 354 | |
| 4261 | 9758 | A | 4556 | 1 | 95 | |
| 4262 | 9759 | A | 4557 | 156 | 364 | GPVE*KPVEEESRGLLD*GLPGMD WGWVFGKGGDPPLAQSLNCPSFTV SEIIGRDLSGFPAPPGEPPA |
| 4263 | 9760 | A | 4558 | 1 | 2523 | |
| 4264 | 9761 | A | 4559 | 3 | 469 | |
| 4265 | 9762 | A | 4560 | 3 | 132 | |
| 4266 | 9763 | A | 4561 | 1 | 2961 | MGAASCEDEEELFKLVFGEEKEAPP LGAGGLGEELDSEDAPPCCRLALGE PPPYGAAPIGIPRPPPPRPGMHSPPPR PAPSPGTWESQPARSVRLGGPGGG AGGAGGGRVLECPISIRTSISPTPEPP AALEDNPDAWGDGSPRDYPPPEGF GGYREAGAQQGGGAFFSPSPGSSSL SWSFFSDASDEAALYAACDEVESEL NEAASRFGSLGSPSPRASRPWTPE DPWSLYGSPGGRGPEDSWLLLSAP GPTPASPRPASPCGKRRYSSSGTPSS ASPALSRRGSLGEEGSEPPPPPLPL ARDPGSPGPFDYVGAPPAESIPQKT RRTSSEQAVALPRSEEPASCNGKLP LGAEEVAPPGGRKEVAGMDYLA VPSPLAWSKARIGHSPIFRTSALPP LDWPLPSQYEQLELRIVQPRAHR AHYETEGSRGAVKAAPGGHPVVKL LGYSEKPLTLQMFITADERNLRPH AFYQVHRITGKMVATASYEAVVSG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; v=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TKVLEMTLLPENNMAANIDCAGIL KLRNSDIELRKGETDIGRKNTRVRL VFRVHVPOGGGKVVSVAASVPIE CSQRSAQELPQVEAYSPSACSVRGG EELVLTGSNFLPDSKVVFIERGPDG KLQWEEEA TVNRLQSNEVTLTLTV PEYSNKRVS RPVQVYFYVSNRRK RSPTQSFRFLPVICKEEPLPDSSLRGF PSASATPFGTDMDFSPRPPYPSPH EDPACETPYLSEGFGYGMPLYPQT GPPPSYRPGLRMFETRGTGCAQP PAVSFLPRFPSPDYGGRGSSFPLGL PFSPPAPFRPPPLPASPPLEGPFPSQS DVHPLPAEGYNKVGPYGPGE GAP EQEKSRGGYSSGFRDSVPIQGITLEE VSEIIGRDL\SGFPETSLEKKPPALKP RETVITLATPAPASALPPFPFLELV ATEAWGQPLAPLSPSFCLSHCLPLPS PSLGCGPQAWLA ALEGLGGKECVE EGGG |
| 4267 | 9764 | A | 4562 | 19 | 387 | |
| 4268 | 9765 | A | 4563 | 1 | 373 | |
| 4269 | 9766 | A | 4564 | 2 | 343 | |
| 4270 | 9767 | B | 4565 | 19 | 507 | MEANGLGPQGPELKNDTFLRAAW GEETDYPVWCMRQAGRYLPEFRE TRAAQDFFSTCRSPEACCELTLQPL RRFPLDAAIIFSDILVVPQALGMEVT MVPSKGPSFPEPLREEQDLEALRDP EVEASKLGYGFQAATPYPTTTGWDV CRLIGFCWCPHGP* |
| 4271 | 9768 | A | 4566 | 3 | 339 | |
| 4272 | 9769 | A | 4567 | 3 | 679 | |
| 4273 | 9770 | A | 4568 | 1 | 139 | |
| 4274 | 9771 | A | 4569 | 1 | 526 | HERFETTYFKKFPAGYYVTGDGCQR DQDGYWITGRIDDMLNVSGHLLS TAEVESALVEH*RLLQEA VVGHP HPCEGVNASYCFVTLCDGHTFSPKL TEELKKA\VMRKRLAPFATPDYIQN APGLPKTRSGKIMRRVLRKICS/VT DHDLGDMSTVADPS\VISHLFSHRC LTIQ |
| 4275 | 9772 | A | 4570 | 537 | 2357 | GVCHQRR LAPQAWPGAGTDSL LLA TRWATGAPGHCCWHLPARHTCGSP GLSPVPQPASAGPPGGLWERHSRE YIKTWRPR/YFLLKSDGSFIGYKERP/ EAPDQTLPLNNFSVAGCLGMS\EC QLMKTERPRPNT/FVIRCLQWTTVIE RTFH/VDSPDE/REEWMRAIQMVAN SLKQ/RAPGEDPMDYKCGSPSD/SST TEEMEVAVSKARA/KVGTFGKVILV REKAT/GRYYAMKILRKEVIA/KVR APGIALASLCGGCVCLQDEVAHTV/ TESRVLQNTRHPFLTALKYAFQTHD RL/CFVMEYANGAVFHLSRERVFTE ERAR/FYGAEIVSALEYLHSRD/VVY RDIKLCAQEKGDTHSP*KVSPSLSSR ITLAPTGTQVSTVRGTSDP/AVECS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HSGTPHSSWNEQLQLHTTVWTRLIG YVEGKPHRGAVPRYMGVGQRVLE DN/DYGRAVDWWGLGVVME/MM CGRLPFYNQDHERLF/ELILMEEIRF PRTLSP/EAKSLLAGLLKKDPKQ/RL LP/PFKPQVTSEVDTRYFDD/EFTAQ SITITPPDRCECWGPRAESRCLPHAE PSSAAVPDGFAPAGPLSPQDAWRGR RGWRRRERAGAAGRTRVRRGHLPE VMPAFLAS |
| 4276 | 9773 | A | 4571 | 64 | 1537 | VTAYHAATMNEVSVIKEGWLHKR GEYIKTWRPRYFLLKSDGSFIGYKE RPEAPDQTLPLNNFSVAECQLMKT ERPRPNTFVIRCLQWTTVIERTFHV DSPDEREEWMRAIQMVANSCLKQRA PGEDPMDYKCGSPSDSSTTEEMEV AVSKARAKVTMNDFDYLKLLGKG TFGKVILVREKATGRYYAMKILRKE VIIAKDEVAHTVTESRVLQNRHPF LTALKYAFQTHDRLCFVMEYANGG ELFFHLSRERVFTTEERARFYGAIEVS ALEYLHSRDVVYRDIKLENLMLDK DGHKITDFGLCKEGISDGATMKTF CGTPEYLAPEVLEDNDYGRAVDW WGLGVVMEYEMMCGRLPFYNQDHE RLFELILMEEIRFPRTLSPKASLLA GLLKKDPKQRLG\GGPSDAKEVME HRFFLSINWQDVVQKKLLPPFKPQV TSEVDTRYFDDEFTAQSITITPPDRY DSLGLLELDQRTVHFPAQFSYSASIRE |
| 4277 | 9774 | A | 4572 | 2 | 423 | |
| 4278 | 9775 | A | 4573 | 1 | 106 | |
| 4279 | 9776 | A | 4574 | 3 | 58 | |
| 4280 | 9777 | A | 4575 | 1 | 191 | |
| 4281 | 9778 | A | 4576 | 3 | 325 | |
| 4282 | 9779 | A | 4577 | 3 | 277 | |
| 4283 | 9780 | C | 4578 | 77 | 292 | MVDFCPPCSICFXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX HWSIC IS* |
| 4284 | 9781 | A | 4579 | 645 | 849 | |
| 4285 | 9782 | A | 4580 | 3 | 140 | EANKENREAQMAAKLERLPEKD*A /HLEEVKRNK\ESKDPADETED |
| 4286 | 9783 | A | 4581 | 49 | 605 | NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASGQAFELILSP RSKESVPEFPLSPPKEEGFFPGGKFR EN*EAAEERRQSP*SCSS*RQLAEKR EHGKEVL\QKAIEENNNFQ*NGQK RKLTPHKMEA**RDPREATNGLPKL EPFAEEKDKAH*KKCRKNKESQRP CPRRDLKPD |
| 4287 | 9784 | A | 4582 | 1 | 567 | VVREPAFSLA/EAQFTARYFSTSSIP NV\NKAPVARIRRSKHM*QGVTLPI EHYHEGTDSL*TALV*ARVGNQLA KLKRNYAKAVELLVQLASLQTSFV TLDEAIKITNRRVNAIEHVIIPRIERT LAYIITELDEREREFEYRLKKIQEKK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KILKEKSEKDLEQRRRAAGEVLEPAN LLAEKDEDLLFE |
| 4288 | 9785 | A | 4583 | 1 | 748 | MSGKDRIEIPSRMAQTIMKARLKG AQTGRNLLKKKSDALTLRFRQILKK IETKMLMGEVMREAAFLAEAKFT AGDFSTTVIQNVNKAQVKIRAKKD NVAGVTLPVFEHYHEGTDSYELTG LARGGEQLAKLKRNYAKAVELLV ELASLQTSFVTLDEAIKITNRRVNAI EHVIIPRIERTLAYIITELDERVREEF YRLKKIQEKKKILKEKSEKDLEQRR AAGEVLEPANLLAEKDEDLLFE |
| 4289 | 9786 | A | 4584 | 166 | 238 | |
| 4290 | 9787 | A | 4585 | 53 | 203 | |
| 4291 | 9788 | A | 4586 | 357 | 498 | |
| 4292 | 9789 | A | 4587 | 262 | 397 | |
| 4293 | 9790 | A | 4588 | 68 | 422 | |
| 4294 | 9791 | A | 4589 | 70 | 361 | |
| 4295 | 9792 | A | 4590 | 259 | 2603 | |
| 4296 | 9793 | A | 4591 | 246 | 667 | |
| 4297 | 9794 | A | 4592 | 25 | 471 | |
| 4298 | 9795 | A | 4593 | 2 | 3788 | |
| 4299 | 9796 | A | 4594 | 1 | 700 | |
| 4300 | 9797 | A | 4595 | 604 | 1047 | SNNRTDNPTSVAYLSKETDVVAKG WPHCLWVVAVAILVLEAIKIIQ GK DFTVWTS HDVNGILGAKGNSWLS D KRLRYQALLLEG PVLQIHTCVALN PAIFLPEDGEPIKH DYQQIVAQTYVT *EDLLEVPLANPD LNLYTNGSSFV |
| 4301 | 9798 | A | 4596 | 1 | 1410 | |
| 4302 | 9799 | A | 4597 | 510 | 755 | |
| 4303 | 9800 | A | 4598 | 59 | 411 | SWPSDKQTLVVQRGQKMEQANHP DPTDHMSQLMWT/VLPQGFRDSPH LFGQALAQDLGHFSSPGTLVLQYV D DLLLATSS EASCQQATLALLNFLA NQGYK/LSRSKAQLCLQQVKYLCL |
| 4304 | 9801 | A | 4599 | 1 | 565 | |
| 4305 | 9802 | A | 4600 | 126 | 492 | CNNSMTSLQVRLKVCPRPCRTSM/L PIRII*KLPQVCLDLL*IREGEWDMY PCWAKFPCPYSLKGT*PIAWGILWS FGDFFAY/IPLMQQKH*FSSQNTRR NEEGQI*WPLLMHSQKPAPLPVV |
| 4306 | 9803 | A | 4601 | 1 | 342 | |
| 4307 | 9804 | A | 4602 | 55 | 219 | LGNKHLLGSIDPRGSWVTGEYIFLR PPIAA*GRQ*DFLPPELWWTSLNNS WAFS |
| 4308 | 9805 | A | 4603 | 339 | 1371 | ASHPLRGLLCGPSLPNEPCPLLHGT QSHRPLKG*GVRAHSTGLAGSSTCR PLRDPLGEASWAPESAQGL*IHQSA LCI*LKLKPAGQRAKLGDRLDIPDR RKSSTILGRAGDLQAMPPEPTLSV GSCAAQASPMNPAPCSTAPSPIDHS RAEECGRIARDWQAAPPAGPCGIH WVKPAGLLSLLRDCKYTNRHSVSS SRFANTNQHPASSSGFVNAPIDTLY LANLVGTWRTFVASSGIVNAPISTL SKQTTWLYQSAGCGKESTQASGAQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TGGTSFKSLETTGSISEASSAKHCTE LFSRFTTFNPDSVPSDGVVGDTAGT VWPGVLKGEPCHLGTCTYRCVLDPH PTPSESDTIQGIHVQVCYMSTLHDA DVCDTNDPVTHTNTKKYIYSTEIFTS NNPELRSEDETVFRALEKWKTSSEQT IGEMDFYICNDPHPDALYQNGLSK MQDTVLSLVFSPSVAA |
| 4309 | 9806 | A | 4604 | 749 | 1002 | QLKKGTNSLLVSKPSPVWIPTGTLT QIMGTGVANIC*PVF*KD*GELGKM NYAMMSTITQGKEENPAFLKWLWE ALRKYTPLSP |
| 4310 | 9807 | A | 4605 | 1 | 1632 | |
| 4311 | 9808 | A | 4606 | 307 | 543 | |
| 4312 | 9809 | A | 4607 | 1 | 1149 | |
| 4313 | 9810 | A | 4608 | 119 | 409 | GDICHHLGLTPVGSHSLLSCSR*QV A*VGAVTAATIGTGILLOQLAFLVC NWLLSGSSENFPRALICFKSEREK GTCIQVGPNSPPPTACKGHN |
| 4314 | 9811 | A | 4609 | 1 | 2433 | |
| 4315 | 9812 | B | 4610 | 97 | 1065 | MHAVHTSLLVERTILTTTKERGSTL QYPLRPGAHKGLQDIVKRFAQALI RKCSSPCNTPILGVQKPNGQWRLV QDLRLINEAVIPLYVPVNPYNLLSQ IPEEAEWFTVLDLKDAPFCIPLHSDS QFLFAFEDPTDHTSQLTWTVLPPGF RDSPLFGQALAQDLGHFSSPGTLV LQYVDDLLATSSEASCQQAATDLL NFLANQGYKTHSRDSDAPVGFTDR HLVATEKIPRGREPLSSLAVYTRGR PTRTGARRTIVSRIRDRFFRYLA QREPPLYQQSLLIHLQLDSQPALSV VIGKVPNVVELTPNFGTAAQV* |
| 4316 | 9813 | A | 4611 | 1 | 2403 | |
| 4317 | 9814 | A | 4612 | 1 | 2838 | |
| 4318 | 9815 | A | 4613 | 1908 | 4698 | SNDRTEDDCGKHPFMSSPPATEPWV CLIEGQEIDFLDTGTTFSVLIPCLG RLSSRSVTIQGILGQPVTRYFSHLLS CNWETLLFSHAFLVMPESPTPLLGR DILAKAGAIISMKTGNKLPICCPLE GINPEVWALEGQFGRKNAHPLQIR LKDPISFPYQRQYPLRPEAHKGLQDI VKHLKAQDSVRKCSPCNTPILGVQ KLNSQWRLVQDLRLINEAVIPLYPV VRNPYTLQSVPPEAEWFTVLDLK DAFFCIPLHSDSQFLFAFEDPTDHTS QLMWMVLPQRFDRSPHFGQAQA QDLGHFSSPGTLVLQYSEIAKTLYT LIKEMERANTHLVEWEPEAETAFT LKQALVQAPALSPTGQNFALYVIE RAGIALGVLTQTHRTTPQPVAYLSK EIDVVAKGWPHCLRTVVAVAVLVS EAIKIIQKDFTVWTTHDVNGILGA KGGLWPSDNCLLRYQALLLEEPVL QIHMCIANPATFLPEDGEPIKHDCQ QIIVQTYATQDDLLEVPLANPDFNL YNSGSSFVENGIRAGYAIVSDVTV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LGSKPLSPGTSTQLAELVALTRALE LGKGKRINVYTD SKYAYLILHAHA AIWKEREFLTSGGTPIKYHKEIMELL HTVQKPKEVAVLHCQSHQKGSARR IFCLTRIPGTRVCKNPHVSLSGISEW PLRDHTPLCFRPKALLAWVHEEICS MGCKDPGWNSLVSEEDRKMQUES LETSRDLLNGFDQNVNDNDMSKVQ AEGASDGDEELIGKWRKGLSMLW KILSIENMMNVWKDGTIKDAIVIEK AVKAIKPETINSCORNLCPDVVHDF TRFTTEPIKDIKEIGDLAIKLGIFESS NSTQFLNQFVPDDRSLPHNKLLKFY KPEFYSSYPLVSCLDHYVDQVGARI SMSFCVTTVTASGSGSWTCGVSQ LKLSYAD |
| 4319 | 9816 | A | 4614 | 1529 | 2945 | |
| 4320 | 9817 | A | 4615 | 3 | 374 | |
| 4321 | 9818 | A | 4617 | 3 | 112 | |
| 4322 | 9819 | A | 4618 | 359 | 465 | |
| 4323 | 9820 | A | 4619 | 3 | 381 | MRILMVGLDAAGKTTILYKLKLGEI VTTIPTIGFIFVDSNDRERIQEVAD ELQKMLLVDEL RDAVLLLFANKQD LPNAMAISEMTDKLGLQSLRNRTW YVQATCATQGTGLYEGLDWLSNEL SKR |
| 4324 | 9821 | A | 4620 | 395 | 552 | |
| 4325 | 9822 | B | 4621 | 1289 | 1603 | MVVTISP NFSLYRMVVLPAASNPTI KMRICFLPNSREKREEIVRPMAVVA LVMGRSRRGLGRPRAFSFQAPRQT KREGRERAEEERGRQKRLSGPCAD EDPAQE* |
| 4326 | 9823 | A | 4622 | 2 | 116 | |
| 4327 | 9824 | A | 4623 | 156 | 403 | |
| 4328 | 9825 | A | 4624 | 8 | 2648 | WIQYSSTTLPNDWNKRKKKEKKA MLSARAKTPRKPTV/KKGSQTNLKD PVG\YCRVRLGFPDQECCIEVINNTT VOLHTPEGYRLNRNGDYKETQYSF KQVFGTHTTQKELFDVVANPLVND LIHGKNGLLFTYGVGTGSGKTHMT GSPGEGGLPRCLDMIFNSIGSFQAK RYVFKSNDNRNSMDIQCEVDALLER QKREAMPNPKTSSSKRQVDPEFAD MITVQEFCKAAEEVDEDSVYGVFVS YIEIYNNYTYDLL EEPFDP/IKPKPP QSKLLRED\KNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRIANTHL NRESSRSHSVFNIKL VQAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTRAEGNRLREAGNINQSLMTLRTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAICGLTPGRRYRNQPRGPVGN EPLVTDVVLQSFPLPSCEILDINDE QTLPRLIEALEKRHNLRQMMIDEFN KQSNAFKALLQEFDNAVLSKENHM |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QGKLEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIEEDKRNLOQ ELETQNQKLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFQPDQNAPPIRLRHRRSRSAG DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAES\EW\TDVETRCVGC GR*GAGSQLGPGYQHHAQPKRKK P |
| 4329 | 9826 | A | 4625 | 1 | 331 | |
| 4330 | 9827 | A | 4626 | 142 | 461 | |
| 4331 | 9828 | B | 4627 | 136 | 906 | XPELKPVDKESEVVMKFPDGFEEKFS PPILQLDEVDFYYDLKHVIFSRLSVS ADLESRCVVGENGAGKSTMLKLL LGD LAPVRGIRHAHRNLKIGYFSQH HVEQLDLNVSACGTAGHASFLGRP EEEYXGWCDSGVPRMKRFKAGVP GSCGYAKEGGVTRVERKDFDQYRA LLQGTVSAAKAFL* |
| 4332 | 9829 | A | 4628 | 1 | 233 | |
| 4333 | 9830 | A | 4629 | 1 | 312 | |
| 4334 | 9831 | A | 4630 | 2 | 119 | |
| 4335 | 9832 | A | 4631 | 1 | 145 | |
| 4336 | 9833 | B | 4632 | 78 | 236 | MSYIPGQPVTAVVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFS EDT DK* |
| 4337 | 9834 | A | 4633 | 102 | 583 | IRVEMSYIPGQPGTAVVQRGEIHKL ROGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIALGLQ IGDKIMQVNGWDMTMVTHDQAR KRLHQALRRRLVRL\VTRQS\LQK\ AVQQSMPVLAATTILRLPAASLYS NATSTLWSPSGFC |
| 4338 | 9835 | A | 4634 | 1 | 373 | |
| 4339 | 9836 | A | 4635 | 3 | 86 | |
| 4340 | 9837 | A | 4636 | 1 | 204 | |
| 4341 | 9838 | A | 4637 | 1 | 767 | |
| 4342 | 9839 | A | 4638 | 20 | 515 | |
| 4343 | 9840 | A | 4639 | 3 | 391 | HEESRSVSQAGVQWRYLGSLQRPP PRFKRFSCLSPPSSWDHRCTTS*LAN F*YLVETGFHHVELLTSSDLPTSAS QSAGITGVSHHAWPWALNVFKDG CESPWPHNKLEFYTAYNFFNTGTT LRPPL |
| 4344 | 9841 | C | 4640 | 201 | 368 | MGKSKXAFRXKSXGIVFIQGTFPXE YNXXPRGIKVSQEXNXXXXXCXKI GGEDVX* |
| 4345 | 9842 | A | 4641 | 1 | 307 | RLFFFFETVSHSVTQARVHLSHLGS LQPLLPTFKQFSCLSLPGS*DYRRL LHPANF*FSVETGFHHVGQAGLEL LTSGDPPTSASQSAGITGVSHRAWP ST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4346 | 9843 | A | 4642 | 1 | 310 | |
| 4347 | 9844 | A | 4643 | 49 | 360 | DRVSVTQAGVQWCNLSLQPLPPR FR*FSCLSLSSWDYRRPPRPANF* FLVETGFHHVGQAGLKLLTSSDPPT SASQSAEITGVSHRAWPVLSSPQPFF FF |
| 4348 | 9845 | A | 4644 | 2 | 119 | |
| 4349 | 9846 | A | 4645 | 1 | 276 | FFFFFFFFLTQSLTHSVTRLECSGVI SAHCNLCLLGSSS*LASAS*VAGTT GANHYAQLIFVFLVEMGFHHVGRA GLKL/HDLK*SKVLGLQA |
| 4350 | 9847 | A | 4646 | 2 | 273 | LRQFSLLLPRVECSGAISAHCNLCLL GSSDSPASASRVSGITGTHHQTWLT FFVFLVEMGFHHVGQAGLQLLT*V IRPPRPPKVLGLQA |
| 4351 | 9848 | A | 4647 | 1 | 106 | |
| 4352 | 9849 | A | 4648 | 1 | 485 | SSIDTLGRRVGQPAPGSPGASNHLC CESYPWQLLQPCPVQAGARAELVP VPAHHPGDPVKTEP*RGQGASSGSC TCWGCPTAQAQAQAPSSPAAPMRK EGPPSL*SERTGRPSRGVTSAGSDG AQPQSA*HSPWPGIVLLSVRYLQETI NHRPGGRPTGFSS |
| 4353 | 9850 | A | 4649 | 1 | 623 | CDLNSQPRSTDGTFDLTVLSNDGVH STVTSNIRVFFAGFSNATVDNSILLR LGVPTVKDFLTNHYLHFLRIASSQL TGLGTAVQLYSA YE/GEQ*NVSFGQ L*SENHNQYVNPGRSHLLERHSK RSF/FRQSGVKVESVDHDSVHGPGC QNGGSCLRRLAVSSVLKSRESLPV VANEPLQPFCKCLPGYAGSWCEID IDECLPSP |
| 4354 | 9851 | A | 4650 | 1 | 446 | LMLRPRLKLQEPVPHHHLGFQCPSS PLLPPAGPPPHKV*PLGFQEGGQHS SSLNFVAHSTPAKP/PPGCVCPSLPA SHAHCLSRVIGGVGLRNCTVVPTRG GGSQLPWLLPSLIVPLIVHQSPVSS LQPIRHDLPAPGDGTHSSAYC |
| 4355 | 9852 | A | 4651 | 2 | 388 | SHGSYVMYHDQVEFISGMKHW/FN TKIQTHY*KNEEKNKMIISTNAENG HDKILLPFMIKTHITLGI*GNVLILIT GIHKQFFWQGGGWGGACGGGRVL LFPQAGVQWWDHSSLQPQPSLNSF SNSSL |
| 4356 | 9853 | A | 4652 | 115 | 413 | LHIYSQPKFRKGTKKIH*W*KDSVFH SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSPMQLIQENTG/IMLQDI GFGKDYLSKTSKAQATKQK*TRKH WEMLQDIGFGKDYLSKTSKAQATK QK |
| 4357 | 9854 | A | 4653 | 3 | 129 | NTLLKKTVSFHQCCWKNWISICRKI KLDSYLSPTYTKIKSKLIKLNKVRPET MQLIQENTG/IMLQDIGFGKDYLSK TSKAQATKPK*TRLLSLTYKNQVK VD |
| 4358 | 9855 | A | 4654 | 1 | 405 | LTLKPNSGFRFPFQVATR*IKYPGIH PAKEVKDLRYRKT*KTLLKGITDGP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | Q*KTIRGSWIGRINITEMAILPKAIYR FNTTPIKLPMAFUTQLEKTIQKFIWN QKGAQIAKRILSKKTNSQTSHITVL QTIRI |
| 4359 | 9856 | A | 4655 | 3 | 448 | FFFFFAFLLLGLLHQIPDVSPTGKYT TLLPLMIILMISGIKEVTYIINDMADK IVKEHKTVMTRLWDTFKWKEVKC GLNTVKALEMGELPSLQDTSPDVFI *QHSNPG*RDCKCTRQGFDRQQLLY QCRDILPPRQQAFKLQSLRAQP |
| 4360 | 9857 | A | 4656 | 2 | 502 | KKKKERKRKRTPAIKKWAKDDRHF TGDKIKMVNKNIKICISLVIS*MQI KAITIHPTRLAKVKCLPRMGR\KGIL FYCWWARKLEQ/SFRKIFIP*NPGVR LLSTNPRKICAPFAKNTRASETWTK LLLAALCVVTPN*KQTNCPSTAGMS NLLASMDHTGRTVSGHA |
| 4361 | 9858 | A | 4657 | 61 | 364 | KTVWFCARVEGQGQNLG*WKPRLP GLKHFPGLSSQ/WNRKLPDGPNTNG *FWNFKKKGGFPLWPKRI*IFGPGD PPSRASKRAGITGITHGAGPRFNFKK WR |
| 4362 | 9859 | A | 4658 | 2 | 436 | KLIIFLYTSNEQREFEIKNTIPFTLAPP KIK*LGTNLT\WIQELYEKIYKSVM KNIKELNKWRSSYGKGKSSSSSSSS SSSLDIACSWLRLKIVKISGLHNLI YRFNIVPIEIPETYLVDVNKLIPQFIW RGKRHRIVNKIVE |
| 4363 | 9860 | A | 4659 | 3 | 480 | GSHDFFDKLILKFIWNSRPRIAKTIL KKKNKVGGTLCDFKTYRATV*I KTVWYWD/QIRHI/DQWSRITSPEIN PYIYCQLIFNRYTKTIQ/YGNNRLFN K*C*DMRRVKSDPFLTY/PYIIN*K MIIDVKAMIMKL/LEGNTGMSLSDF GLRKALDVTTKV |
| 4364 | 9861 | A | 4660 | 362 | 408 | CQVISVLWFYSSVLGWLWVFCFSL KF*/WKSRSRQANPILKNKTRVLIL PDIKTPK\AGVIKPVW*QCS*KVW GEKVWYWQKMTQIVQWDRTESPQ IDN*SLTKEIQWRKDSLFNKW*GNN WTAPFSS/RSLNLNKDLTAVTKIKSK WVTDLNVKHKTINLL |
| 4365 | 9862 | A | 4661 | 93 | 367 | KVWGEKVWYWQKMTQIVQWDRTE SPQIDN*SLTKEIQWRKDSLFNKR* GNNWTAPFSS/RSLNLNKDLTAVTK IKSKWVTDLNVKHKTIKLL |
| 4366 | 9863 | A | 4662 | 123 | 397 | KVWGEKVWYWQKMTQIVQRDRA ESPQIGH*SLAKEIQWRKNSLFNKW *GDHWAAAFSSSSSI*TKTLQP/CTKI KSKWVTDLNVKRKTIQLL |
| 4367 | 9864 | A | 4663 | 2 | 433 | ETADFGPLVLDS/DDDSVDRDIAEAI REYLKAKSGAAQTGAGRGQPGAA QPSRAAGSGSRCKPELSHGSAPTSV CPPKLVPGSGGGPGSQVRSSD*GS AFPVRASSNDSFEQSIKAEIEQLNE KR*HATPKCDGASIDKKPDP |
| 4368 | 9865 | A | 4664 | 94 | 445 | HHQLTLESLGKSKNSPRLSPSLGAC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LSCIIWQPAKGQG\SGDGGNWQRG KTAETE/SAAIGGETEWTAKCP*YSC L/GVGPTALTSQPPT/PEAEHPQA/GG TYRDLHPDPTWKTGWCHFVFC |
| 4369 | 9866 | A | 4665 | 52 | 119 | |
| 4370 | 9867 | A | 4666 | 987 | 1324 | VSNTPSARNQGRASSPGNSSPE/SSS ESAPAAATANGCDEAHLIPGGKFREP LKGQRGPELGPRPRALGGPRGSI/RP GSGGSFRG*LGGQMLLEPAASPGTQ PSGHLPALCGLSN |
| 4371 | 9868 | B | 4667 | 3888 | 8771 | MRLWSWVLHLGLLSAALGCGLAE RPRRARRDPRAGRPPRPAAGPATCA TRGPRPPRLAAAAAAGRAWAVR VPRRRQQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPRDAFTLQ VWLRAEGGQSPAVITGLYDKCSYI SRDRGWVVGIHTISDQDNKDPRYFF SLKTDRARQVTTINAHRSYLPQW VYLAATYDGQFMKLYVNGAQVAT SGEQVGGIFSPLTQKCKVLMLGGS LNHNRYRGYIEHFSWLVARTQREIL SDMETHGAHTALPQLLLQENWDN VKHAWSPMKDGSSPKVEFSNAHGF LLDTSLEPPLCGQTLCDNTEVIASY NQLSSFQPKVVRVYRVNLYEDDH KNPTVTREQVDFQHHQLAEAFKQY NISWELDVLEVSNSLRRRLILANC DISKIGDENCDECNHTLTGHDGGD CRHLRHPAFVKKQHNGVCDMDCN YERFNFDGGECCDPEITNVTQTCFD PDSPHRA YLDVNELKNILKLDGSTH LNIFFAKSSEEELAGVATWPWDKE ALMHLGGIVLNPSFYGMPGHTHTM IHEIGHSLGLYHVFRGISEIQSCSDPC METEPSFETGDLCDTNPAKHKSC GDPGPGNDTCGFHSFFNTPYNNFMS YADDDCTDSFTPNQVARMHCYLDL VYQGWQPSRKPAVALAPQVLGHT TDSVTLEWFPPIDGHFFERELGSAC HLCLEGRILVQYASNASSPMPCSPS GHWSPREAEGHPDVEQPCSSVRT WSPNSAVNPHTVPPACPEPQGCYLE LEFLYPLVPESLTTWVTFVSTDWDS SGAVNDIKLLAVSGKNISLGPQNVF CDVPLTIRLWDVGEVYGIQIYTL EHLEIDAAMLTSTADTCLCLQCKPL KYKVVRDPPLQMDVASILHLNRKF VDMDLNLGVSYYQYVWITISGTEESE PSPA VTYIHGRGYCGDGIQKDQGE QCDDMNKINGDGCSLFCRQEVSN CIDEPSRCYFHDGDGVCEEFEQKTSI KDCGVYTPQGFLDQWASNASVSHQ DQQCPGWVIGQPAASQVCRTKVID LSEGISQHA WYPCTISYPYSQLAQT TFWLRA YFSQPMVAAA VIVHLVTD GTYYGDQKQETISVQLLDTKDQSH DLGLHVLSCRNNPLIIPVVDLSQPF YHSQAVRVSFSSPLVAISGVALRSF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DNFDPVTLSSCQRGETYSPAQSCV HFACEKTDCELA VENASLNCSSD RYHGAQCTVSCRTGYVLQIRRDDE LIKSQTGPSVTVTCTEGKWNKQVA CEPVDCSIPDHHQVYAASFSCPEGT TFGSQCSFQCRHPAQLKGNNLLTC MEDGLWSFPEALCELMCLAPPPVP NADLQTARCRENKHKVGSFCKYKC KPGYHVP GSSRKS KRAFKTQCTQ DGSWQEGACVPVTC DPPP KFHGL YQCTNGFQFNSECRIKCEDSDASQG LGSNVIHCRKDGTWNGSFHVCQEM QGQCSVPNELNSNLKLQCPDGYAIG SECATSCLDHNSEIILPMNVTVRDI PHWLNPT RVERV VCTAGLKWYPHP ALIHCVKGCEPFMGDNYCDAINNR AFCNYDGGDCCTSTVKTKKVTPFP MSCDLQGDCA CRDPQAQEHSRKDL RGYSHG* |
| 4372 | 9869 | A | 4668 | 1 | 183 | GRDGVLPCCPGWP*SPELKQSA/CL GLPKCWDY/RARATAPGLLFFSYAK ICPCLTSCQYSKC |
| 4373 | 9870 | A | 4669 | 3 | 462 | TYQSFSPSHMPLRGYDVW*TTLFQN P*HG*PGLQRFPLANMLCGPSGSHL VLLKL*RSVTLNHREALICLPPE*YV EPSGTKACIAGWGETKGTGNDTVLN VLLNDISNQE*NNQHRGHVR*S*M STDGLQASVGAL***YGGPHSWFIH HRG |
| 4374 | 9871 | A | 4670 | 1 | 360 | ARGPQRSERSSRRPAPPSRSSGS*RC SCIPWPTLLLRGPR*RPL*NARYMKI LASPFQLSHPRKGPRRWH/AGVLS PPAAPPSSSSVPEAGGPPIKKQKAD VTL SALNDSDAHS DVDM |
| 4375 | 9872 | A | 4671 | 70 | 631 | RQRPQRSERYYWRAAPPS*GDKVG PQMASQQPSASLYPYPSTSHITAGS RLGEFHELGWLEVRWFVVDPLAC RENCETGVWAMGLSVFLSVIHS L T QRSFINTDSVLCHAQRETNVCPCAR EGPCL*PSPSARSQRPRSPGSRTPQ EKSRRDAAASSAPRAS*RRRRPPII PLRPLWTLTSWPRAPPHGDAAAAA TREPEFHL |
| 4376 | 9873 | A | 4672 | 93 | 338 | |
| 4377 | 9874 | A | 4673 | 1 | 660 | FRRFRWRRRLH*AGPASSAGGSPGE ASGTMSGELPPNINIKEPRWDQSTFI GRANHFFTVDPRNILLTNEQLESA RKIVHDYRQGIVPPGLTENELWRA KYTYDSAFHPDTGEKMLIGKNGQ AQGF PWNMTNTGCM DGRFTGTTP AVLFWQWINQSFNAV VNYTNRS GD APLTVNELGTAYVSATTGAVATAL GLNALTKHVSPLIGPFGPFACVA |
| 4378 | 9875 | A | 4674 | 1 | 387 | FFF*RWVSHSVAQA AVRWRNHGSL *PKTLGPK*SSH/CQSP*RAWDS*AH AHYHPA*FLNFFL*RQGPHLSMFPK MVLNSRPQAVPPT*ASQSDGITGVS HHTLALKV/CLFKMKYFE**TEKGI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HFKRTK |
| 4379 | 9876 | A | 4675 | 3 | 383 | GQLQARPPAPAAADCPPWTLRGSA LVPWLVPWRKASPQLSPGSPECP*A PSARPQDPPRPAGQIQDRASEHAAR GGPCGVLRADGALPALPPDRARPQ VCGRGEVAARARW*RSSGRRGTRK RNGE |
| 4380 | 9877 | A | 4676 | 490 | 1013 | WASCSSSREYQCCFQTVPPGFSRVM KFFTFPPGSKHFPAPLPAPQACTSF GLAGLPNALPLILVPAPPA/SSLAN PQLVQPPV/PGLVPRPSRSCSA/RP SA/RLARPPETPAR/PRAPSSAPRTRT PS*GRARSGGSAGNAPSARRTPQGP TRAACSLARILDASGSWRVLRP |
| 4381 | 9878 | A | 4677 | 1 | 447 | KKFVIPDFEFTGHVDRIFEDVKELT GGKVAAYIPQLAKSNPDLWGVSLC TVDGQRHSEGH TKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAIVVS SLIKMDCNKA*KFDFVLQYLNKMA |
| 4382 | 9879 | A | 4678 | 3 | 284 | QLGQYGETPSLLK/IKIRIQKVAGHG GRHL*SLLRSLRQKNLLNPAGGRS CSEPRLRHCTPAWVTERDSVSKKK KKKKEKERKKKKAGCGGSRL |
| 4383 | 9880 | A | 4679 | 122 | 196 | CWFENVNSKSGFWVLF*FKAKLVN |
| 4384 | 9881 | A | 4680 | 2575 | 2786 | ADTESITL*FYHFFFFLRL/DSVAQA GVQWCDLGLLQV/LPPGFTPFSCLS LPSSWDYR/RPVITPS*FFVFLVEM/G FTALARMVLIS*PCDPPVSASQSAGI TGVSHCAQPTFIPK |
| 4385 | 9882 | A | 4681 | 3 | 512 | YNQKVDLFSLGIIFFEMSYHPMVTA SERIFVLNQLRDPTSPKFPEDFDDGE HAKQKSFISWLLNHDPKRPTEL IKSEL/LPPPQMEESLHEVLHHTL ANVDGEGPYRTIDGPRSFQRISPAI DYTYDQRHS*KGTSSIRA/AKLLHL VRETMRICTRHGACQT |
| 4386 | 9883 | A | 4682 | 1 | 382 | EESILGEVGEALTSAGEELKIDRFF*I VEGLRHNSSQLNVTSMLINALDTS PDDLDFRLHIINEFMRCGLKEILPHL *GIKNDGLDMQLKDFDEHNEEDLL ECNHRLEDIRAELDESVDVHMLW S |
| 4387 | 9884 | A | 4683 | 1 | 472 | GIMLPDLKLYDIAMVAKSAWYWH KNGHKVLWNKMAQN/HYGGQLVF VKVPKYTQWGKGSLFNEWNQEN/ WISACRRMKLDPYVSTKINSKWIK AYTIR/PETVKLLEENIGKKLIDI/GP G**FLALAPQTQATKA*IDKWDFIK VKTFCTARETVNTEKRH |
| 4388 | 9885 | A | 4684 | 182 | 345 | RFPLCSFPPTLPCEGICFPFA/FCHDC KFPEAFPTRLPEPAEL*VNSTSSLH KL |
| 4389 | 9886 | A | 4685 | 205 | 395 | VNLGIFGKNGAPPG/PEGRGGILGHR NPPPRGLNK*PPLTFQGTGTPGSSSS S*VNLGIFGKNGAPPGGQGGPKTPG PKEWAGLAPQKGGTTGLDPLGPPK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KGFNNHPGGIREFPGN |
| 4390 | 9887 | A | 4686 | 35 | 389 | NLFYKVLQSAGFFSMDHEDDVDFL ARFSQLVTGKRQSLIVSWTT*IQNG DIKNAQEALAAETRMALTLR*LAP DDGTSSKI/LGFCCDYVQILKHL\AQ QKAGAAAIMSVATKELMMKT |
| 4391 | 9888 | A | 4687 | 3 | 547 | GGAGRRAWAGVGGAPGAGGGPAE AGAAAEEGAHRGDGAVRAGAGG GRRYRPRRVQDPGGPAE/G*TWPPS PSSRCSSPCVPGRG*/PSEPQDPAAV SLPTSSVPETRGAPAGPIRG\PAPGL RCQP*EARPGCVYWLISGGWCSPLF PWKLPGPRRPKQL*APRAGPCRPSL PCRLATGHDF |
| 4392 | 9889 | A | 4688 | 65 | 414 | WKCADTNVAQGPRVQQVLQLRGT PIPNHCALCLLREKQRQLCPRGSNG PAERSKPRRIQPEDATPAQALPRLP KGGGPGKSPTRGKHLGWGRDLFAS LSPAKATCLPPSIDNKPFF |
| 4393 | 9890 | A | 4689 | 75 | 787 | HVAFASGQRCNKSLPTPKVVPVPRVG LFPRPRPPWAALVALGLAWHPLAGI PRGCCVPHRHNAPEGKRLPFVSPS GHRARSTWAETRPQGPRGSLASLCP AHMDLSIWKTARGATFSFQQGPPG SWRGQT/RGPVSPLRPAPPPP*RPDK DGGGGS\PDQAGRTRKAEVGGCL ASMRPPPAPLT*TRRGR*RRPAPAP ARTAPSPRCSAPSSAAAPASAGPPP APGAPPTPAPRPRPYALRR |
| 4394 | 9891 | A | 4690 | 8 | 382 | QEYWE*LYAYTF*NRDELDEFFDRH ILPNFTQEEYTT*NNPVSVKEIEFVI/ NNISTPKKNPK*TSDDDDFTSKFC*T FKEELIPVLYKHFOKIVEEEVLPHLF CELSITFLKLDRCCEVRLHR |
| 4395 | 9892 | A | 4691 | 2 | 389 | NRKRIELTRKVLFEKHMARDVQNE HLTRFVGACTDPPNICILTEYCPRGS LQDILENESITLDWMFRNSLSSDIC* GMLFIHNAA/IC*HGNLNSFNLSVLIR DLSRFN*FSFSSESPVNCIQIIVIIISP |
| 4396 | 9893 | A | 4692 | 2 | 544 | TKAPKYIKQTLIDPKGEVDYNMIIV G/DANTPLSKTDRSSIQ*INKETVEL NHILDLIGLTAIYRTFHPTATE/YFFS SAHGTLRSRINYTLGPKPGCEKIVKH RNYIKYPFLNTIELEINNKRNSENT NTWKLNNMFLKD*WINEEIKKEI*K LLETNENGNTM*QNLWDMTKAVL RMKFTT |
| 4397 | 9894 | A | 4693 | 1 | 373 | MPHSVPGMLMSPGIIPPTGLTAAAAA AAAATNAAIAEAMKVKNIKLQAMS NYHASNNQHGANSHQGDMSRVAL DLPLSILPNLYTMPLVLQHSHTYN HLTYS*LHNLQTIP*INLDQRAPSLP |
| 4398 | 9895 | A | 4694 | 185 | 417 | NSELNGKEAALQ/IMILEREIGVEKA LNVQKGRVSESLKLLANRPGMVAH ACNPSTLGGQGGWVIVIRSGVRDQP *PHG |
| 4399 | 9896 | A | 4695 | 88 | 432 | TDLFLFVCLRLS\LLSVAQAGVQWF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DLSSPQPPPRFKRFSCLSLSSWNH RCTPPRLV/N/FFVFLVEMGFTMLAR MVSIS*PCDLPTSASQSAGITGINCR TQLTY*F*KFSVDSL |
| 4400 | 9897 | A | 4696 | 3 | 390 | YRIPYYVSTDCENLLKRFLELNPVK RLTLKQIMNDRWINARHEEDELKPF AEP*LADILDQKGIYIIGGMGYSQEEI WESLTKMKYDEITATYLLLGRKSS HLDASDSTSSTNLSLAKGRPSTDFN NSTG |
| 4401 | 9898 | A | 4697 | 289 | 365 | SPRLGLPKCWDYRHEPPHPAAFH*G CVLFIFYFIFLKQEL/NSLTQAGVQW RDLSSLQPPPPGFK*FSRLSLQSS*D YSCVPPRLAFCIFFW*KRGLTMLTR LVSNS*PQ/CDPPALASQSAGITGMS HHTQPHSIVL |
| 4402 | 9899 | A | 4698 | 33 | 397 | NAYNQLKVCASSPWLFCCANFSSY YFYDSHNVIQG*NMTYCT/VM*YLL ITGSLSAHLKNMSLKRIMKSYRSGA ESATEEPFTILYESQFSVGGNELDFQ VKTLSSLPEVVIVHGSQDNNATA |
| 4403 | 9900 | A | 4699 | 2 | 371 | LNTVIANGVAMASRPYQPTHVNVH IHQUESTLTHLLKAGGTLKKTLEHFG DTVSSSTATIGYEQLALWVTQILLGR *E/CVILECVLILGPWTALSASRCF WAESVEIVPRAGAIVHDKQPVKLA |
| 4404 | 9901 | A | 4700 | 3 | 441 | GFEDKVFYVWFDATIGYLSITANYT DQWERWWKNPEQ/ALGAEDNYTL VSHLIATEYLNVEDGKFSKSRGVGV FGDMAQDTGIPADIWRFYLLYIRPE GQDSAFSWTDLLLKNNSELLNNLG NFINRAGMFVSKFFGGYVPEMVLTP |
| 4405 | 9902 | A | 4701 | 2 | 375 | CITRDLKWGTPVPLEGFEDKVFYV WFDATIGYLSITANYTDQWERWW KNPEQVDLYQFMAKDNVPFHSLVF PCSALGAEDNYTLAKLLDLKKQLA VAEGNPLKPLKARRKSKRPWLIESH FNR |
| 4406 | 9903 | A | 4702 | 1 | 3093 | |
| 4407 | 9904 | A | 4703 | 2 | 2717 | GEMRLFVSDGVPGCLPVLAAGRA RGRAEVLSTVGPEDCVVPFLTRPK VPVLQVDSGNLYLFSTSAICRYFFLLS GWEQDDL TNQWLEWEATELQPAL SAPLYYL VVQGKKGEDVLGSVRRAL LTHIDHSLSRQNCPLAGETESLADI VLWGAQYPLLQDPAYLPEELSALH SWFQTLSTQEPCQRAAETVLKQQG VLALRPYLQKQPQPSAEGRAVTNE PEEEELATLSEEEIAMAVTAWEKGL ESLPPLRPQQNPVLPVAGERNVLITS ALPYVNNVPHLGNIIGCVLSADVFA RYSRLRQWNTLYLCGTDEYGTATE TKALEEGLTPQEICDKYHIIHADIYR WFNISFDIFGRTTTTPOQTKITQDIFQ QLLKRGFVLQDTVEQLRCEHCARF LADRFVEGVCPFCGYEEARGDQCD KCGKLINAVELKKPQCKVCRSCPV VQSSQHLFLDLPKLEKRLEEWLGRT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LPGSDWTPNAQFITRSWLRDGLKPR CITRDLKWGTPVPLEGFEDKIVFYV WFDATIGCLSITANYTDQWERWW KNPEQVDLYQFMAKDNPVPHSLVF PCSA\GAEDNYTLVSHLIATEYLN YEDGK\FSKSRRVGVFGDMAHDTG IPDISRFYLALYIRPEGQDSAFSWTD LLLKNSELLNNLGNFINRAGMFVS KFFGGYVPEMVLTPDDQRLLGHVT LELQHYHQ\LEKVRIRDALRSILTIS RHGNQYIQVNEPWKRIKGSEADRQ RAGTVTGLAVNIAALLSVMLQPYM PTVSATIQ\AQLQLPPACSILLTNFL CTLPAGHQIGTVSPLFQKLENDQIES LRQRFGGGQAKTSPKPAVVETVTT AKPQQIQALMDEVTKQGNIVRELK AQKADKNEVA\AEVAKLLDLKKQL AVAEGKPPEAPKGKKKK |
| 4408 | 9905 | A | 4704 | 180 | 490 | VENGNNSLTIMNRRARQKINKE\TA DL*NTMNQMDLTDIDGTFYPKAEY TFFSSKCGTF*RTDHMLGHKTS\LD KFKKIKVIQNYLFNHNGVKLEINNS KKMRKF |
| 4409 | 9906 | A | 4705 | 2 | 405 | KNLNNRLFIFP*IKKEIKRQIRK*FEW NEKEKTTYQNLWDAPKAKLKEKCI VLYV\KEETSQITDLSFHLKTPEKEE HVKPKVNRMEIIRIRAEI\AVKYRK PTETNETKSWSFENFSKIDTPLIKMI RKKKVD |
| 4410 | 9907 | C | 4706 | 217 | 486 | MDDPRGHASPVTRTQKPQASRLLV GLRAGGLSWGHWGRGKPPRGRV PAAALGAAVVAAMASPDWPAPGP KQPGRWADLAALLLCGLRPA* |
| 4411 | 9908 | C | 4707 | 13 | 216 | MLYWDCKRYKV\KDKTQAWDFAG NISVKGAE\LSQTRAASGPRRQAQVT FSVWRGGLQVMAEEGRVDVC* |
| 4412 | 9909 | A | 4708 | 132 | 1424 | VKHGPQGGP\RRQAQGD\IQVFGVGV LPGEWPEEGTQKGGPPLKTLGTGD GDKIGEPPTRAPRFR\TGQPGPRDGL VGPGGELAKPWGPPRGLGPASCPP GNTPLPARPEY*HLGWVGCP*RMG QGNLGVPSK/PVFGSSGPNVGSTNC DNFGSFGLSVPMF\PNGP\IQRALFEG DLWDLGRTGHGTT\PGGQCKPLSPG PKKLQGL*TC*SSLALQG/RLSLGAQ SGGRGK\POESES\PCPNP*APPVVC YGITRPVGF\RGPSQPG/LMGRPGSSS ALWA*NPELPNCPGL\POPCPQEV QSF\GPPGV\RGRLKGGQDCHRG EGSSKCAQGGHPAPA*WNPLVYTP ASPF\FRPASGKPRS/RPSCGLRAPS* HLRRPCLTPPFRPQGLLGSSPCPQKP APDSGLLH\SP\LTSPRGLSGQCNP RR LHPQLNQSNRDR |
| 4413 | 9910 | A | 4709 | 1 | 340 | RHEERTTGILTSVGLASDTSLICVIE DFFDTAL\ISRSSSEGKIQMLDSFLLS L*LLVTEETVNHLLQ\QEDRPCMDTL DCG/LQVAISEALRRLTTSKSRDDL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HIWYDDESIV |
| 4414 | 9911 | A | 4710 | 12 | 398 | TYLDLPLPGFCIYDF/VPPFSSECFIF VFMVCFFLAFILSFSSSSPNSFFDLF FLALPQLPTLRGLFV*ALFQILSWVV FPVKFSLGCVFYLFQFIFKQLAFFH HV*ETFSVPFLICKYWDD*TYFS |
| 4415 | 9912 | A | 4711 | 111 | 453 | YPFIIITFNTLGVAGNCL/KLTYTI** MPTANILKKLKAFSLR*RTR/H/GCP QSI*ARRII*DIQIAKEDVKLYLFTDD MILYVENPEESTQKDLLANKVNKVS GYNINMIIRCISM |
| 4416 | 9913 | A | 4712 | 1 | 184 | SSRDILLCTDIASRGLDSTGVELVVN YDFPPTLQD\ELAARRRRSLPGLASS VKEPLPQAT |
| 4417 | 9914 | A | 4713 | 1 | 1630 | MALTRPVRLFSLVTRLLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRRNLPVPVLRPGPLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQQEAPAVRKLSS KGSFADLGLEPRVLHALQEAPEV VQPTTVQSSTIPSLRGRHVCAAE TGSGKTLSYLLPLLQRLLGQPSLDS LPIAPRGLVLVPSRELAQQVRAVA QPLGRSLGLLVRDLEGGHGMRRIRL QLSRQPSADVLVATPGALWKALKS RLISLEQLSFLVLDEADTLDESFL LVDYILEKSHIAEGPADLEDPFNPK AQLVLVGATFPEAGVGQLLNKVASP DAVTTITSSKLHCIMPHVKQTFLRL KGADKVAELVHILKHRDRAERTGP SGTVLVFCNSSSTVNWLGYLDDHK IQHLRLQGQMPALMRVGIFQSFQK SSRDILLCTDIASRGLDSTGVELV VNYDFPPTLQDYIHRAGRVGRVG SEVPGTVISFVTHPWDVSLVQKIEP AARRRRSLPGLASSVKEPLPQAT |
| 4418 | 9915 | A | 4714 | 79 | 410 | IVYWVEVENRDHYAAYLGWEEAP YSDRAYAPQEKDLGPMDIRIGLL*K NWIPLQDDLYPVDMLHTSVG*EMEI LNNCRNQGV*RMASKDRRETLETYQ QL/L*LLQTSPLYLA |
| 4419 | 9916 | A | 4715 | 185 | 449 | TTILAWGDYLSLENSRSGPN*L*LLS GCTVQSFGLDWNGLLK*DSLTRL ALCSLQLGRK\VETTTIHYDCEGLGL KHLWKPAVEAYG |
| 4420 | 9917 | A | 4716 | 154 | 364 | MWRWFSLPPPFSLAGVELAPPVSRR SPRGP/TPYGLPRVPLWPLHSTALYC PPSPRTSAPFTPHPLPKLRG |
| 4421 | 9918 | A | 4717 | 9 | 1805 | SPATSP*ETAGPVKRSRNGSSPAADP EALSPPTARLQRVTVPPI*LNGQLSS PLHFAAGGGHAEIVQILLNHPETDR HITDQQGRSPLNICEENKQNNWEEA AKLLKEAINKPIEDPLAILILFDEAR YNLLKGFYTAPDAKLITLASLLQI VYGNYESKKHKQGFLNEENLKSIVP VTKLKSAPHWTNRILHEYKNLSTS EGVSKEMHHLQRMFLQNCWEIPT GAAFFTGQIFTKASPSNHKVIPVYV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GVNIKGLHLLNMETKDFQYFQYYVD |
| 4422 | 9919 | A | 4718 | 200 | 529 | EDVSKPVPWTLNGSCTSPLISHSDN QKCPYFPVIPAMGNPENIEDAYVA VIRPKNTASLNSREYRAKSYEILLHE VPIEGQKKRERKIFYWKRNFKATV K*HKAYWIT |
| 4423 | 9920 | A | 4719 | 177 | 321 | QTCSMDTKWQLYISPHQS**QPEMP SIFSSDPSLQCVCLHICKRLLS |
| 4424 | 9921 | A | 4720 | 166 | 627 | MWRWFSLPFPFSLAGVELAPPVS/S KDTERSHPYGLPRVPLWPLHSTKW VGQSPGEGGQGPSLSHSSFPFPRHS SPAQLPVAEKPSVAKRKPS*GFRA PTRAPKAQVSGVGDPPAHLFTVLP SPRTSAPFTPHPLPKLRGPRSSKALA FHSA |
| 4425 | 9922 | A | 4721 | 3 | 610 | STFNNEP*PEKQEQNKHKIRRKQIK IRA*INKIE/TKNQCKRTMKQKVAFF QKLNKTDKPLARLRKKRQDKIRNE KDITTDTAEIQRIRGYEQLYANKL ENLEEIDNS*THTTY*DLDQEEIQNL NRLITSNKVEAIKSLPVKSLGPDG FTAIFYQTKEELIPILLKLF*KVEEE RVLPN*FYEASITLMPKPKDKDT |
| 4426 | 9923 | A | 4722 | 1 | 454 | LAHCNICLLGSSNSASVSQVAGITG GCHYTQLIFLFLVEMGFHHVGQVG LELPTSGDLPALASQSVGITAVSPLC PTRIIFFEAESCLCWPGWSPNPGLKQ SPCLGFPKCDYQPDLTMP*FYL LELEIKFGVHVLWKSFLIKIENYYC |
| 4427 | 9924 | A | 4723 | 1 | 318 | KEECNKEEKESREKK/NEKEKIE*KE EEVRKEEKSLNKDKDKKRRRKREK GEGRKKEGILKVKKDGNPSNGHA RMPKER*LYDVRGTPHSSDHGDT AIFQTCIL |
| 4428 | 9925 | A | 4724 | 42 | 200 | LICT*MLIVALLVIARNWKQIRC/SST /DEWLNKLW*IPMEYY*AIEKEPTIG TC |
| 4429 | 9926 | A | 4725 | 50 | 403 | VVYHVMVLLKVVICHHFLTLFFS FRSLILYLFFILFMISLYLSCFLYNFL FIPSSSIFSHICFLMIIVLI*FFFYALFIMI FNPIILYLN\YLLSLFLIESLFDYYLCL ISFVIFY |
| 4430 | 9927 | A | 4726 | 3 | 282 | VQGQEPLTASMLVAA/PPQEQKQM LGERLFPLIQTMHSNLAGKITGMLL EIDNSELLHMLESPELSRSKVDEAV AVLQAHHAKKEAAQKDSKAK |
| 4431 | 9928 | A | 4727 | 780 | 1249 | LVVFMSIPLCSSTHPSILQGLKLVPL EQGQPPPLLHIVRCSDEIQAALNHH QVLSFPQC*PTAFPGSQAPQPAVHV QGQEPLTAS\MLAGAPPQEQKQML GERLFPLIQTMHSNLAGKITGMLLEI DNSELLHMLESPELSRSKVSWSGSDP AASVLM |
| 4432 | 9929 | A | 4728 | 510 | 2771 | NLEPSHQDRGEVQSRGEGRIVRRAF CLRCCGRGSRPPPPVSVSPSPPTPA RPRRAGATCEPARARAPAPKAPLCP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AAGPIRSPLAGLGVVGGGEMNAAA SSYPMASLYVGDHSDVTEAMLYE KFSPAGPVLSIRVCRDMITRRSLGY AYVNFQQPADAERALDTMNFVVIK GKPIRMWSQRDPSLRKSGVGNVFI KNLDKSIDNKALYDTFSAFGNILSC KVVCDENGSKGYAFVHFETQEAAD KAIEKMNGMMLNDRKVVFVGRFKSR KEREAEKGAKAKEFTNVYIKNFGEE VDDESLKELFSQFGKTLVKVMRD PNGKSKGFGFVSYEKHEDANKAVE EMNGKEISGKIIFVGRAQKKVERQA ELKRKFEQLKQERISRYQGVNLYIK NLDDTIDDEKLKKEFSPFGSITSKV MLEDGRSKGFGFVCFSSPEEATKAV TEMNGRIVGSKPLYVALAQRKEER KAHLTNQYMQRVAGMRALPANAI LNQFQPAAGGYFVPAVPQAQGRPP YYTPNQLAQMRPNPRWQQGGRPQ GFQGMPSAIRQSGPRPTLRHLAPTG SECPDRLAMDFGGAGAAQQGLTDS CQSGGVPTAVQNLAPRAAVAAAAP RAVAPYKYASSVAAALILPYSLCRH PS/PAVHVQG\QEPLTASMLAACNPP /QKQKQILGERLFPLIPTMH\PNLAG K\ITGMLLEID\NSELLHMLESPESLR SK\VDEAVAVLQA\HHAQERSCEPG GRCCCCYLLDPRKTDKAK |
| 4433 | 9930 | A | 4729 | 7 | 365 | LYTRHPPSPSCIMTACFGSHIRYRSD *VPTPVL RPAVIRSVGGGDCSERLG LRPRPI/PELGPHPTTRPPPPWQNV QRADPVAVTPCRSREGSQAEP LPRG RGAVSSSTTRPGLPAPNRP |
| 4434 | 9931 | A | 4730 | 1 | 1520 | AEGACGPRQPNKGAGAPPQGPAT LPGPRSGLSSTATMTANGTAEAVQI QFGLINCGNKYLTAFAFGKVNAS ASSLKKKQIWTLQPPDEAGSAAVC LRSHLGRYLAADKDGNTCEREVP GPDCLFLIVAHDDGRWSLQSEHR RYFGGTEDRLSCFAQTVSPAEEKWS VHIAMHPQVNIYSVTRKRYAHLA RPADEIAVDRDVPWGVDSLITLAFQ DQRYSVQTADHRFLRHDGRLVARP EPATGYTLEFRSGKVAFRDCEGRYL APSGPSGTLKAGKATKVGKDELFA LEQSCAQVVLQAANERNVSTRQGM DLSANQDERPTRRPSSWRSTATPKS VPSVPTRASTGR*RPPGACSPPPPAR MPAATLTSSGVTGASH*GRPMASL* PPRRMGSWPPRWRQQGTQSSSS*SS STAPSSCSAGSMASAAARSRAPWT PTAPAMTSSSWSSSTMAPTTSKTPQA NTGRWAVTPRSPAAATLLWTSSSSS ATITRWPSRWAGAT |
| 4435 | 9932 | A | 4731 | 131 | 677 | PSSLS/CDIFLRSPISTPSPSPLPRTPTS TPVHVKGQTAGSVINNPYVIMDKQ PGQVIGATTPTSGSPTNKISTASQISQ GTGSPVPKIHGSSFVTSTVKVIKQE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PGEAPHVPATGAASQSPLPQYVTVK GGHMIAVSPQKQVITPGEGIAQSAK VQPSKVL/GQIG*CLPTLARADLLYS VC |
| 4436 | 9933 | A | 4732 | 131 | 362 | PSSLS/CDIFLRSPISTPSPSPLPRTPTS TPVHVKQGTAGSVINNPYVIMDKQ PGQVIGATTPSTGVY*IHICTI*RV |
| 4437 | 9934 | A | 4733 | 1 | 4461 | |
| 4438 | 9935 | A | 4734 | 2 | 614 | STTTERENYRPIFLMNTDGRILSILP SQI***MKKIIYHDQVGFIPGMQRWL NVHKVTMHVHHINKMKGKNYLIS ADAEKSLGKTYHCFMMKTLNKLGI EGTLNIRKGIYD*STANILLTGKN*K AFPLRTGIRQGCPLSPLLFNTVWDIQ AKVIRQDKQIKGIENGQEEVKLSHF ADDIILYL*TEKPKDSTKKLLKWN |
| 4439 | 9936 | A | 4735 | 164 | 613 | NLNMEATGTDEVDKLTKEFISAWN NMRYSWVLKTKTYFSRNSPVLLLG KCYHFKYEDEDKTLPAESGCTIEDT *LREM*KNFRKDSISRIWLTREEFP QIEGSALTDCGWGCTLRTGQMLL AQGLILHFLGRAWTWPDALNIEKLE L |
| 4440 | 9937 | A | 4736 | 40 | 359 | |
| 4441 | 9938 | A | 4737 | 4274 | 5256 | HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLQHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRYVYVMVVIDFVLV SNIILPKFNHLCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*LAESLEF GGSGENVNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV |
| 4442 | 9939 | A | 4738 | 133 | 359 | LLNFMLLFHRYYALKVSYFKSSLDR KLELLWNKYWVNTLSSSSSLTVS/ DYTCKECI*ILSKLHSRLISETLFHRK |
| 4443 | 9940 | A | 4739 | 1 | 353 | NWTL*TLKKIFSLKDAIKRIKQSVR WKKIFAKHTSDKGVESNIYKELS*I NKASSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSYHYTSIRVA KMKKTDYVTSW |
| 4444 | 9941 | A | 4740 | 1 | 375 | LVPKRA*YWHKNTSSSSSSSSSS/PSS HLHIYSQPKFRKGTKKIHW*KDSVF HSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSPMQLIQENTG/IMLQD IGFGKDYLSTSKAQATKQK*TRKH WEMLQDIGFGKDYLSTSKAQATK QK |
| 4445 | 9942 | A | 4741 | 1 | 296 | FRRSL/DSVAQAGVQRRHLGSLQAP PRGFTPFSCVSLASWDHRSPLPRPA NFFVFLVETGFHVLARMVSIS*PCD RPT\SGFQSTGNTGVSHRTWPLLL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4446 | 9943 | A | 4742 | 3 | 380 | FLEEYNPPKVSQEEITSSSSSSSSSSSS SSSSLSSDIES/VIKNTSSNNNKKNPG PDGFTAKFYQM*KDELISTLLKIISK/ IFHSNSFCE*QTTR*FAISITWRAKPD KDTPQKEPYRLISLNIHSC |
| 4447 | 9944 | A | 4743 | 3 | 369 | SFTLIKKTKDIIRKANYKTMSLRKIA AVILNKILAN*IEH/RIKRJIHHNQIRF I/SGTQVWLNI*K*INVTHHINRLKK KNYMILIYEEKTFDKIKHPFM/IK/V LSKLGTEFFKLIKHIWRKI |
| 4448 | 9945 | A | 4744 | 70 | 345 | KVWGEKVWYWQKMTPIVQWDRT ESPQIGN*SLTKEIQWRKDSL FNKW *GNHWTAPFSS/RSLNLNKDLTAVT KIKSKWVTDLNVKHKTIKLL |
| 4449 | 9946 | A | 4745 | 3 | 345 | KFNNLDEMDKFADRQKLPYLAQEE RQNLN/*PYLLKNLNVQNLPIKTS PDELICKFYETFKNEIILLCSLFQK MELSQHIDSNTLTQKI*K*YRTE ENYRDISLINTYAK |
| 4450 | 9947 | A | 4746 | 35 | 355 | PHPPWWSLSSSPPSQHSFLPSPAYM PSPSGNSM/CYLSPSRGM*APSRQGP SSFHQLCPKCLKGCWARHMPSK*G WNGNPFVSLNYPWARNRPSLLTH FVMWEAPRP |
| 4451 | 9948 | C | 4747 | 27 | 416 | MMKRLGMFNIQHCKKLSSWVLLM KYLGNAPPSSSCLMRGNYSTWKMN SPTISSPSSWENEDRRSASLHLPKLSI TGTYDLKSVLGSTGASLKVFQQWG AGPLPGFTEGGHPXKVFQGPCIKAV LEPFDE* |
| 4452 | 9949 | B | 4748 | 5 | 763 | MPSSVSWGILLLAGLCCCLVPVSLAE DPQGDAQAQKTDTSHTDQDHPTFNK ITPNLAFAFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEAFVNFVDTEE AKKQINANGTRPFVKDTEEDFPR GPGDHREGAYDEAFRHV* |
| 4453 | 9950 | A | 4749 | 11 | 368 | GLKSLIN*LLAVYPREQTTL EEVMR DPWVNS/GSGVAFDN/TE*QILDHLN PETTQLLVAMGFQADNLSVAVREQ LFSYAMATYLDLEHTLLKKRSTIRS QTLPPGDPTWPLYIEVCTFRLS |
| 4454 | 9951 | A | 4750 | 175 | 349 | PSVAGRPRRKGGGRQPAQTRAVGI AGTEPPLYLGLWGPVGVDQG*QP ASFPGPPQVPKAPSNTKEASPSNA HSSSLGRLPSSPLPPRPASNTGSLSPR QGTMTTL*GATHLPQHSD*EESTRE SPPPTLEQPLPPSVQLIRMPCPPLPVT Q |
| 4455 | 9952 | A | 4751 | 2 | 354 | ENCQINNLRFHRLKPKKEEYTKPTA SRRK*IVNIRIERNGIEQKNNRTSSSS SSSSSSSSSSSLTFR*MDGRSSSSSS SSSSSSSSSQ*QRKKTRLIKI*NERG DITADLTEIK*LLILQKLNNY |
| 4456 | 9953 | A | 4752 | 121 | 363 | WRDFKTKTVIRAK*GYLIITG*NHQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; Δ=possible nucleotide deletion; ▴=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | EDTTVINMYA\PKTAPKKYMKQKL TDWKRAV/DSKTTAGDLNILLIMD KTKQKINRV |
| 4457 | 9954 | A | 4753 | 178 | 439 | GPALINALLKWRIPSGEDREP*GRD WEKEKE/R*LEEGRERGGKGEGGK RRNKGRKEGREERGKGEREEGYIM CIHGIGNRSLAVLGA |
| 4458 | 9955 | A | 4754 | 193 | 355 | GLFSIEEH*HDSTHLGINTLLISRLFI EK*LLKR VYQVTQACELYAWNPN DQCLPPPLVRPVQHRGAYPGEDWQ IDYTQMPCKGFKY*LVFIDTFTVWI EAFPTKIEKAIKV |
| 4459 | 9956 | A | 4755 | 3 | 227 | NIKIGKEEVKLSLFA GDVYLEKPKD STKKLLELI/NFSKVAAY*INIQKVA FLYANSE*SEKEIRNIIPFTIAT |
| 4460 | 9957 | A | 4756 | 115 | 487 | CSLCFVAEWSPWCGWTQLIYPW*E/ ITHSPVHTQRLGLETHRTAEMRLFS FSLFFFLRQSFALVTQPGVQRCDLG LLQPPSPGFK*FSCFSLPSSWDYRHA PPRLANFVFLVQTGF\SM LATLVSN |
| 4461 | 9958 | A | 4757 | 2 | 436 | GTEAEQPSYQPGLELPQGDQEEP LAGKTGLGPRFPRTTGGSQGTLL EGLSHSPFQSPGIPGEFEKARKIL*A GS*HNSC*ATE/GLGERPPGICGVSS SVSTQGPMP*CGQQGN*ALESCRGP ATAALSEQSPASPSSRAARA |
| 4462 | 9959 | A | 4758 | 76 | 194 | |
| 4463 | 9960 | A | 4759 | 310 | 551 | SSKQSSAKPPFCLPNPGKVCRSGRS RT*GCNLQKSGSGPEKGRRFGHPPE WTIFPSVQRQQA*FSDSPPTNGIP GEWKG |
| 4464 | 9961 | A | 4760 | 1 | 1165 | LRWQREEGQKAGVHVGTMTQHRL PQGA AVLPAALAPPPKHQFSLQAS SPSRLGRAGLAGGPSRAGLLC*WRR LSFLPSSFPSPRSWGARSRRRARGQ VGPREPAGRSAGDRGVGGRFGGPL ALSFFATGLLRASCAPAFQEVTVLG KAVQWRLEPGEPFTEG*ALAGTLG LGKH*QGRQK*GWG*PSLANARQ LGKPLQVLGWLGHVEGRPGRAVK VTGVRSWSCLPGSTGVGDRSRATQ LPAGP*VSLRVDQGEAVTGWGGRA GARGSPGRQ\GEPRHSARG*GPESLP LPVTRNSLVGGLSESN*ACPCR*QK ERLSIRGVPERRPFSGPEPGRGPASC SGLPTTGGTEERRKEGKRAAAISKA ALPGWARLPDQPGPAATGSK |
| 4465 | 9962 | A | 4761 | 1 | 389 | EETLPLFADDMILYIKKKQKTKKTT KESTKRY*N**MNVFGKVAGYKV NTQKSIN*QYTI*KVKLASFSSSPQK NKIGINLTKEIQNVYSENYKTLKEIK DLNK*ESIPCSQIRRFNIVKMTVLLK LI |
| 4466 | 9963 | A | 4762 | 1 | 346 | RACL*FQLLGRRLRQGDGLSLGIRGC SGPGWHHHSPA WATEKDPVSKTNK QNIKH/LRKSPLSRDEKILREKREEE KILAYHYLEKSAIYSISFFFLTKHILN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TPVCWFSSEHIIYF |
| 4467 | 9964 | A | 4763 | 2 | 468 | FPSLPSSFFSRFLFCIITVMF*VLDPLS LSYLTLLILPHLKIEFNFEK/CVNH/CF LLMLLLFLLACTY*MCLGPFYFLP CLSFSSVFHFLSLCCIIIGNLFRYIFKFI NFELCACYVLYT*DLFYF*KFSLVIF* IY*FFLSIMLSL*VFFHLKHFI |
| 4468 | 9965 | A | 4764 | 3 | 364 | RNLKLISEYCKISG*KVNIENQ\VFL YISNGQVEFEIKNTIPL*AHT*KMKY LDINVTKYVQDPYEENYKILMKKIK EQME/NIPCL*I/GRLNTKTSVLPNLE **ITAIPKIPASYFVDN |
| 4469 | 9966 | A | 4765 | 1 | 755 | EESILEE\VLEALTSAGEEKKIDRFFC IVEGLRHNSVQLQVACMQLNNGLG TSSGELEFKLHIKNEFMPCGLKEILP NLKCLKNDGLDIQLKGFDEHKKE LVELSHRLEDIRAELEAAYVYNM VWSTV*ETRAEGYFISILQHLLLRN DYFIRQQYFKLIDECVSHIVLHRDG MDPDFTYRKRLNLDLTQFVD\CV QAKLKEFEKALELYKKFEKEFTD PQENS*NCAKKEAQYGFNPNSK TF |
| 4470 | 9967 | A | 4766 | 12 | 321 | KSCDWAERLVTLV\WN/PYFKNLSN SYYKQLSPMGGYLNSWAHTLTEWI IDNILDQLIFPKLQKEVG*ESWETVV ITNHRDLFSLWLHYLSAVKTPGINGI CQHNY |
| 4471 | 9968 | A | 4767 | 2 | 375 | MSSPLPSPWSPCLLPQAPGPTLPVP PAETLSVSPACFLRLPINSPSQ*APA WRQLTADWGGHSALGLPGCPGPS\ TWPSHSASHLLPQRNQGPPMLGYA HLPGLPTNVLP SGHTPALERP |
| 4472 | 9969 | A | 4768 | 3 | 338 | QSLALSPRLECSGAILAHCHFC/LPG FT*FFCLSLPSSWDYRSPPT/RQLIF VFLVEMGFHHLGQAGLELLTL*SA HLGLPKCWDYRHEPPRPAQRPKLK NLK*LTTVARFTI |
| 4473 | 9970 | A | 4769 | 66 | 365 | LRDEQQHGGPWTSPLSRPPTGKRA RGRSACPQLTH*PGTAARKGASGR SRALALPTRCPGPACGGREPRLQAR GVP/R*IPPRRGPHGAPSGLP GPVG C |
| 4474 | 9971 | A | 4770 | 3 | 345 | KRGTPLAGEMAEGHCL\CLPLGTEY LTVNPIVHLFNSEIG*KIRPVA\KVR HVYSITASIFFTPLRCLCGEKHISGLR ARSGIVLSLELNHGIDSFAHM*SCDL ILINTLLSYYI |
| 4475 | 9972 | A | 4771 | 2 | 352 | KRGKPLAGEMEEGHCL\CLPLGTEY LSVKPIVHLFNSEIGEKIRPVAGGR HVYSNTASLFFTPLRCLGGEKHKSG LRARPGIVLSLELNHGIDSFAHM*FV DLLLITLLSYYIPFR |
| 4476 | 9973 | A | 4772 | 1 | 296 | QRSVKISISENGNSHMEIVSFLIFCQ FLLHVFCSTHIDYCYIFLLI*YPINRQ CLFAY*YSDIKFYSDIN/ISYFLCLLC MSFYPLSTCIYMGLVFIF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4477 | 9974 | A | 4773 | 2 | 859 | GRWPTQPTSLQGGQTLGDVREAFS RRP*NGERQGAPPACPLPRSLGLWR PWGPLSVTT*NRSWSCYCWLRLV/ GWKGSRAVVKALGSPEAAWHLLG PDAALQPCHFSQPQRRRCRGRPPFLP LSGWAGPWECWPTCQAGRT*IPEG GGGSC*GPQVNDLQRHTEENVLRC DLPHPALAAWGTVSPG/SHPAPQ*T EV*RSAQSSFRPQCPLTSPARGTPGS SRRLLCGVPP/CGPLLMLCPLPVPEV GLGPFLRELLNTKKLNCFVNKQKV PNKPACHLGDGPSLPHQIC |
| 4478 | 9975 | A | 4774 | 158 | 517 | RCRSGYVDQVAGLFCFVLRQSLTF VTQAGVQWHDLSLQPLPPRFN*FS CIILLSSWDYRCMPCLANFGIFLR/E RGFTMLGMLVLNC*PQ/CDPPTSAS QSAGITGMGPPHLGLSCSIKK |
| 4479 | 9976 | A | 4775 | 1 | 165 | GSLLPLLFNILEVLAKAIRQEKSIQN EKEKV*LSLLTDHMI/YM*NPTVKK LTT*KLTT |
| 4480 | 9977 | A | 4776 | 2 | 516 | QNPCISERQYCCEKLPLERSSRPQDS AGQPVT/HAHCSLSSTVDLCPLLAT HRISCWH*QDEVQGGRDASVDKGD LVALSLPAGHGD TDGPISLDVPDGA PDPQRTKAAIDHLHQKILKITEQIKI EQEARDNDNAEYLKLANNADKQQ VSRIKQVVQKKNPEAAQTIGQLD |
| 4481 | 9978 | A | 4777 | 154 | 406 | CTDIQGYPGSRVAQAGVQWHNL/ CLSLPSSWDYRRPLPRPANFLYF*ER RGFTVLARMVVIS*PCDPPASASQG AGITGVSHRT |
| 4482 | 9979 | A | 4778 | 1 | 429 | ARLETNSRSVAHGGVQCHDLSSQQ PPPPGFKGFSGLSLPSSWDYRRPPPC PR*F*YFY*RRGFTVLARMVVIS*PC DPPALASQSAGITGLSHCAR/LERES HSIA/RAGGQWFHLGSLQPPPPRFK* FSCLSLPSSWDHRC PVD |
| 4483 | 9980 | A | 4779 | 1381 | 1787 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 4484 | 9981 | A | 4780 | 1147 | 1553 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 4485 | 9982 | A | 4781 | 1456 | 1862 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCLSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 4486 | 9983 | A | 4782 | 889 | 1295 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSI*PRDPPTSA SQSAGITGMSH |
| 4487 | 9984 | A | 4783 | 743 | 1149 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSI*PRDPPTSA SQSAGITGMSH |
| 4488 | 9985 | A | 4784 | 2583 | 3580 | DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTSDSPT LASQSAGITGVNHHAWLFFFC/SD TVSLCYPGWSRVA*SRITATSAVGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRYPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGFTVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLFYFHRDEGSLCCPGWS* TPELK |
| 4489 | 9986 | A | 4785 | 1966 | 2372 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSI*PRDPPTSA SQSAGITGMSH |
| 4490 | 9987 | A | 4786 | 3 | 305 | FFFLRKSL/GSV/TQAGVQWRGLRSL QPPPPRFKRFSCSLSSWDYRCVPP RPA/NFLYF**RWGFTTLARMVSI* PCDPPASASQSAGITGISHRAQPIKY |
| 4491 | 9988 | A | 4787 | 1172 | 1688 | VFFGVFVFVFVFVFFPKLTSGTIPWA SPEVMIYPPTHS*VCEAPSPFYVFSH LFSLQSPSHLVCLFLCSF*DGVSLCR QAGVQWRSLGSLQPLTPWFKRFSC LSLPSGWHH/RRPANFCIF/M*RRGF TMLPRMVISISSPRDPPASASQSAGIT GMSHRARPQSSVFKQSFLSR |
| 4492 | 9989 | A | 4788 | 641 | 1074 | VLNLVEFVTRELAFTNVFFCFFVF FCFFLRRSL/DSVTQAGVHWLDLGS LQAPPPRFTPFSCSLPSSWDYRRPP RRPANFLYF**RRGFTRLARMVSI* PCDPPASASQSAGITGVSHRARPTN VNKAITNGLFTYFFFNEE |
| 4493 | 9990 | A | 4789 | 7273 | 7925 | IVSLFLFILLVFWWWCFFFFFFFETE SCSVAVAQAGVQWHNLGSLAQAPP PGFTH/LFSCSLPSSWDYRRPPRP VNFFFFFFHF**RRGFTMLARMVLIS *PQVICPASASQSAGITGLSHRVRQ GPHNLLTNQVNKFFFFFFLETESHV TQAGVQ*HDLGSLQSPPPGLKRFSC LSLLSS*DYRLPPHPHF/CVFLVE NGNSPCWPGWS*TPDLR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; v=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4494 | 9991 | A | 4790 | 156 | 391 | IPHSYIRKFYSFKMAILSP/KLIYSINA ISKKIK*AFLKKTDELILTFI*KGKES VLDKPILKKKNIVGLKICDFETYY |
| 4495 | 9992 | A | 4791 | 365 | 506 | GRHHACLIVDRALVFPS/CQVGRAA HFLPLPGPCPAWTPPSRSLRPGP |
| 4496 | 9993 | A | 4792 | 2 | 503 | LTHPAGARPVLLTTPESFEGPCFGTP HGQSLSQSAFSRGHSLGDTVGVGTG QVGS/LLSGGGVRAG/GAGGGGGA GFGSRLALKAAGERGEKPREPVPPP *QRIGPHTKAPWT*AGQGQPPGRAC SPG/PPAEPASQPLTPGPGRRLPGGK RSRRDRARGAARKMGLLFPLD |
| 4497 | 9994 | A | 4793 | 3 | 389 | FQDLIKR*KATIIKTLWY*HKNRY/D IDQQNRIEN/SKHRLSHLIFDKGTRTI Q/YGREQLSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSP IPDIGFHNDFLNMTPKAQATTKK |
| 4498 | 9995 | A | 4794 | 27 | 285 | VFFFFFFLRRSLALLPRLECSGTIVF LVETGFTMLARMVSIS*PRDLPALA SQSAGITGVSHRARPASFNFLTINILP PLLLWTF |
| 4499 | 9996 | A | 4795 | 12 | 336 | SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSLRTFSSHSLNMELVQD LTASAPMYSSTSRDPP/CLGLPKCW DYKREPPRAH |
| 4500 | 9997 | A | 4796 | 74 | 463 | HISQHRSYLQVLLASYKTASFLFFF LRQSL/DSVTQAGVQWRDLGSLQA PPPGFTPFSCPQSPK*L/SSWDYRRPP PRPANFFCIFIVEKECFTLLARMVSIS WPRDLPASASQSAGITGMSHRARP AQVS |
| 4501 | 9998 | A | 4797 | 1 | 337 | KKLISGFNVIPIKTPANPCVKIDKLIL KFIWHCKARRIGKAMWNKIKYGGGL IQ*DLKICHKVRHIEIVWY*LQGRQ/I DQ/WEQ/IQSPIDPNYSHLTYDKSP TAIQRRKIYPF |
| 4502 | 9999 | A | 4798 | 3 | 331 | KNYKTLLREI/KEELN*WKDIPRLW LRRLNIVKMSFL/SKFIYRLDSIPIK/ MPSRHLFL*KLILKQILKFTWEGKGP GIAKTILKKNKFGGFTLLNFNTYNK AANSRVLVLG |
| 4503 | 10000 | A | 4799 | 3 | 340 | INRLNIFTMAIFSTLIYRFNTIPIKIPA GFVEMDKLILKL VWKFAHGIGKT TLKKNRVPAPKFSSSSSSSSSYWNE DRNINQWN*IDNLKINPCVCGQLIF NKDAKTNEER |
| 4504 | 10001 | A | 4800 | 46 | 195 | SPATLGRPEVGPDS*GPGDRDHAGL TMVKPPVFYLNKYWIMRSGDRDHP G |
| 4505 | 10002 | C | 4801 | 353 | 442 | MPLLYVQRLFARTGLCATLFGMM SPLYV* |
| 4506 | 10003 | A | 4802 | 1 | 273 | FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPPE*LGLQA PATAPG*FFVFLVETGLCKHNEKSP LSVQGRIVVLRNQKG |
| 4507 | 10004 | A | 4803 | 57 | 231 | |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4508 | 10005 | A | 4804 | 2 | 169 | |
| 4509 | 10006 | A | 4805 | 698 | 1231 | |
| 4510 | 10007 | A | 4806 | 58 | 2674 | |
| 4511 | 10008 | A | 4807 | 7 | 235 | |
| 4512 | 10009 | A | 4808 | 1 | 245 | FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPPE*LGLQA PATAPG*FFVFLVETGFHLVSQDGL DLLTS |
| 4513 | 10010 | A | 4809 | 175 | 394 | NFLRYSHFKKCNRRPGAVVTPVIPA LWEAEAGGS/CRSGDRDHPG*QGE GKRGSLKFQEVSGAPNKFSLWILPL |
| 4514 | 10011 | A | 4810 | 65 | 2712 | SGSGHCLAEAAASMGPWGWLKRW VALLLAAAGTAVGDR CERNEFQCQ DGKCISYKWVCDGSAECQDGSDES QETCLSVTCKSGDFSCGGRVNRCP QFWRC DGQVDCDNGSDEQGCPPKT CSQDEF RCHDGKCISRQFVCDSDRD CLDGSNEASCPVLTCPASFQCNSS TCIPQLWACDNDPDCEDGSDEWPQ RCRGLYVFQGDSSPCSAFEHCLSG ECIHSSWRCDGGPDCKDKSDEENC AVATCRPDEFQCS DGNCIHGSRQCD REYDCKDMSDEVGCVNETLCEGPN KFKCHSGECITLDKVCNMARDCRD WSDEPIKECGTNECLDNNGGCSHV CNDLKIGYECLCPDGFQLVAQRRCE DIDECQDPDTCSQLCVNLEGGYKC QCEEGFQLDPHTKACKAVGSIA YLF FTNRHEVRRMTRTRSGYTSFIPNLR NVVALNTEGPSNRIYWSDLSQRMIC STQLDRAHGVSSYDTVISRDIQAPD GLAVDWIHSNIYWTDSVLGTVSVA DTKGVKRKTLFRENGSKPRAIVVDP VHGKHPCT/WPGVLCTCQVTSAT* DVRATIRR*ML/WFPQRTLEKAHLV SGREKQEESIIRCLR VKVWLTYEMQ DLGGG*TRL*ITQAKMNAENWL*L EEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVL FHNLTQPRG VNW CERTTLSNGGCQYLCLPAPQI NPHSPKFTCACPDGM LLARDMRSC LTEAEAAVATQETSTVRLKVSSTAV RTQH TTTTRPVPDTSRLPGATPGLTT VEIVTMSHQALGDVAGRGNEKKPS SVRALSIVLPVLLVFLCLGVFLLWK NWRLKNINSINF DNPVYQKTTEDEV HICHNQDGYSPSRQMVSLEDDVA |
| 4515 | 10012 | A | 4811 | 49 | 361 | STSYPTGSHAFL*PQNVVDAETNS* HINNVLRLKIKLLEENT EKNCHD LGLSTDYY/SVTPKA*ATTTKNDKL ELIKKNFCTSKDITYKVKRL LIGNNI CK |
| 4516 | 10013 | A | 4812 | 2 | 346 | EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKKNFCTSKDIT*K VKRQLIGENSCK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; ▯possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4517 | 10014 | A | 4813 | 2 | 356 | EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCKSFM |
| 4518 | 10015 | A | 4814 | 1 | 357 | VRPHHTNKKRVRLR/VRVNIKVRD KVSTEVKDKIKNQAAVIVKLGVOIK AGPWVRVKDWVRLEVKIKNRDQV RGEAEVRRIGQQLRTKTRPKLNVHP KRNGSIN*NIHTVECYSTIKKQ |
| 4519 | 10016 | A | 4815 | 1 | 323 | PVRGTEQSNKSWASGLQPGWGRAE QLAWGSFNLSKWPSGGGDPQPILLS RVQNMGRRLAR*EAPCQPQPQLPSR RSSPVPHQHL/PPCHPCGASLSPALA WPPPPPSRS |
| 4520 | 10017 | A | 4816 | 1908 | 2324 | ILASSLRANPGFIRNFHLFFFFFFYFLR RSL/DSVAQAGVQWHDLGSLQAPPP GFTPFSCLSLPNSWDYRRPP/RHHAR LISFFLFLVEMGFTMLARMVSIF*P WDLATSASQNAGITGVSHHTHPRP VIKYLPSSSPNLAG |
| 4521 | 10018 | A | 4817 | 1 | 273 | RPRRRYPHSWWFL/QEVAIFTLIEKV VFYYSHRLFLHPAFYKKIRKIHKKW TAPIGVISL*AHPIEHA VSNMLPVDP VNLRQSI RTVLFHQ |
| 4522 | 10019 | A | 4818 | 3 | 293 | DHVS PGVQDQAGQYSKTP/SLOKQ KQKTNRHGSA YLWSELLGSLRQED HLNPGVRGCSELLGHCS PAWAAK *DPVC*KNKTKNLIAGGHPRSF WIQ |
| 4523 | 10020 | A | 4819 | 2 | 170 | KLGF IKIKDFSSVKDNVKGMR RQAT DW/DFIKIKDFSSVKDNVKGMR RQA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN |
| 4524 | 10021 | A | 4820 | 52 | 228 | WASGHVRPYRVLNNFISNQKMDF KEDLSGIAEMFKTPVKELLIVL*TCL IVAFKSDNS |
| 4525 | 10022 | A | 4821 | 22 | 376 | TGTVIKIAWY*HKDRHMDQ*NRINS SETNPNI*SKVQRPFWRASSSSSSSS SSSSSSSSSSSS/PSSSSSSSSSSSSSSSS SSSSSSSSFIQNTGINLTDFGLGNVF LDMTPKAQAKE |
| 4526 | 10023 | A | 4822 | 151 | 379 | SIPGIQSWFNIQKSINVFYHIVILNTQ HRSSSSSSSSSSSSSSSY*LMIKF/LNK LGIEGNFLILIKAIHGKPTVNH |
| 4527 | 10024 | A | 4823 | 3 | 479 | RDEVSPHCPGWSQTPGLKQSSCLGL PKC*AYRHEPLGL/ILFFH*ATQETQ ARAGWSYASHFVDERTEAQR/V*G TCPRSHANYVLEDLICVLF*DRVCS VAQAGVQWHDLSSLQPPPPGFK*FS CLSLPSSWDYRRFATTAS*ILAF*VE MGVRHFARLV |
| 4528 | 10025 | A | 4824 | 1 | 57 | GKRYTRSDELQRLRRAHTG/EKKLV CPECSQRSMRSDRLTGHIRSHQNKK GIH*SDELQRLRRAHTG |
| 4529 | 10026 | A | 4825 | 3 | 602 | VDKNHTLSLLCQPSHGDCSRFSAST CLIRSRFHFNFNTFKIF*KLGDSMLT AVSVARDCGMILPODKVIIAEALPP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KDGKVAKINWHYADSLTQCSPSA IDPEAIPVRL/CP**LRGSSNDSLFC NEWIILSDTGGIFK/HLVPKGSNLG VCVCSHECIATVF*KNLYYCFQLML HGTVFARMAPDQKTQLIEALQNVE |
| 4530 | 10027 | A | 4826 | 3 | 241 | TSFSCSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR |
| 4531 | 10028 | A | 4827 | 3 | 241 | TSFSCSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR |
| 4532 | 10029 | A | 4828 | 2 | 321 | KAVLRRKFATNT*KK*TSQIKNLL KKLQEKKNFKPKVSRRTIQRSEQK *IQTRKPGEKINKTKGSSSSSSSSSS SSSSSQREDLNQIGNEREDITTGTT EIQ |
| 4533 | 10030 | A | 4829 | 132 | 290 | LVTSE***IYQIFFSPEMESHVSQA GVRWSNLASSLHPLPPGFKRFSCFSL |
| 4534 | 10031 | A | 4830 | 645 | 1201 | GGRDLLRTHSVGPSTPQTIPVLTPPG *CACTQDVSPHS/PPMKELWPGA PQGSPPGRLSPQPPH*RPSHPCTLW PAL/PGLASTEGWGAIALYLEKNW GREGLNLPPA*PFCPPQSPHGSVLF PSKASREAPTSNPCLQPOIPRLPSR PKAQAPATHLGGAATHRISAGVAR VCAGAFGGQA |
| 4535 | 10032 | A | 4832 | 115 | 454 | TMMTSWINCFRKG*DDVEHHAH NLRGKKFILFLPIQEGLTRGRKQ*AN TVGHFQLGFRLYKISGLEKLKLSKL STQWLLKPLHPDQL*TRAELLG*ES LDKYDQDPEALIR |
| 4536 | 10033 | A | 4833 | 1 | 638 | ERQSVPGFKASQDRLTLLVRAYTN Q*LKLRLIFHFENPRALKNCAYS TLVLCQWNNKAWMSAHLFTGW LTKYFKLTIETCYCEKTPFKILLFI DNLAGHPRALMEM*KEMNVFMPA KTTSIMLPLASSFNSYYLRNRIHRTF VVVAQSWLQCPTTAISDIQIGPVAM GLLLIPSAFVLCWLSIQQVSKLKH HSHHSYFLRFWRLTA |
| 4537 | 10034 | A | 4834 | 2 | 6053 | KEILQEYLEISSLVQDEVVAIHREM AAAAARIOPEAEYQGFLRQYGSAP DVPPCVTFDESLLEEGEPLPGEQL NELTVESVQHTVQLLGKRQVLQEA LQGLQVALCSQAKLQAQELLQTK LEHLGPGEPPPVLQLQDDRHSSTSS QEREGGRTPTEILKSHISGIFRPKFS LPPPLQLIPEVQKPLHEQLWYHGAIP RAEVAELLVHSGDFLVRESQGKQE YVLSVLWDGLPRHFIIQSLDGSRL RMEAADPGSPALQNLRLLEGEGFPS IPLLDHLLSTQQPLTKKSGVVLHRA VPKDKWVLNHEDLVLGEQIGRVPQ RGSNSQRAWVRGPNTGAPHPGVGS RMGRKRRREL RDWEGRGRSPRPFQ GNFGEVFSGRRLRADNTLVAVKSCR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ETLPPDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYVMELVQGGDFLTFLRTEGARLRVKTLQMVGDAAAGMEYLESKCCIHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYSSES DVWSFGILLWETFSLGASYPNLSNQQTREFVEKGGRLPCPELCPDAVRLMEQCWAYEPGQRPSTSTIYQELQSIRKRHRPRCSSSAAPAHMLTALHSPGLLPPASTLPAGCSAVSSLCPCCCQGFLFRAETIKPLVPTEHSWHVHSSGRQVSEGTSAGNIEQARKGKGLEEC AVPTGGSTPLPEGRNDRDLRLPGPEPASEAGGPARGRRTERSGCPGAQLGPRQRPPEQGATGERAPAFACVAACTRAAVPGRVCVEASMKLKKQVT VCGAAIFCVAVFSLYLMLDRVQHD PTRHQNGGNFPRSQISVLQNRIEQLE QLLEENHEIISHIKDSVLELTANAEG PPAMLPYYTVNGSWVVPPEPRPSFFSISPQDCQFALGGRGQKPELQMLTVSEELPFDNVDGGVWRQGFDISYDP HDWDAEDLQVFVPHSHNDPGWIKTFDKYYTEQTQHILNSMVSKLQEDPRRRFLWAEVSFFAKWLVGNGQLEIATGGWVMPDEANSHYFALIDQLIEGHQWLERNLGATPRSGWAVDPFGYSSTMPYLLRRANLTSMLIQRVHYAIKKHFAATHSLEFMWRQTWSDSSTDIFCHMMPFYSYDVPHTCGPDPKICCQFDFKRLPGGRINCPWKVPPRAITEANVAERAALLDQYRKKSQLEFRSNVLLVPLGDDFRYDKPQEWDAQFFNYQRLFDFFNSRPNLHVQAQFGT LSDYFDALYKRTGVEPGARPPGFPVLSGDFFSYADREDHYWTGYTTSRPFYKSLDRVLEAHLRGAEVLYSLAAAHARRSGLAGRYPLSDFTLLTEARRTLGLFQHDAITGTAKEAVVVDYGVRLRLSLVNLKQVIIHAAHYLVLGDKETYHFDPEAPFLQVVGWEEAEPMMVLPFRLTEFQDDTRLSDALPERTVIQLDSSPRFVVLNPLEQERFSMVFLVNNSPRVRVLSEEGQPLAVQISAHWSSATEAVPDVYQVSVVRLPALGLGLVQLQLGLDGHRTLPSVRIYHLGRQLSVSRHEAFPLRVIDSGTSDFALSNRYMQVWFSGLTGLLKSIRRVDEEH EQQVDMQVLVYGTRTSKDKSGAYLFLPDGEA\SPTSPPCCVSLKALSQRWFRMTSTFTRSGFTICQWRGCLWYHPWWTSGTTSTRSWPCTSIQTSTAR/VIFFTDLNGFQVQPRRYLKKLPLQANFYPMVMAIYQDAQKRLTLHTAQALGVSSLKDGQLEVILDRRLMQDDNRGLGQGLKDNKRTCNRFRLLLERRTVGSEPFFSKLAAMFR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GLIFHSSRSGNREVQDSHSTSYPSLL SHLTSMYLNAPALALPVARMQLPG PGLRSFHPLASSLPCDFHLLNLRTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFDC GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG |
| 4538 | 10035 | A | 4835 | 1 | 6606 | MGSSELCSPPQGHGVLLQMQEAE RLLEGMRKWMAQRVKSDREYAGL LHHMSLQDSGGQSRAISPDSPISQS WAEITIQTEGLSRLLRQHAEDLNSG PLSKLSLLIRERQQLRKYSEQWQQ LQQELTKTHSQDIEKLKSQYRALAR DSAQAKRKYQEASKDKDRDKAKD KYVRSLWKLFAHHNRYVLGVRAA QLHHQHHLHQLLLPGLLRSLQDLHE EMACILKEILQEYLEISSLVQDEVVA IHREMAAAAARIQPEAEYQGFLRQ YGSAPDVPPCVTFDESLLLEEPELEP GELQLNELTVESVQHTLTSVTDELA VATEMVFRREQEMVTQLQQELRNEE ENTHPRERVQLLGKRQVLQEALQG LQVALCSQAKLQAQQELLQTKLEH LGPGEPPVLLLQDDRHSTSSSEQR EGGRTPTLEILKSHISGIFRPKFSLPP PLQLIPEVQKPLHEQLWYHGAIPRA EVAELLVHSGDFLVRESQKGQYEV LSVLWDGLPRHFIIQSLDGSRLRM EAADPGSPALQNLRYRLEGEFGPSIPL LIDHLLSTQQPLTKKSGVVLHRAVP KDKWVLNHEDLVLGEQIGRVPQRG SNSQRAWVRGPNTGAPHPGVGSRM GRKRRREL RDWEGRGRSPRPFQGN FGEVFSGRRLRADNTLVAVKSCRETL PPDLKAKFLQEARILKQYSHPNIVR LIGVCTQKQPIYVMELVQGGDFLT FLRTEGARLRVKTLLQMVGDAAAG MEYLESKCCIHRLAARNCLVTEK NVLKISDFGMSREEADGVYAASGG LRQVPVKWTAPEALNYGRYSSES VWSFGILLWETFSLGASYPNLSNQ QTREFVEKGGRLPCPELCPDAVFRL MEQCWAYEPGQRPSFSTTYQELQSI RKRHRKHRAKTERKGTRGMRCTD RRQHFPARGAQRQRPKATWAGAG FRGWRTRAEPQRSAPAARGPAGE LQQRAEQGATGGRAPAFACVA AACTRAAVPGRVCVEASMKLKKQVTVC GAAIFCVAVFSLYLMLDRVQHDPT RHQNGGNFPRSQISVLQNRIEQLEQ LLEENHEIISHIKDSVLELTANAEGP PAMLPYYTVNGSWVVPPEPRPSFFS ISPQDCQFALGGRGQKPELQMLTVS EELPFDNVDGGVWRQGFDISYDPH DWDAEDLQVFVPHSHNDPGWIKT FDKYYTEQTQHILNSMVSKLQEDPR RRFLWAEVSFFAKWLVGNGQLEIA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TGGWVMPDEANSHYFALIDQLIEG HQLERNLGGATPRSGWAVDPFGYS STMPYLLRRANLTSMLIQRVHYAIK KHFAATHSLEFMWRQTWDSDSSTD IFCHMMPFYSDVPHTCGPDPKICC QDFDKRLPGGRINCPWKVPPRAITE ANVAERAALLLDQYRKKSRLFRSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLFDFFNRPNLHVQAQFGTSLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTSTRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSGLAGRYPLSDFTLTEARRTLG LFQHHDAITGTAKEAVVVDYGVRL LRSLVNLKQVIIHAAHYLVLGDKET YHFDPEAPFLQVVGWEEAEPMMVL PFRLTEFQDDTRLSDALPERTVIQL DSSPRFVVLNPLEQERFSMVLLV NSPRVRVLSEEGQPLAVQISAHWSS ATEAVPDVYQVSVPVRLPALGLGV LQLQLGLDGHRTLPSVRIYLHGRQ LSVSRHEAFPLRVIDSGTSDFALSNR YMQVWFSGLTGLLKSIRRVDEEHE QQVDMQVLVYGTRTSKDKSGAYL FLPDGEA\SPTSPRSPCCVSLKALSS QRWLRTMSTFTRRSGFTICQGWGR CLWTYHPWWTSGTTSTRSWPCTSI QTSTAR/VIFFTDLNGFQVQPRRYLK KLPLQANFYMPVMAYIQDAQKRL TLHTAQALGVSSLKDGQLEVILDRR LMQDDNRGLGQGLKDNKRTCNR RLLLRRTVGSEPDFFSKLAAMFRG LIFHSSRSGNREVQDSHSTSYPSLLS HLTSMYLNAPALALPVARMLPGP GLRSFHPASSLPDFHLLNLRTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFDC GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG |
| 4539 | 10036 | B | 4836 | 114 | 255 | VQPRRYLKKLPLQANFYMPVMAY IQDAQKRLTLHTAQALGVSSLKDX* |
| 4540 | 10037 | A | 4837 | 1 | 452 | LDGRQLSV/SRHEG/FP/LRCIDS/GTS ELALS/N/RMQVWFSGLTGLLKS RRVDERHEQQVHMQLVYGTRTS KDKSGAYLFMPDGEAKP\TSPRSP CCVSLKALSSQRWLRTMSTFTRRSG FTICQGWGRCLWTYHPWWTSGTTS TRSLHFSFN |
| 4541 | 10038 | A | 4838 | 3 | 3543 | QLGRLGPERRGGRALTVCEASMK LKKQVTVCGAAIFCVAVFSLYLML DRVQHDPTRHQNGGNFPRSQISVLQ NRIEQLEQLLEENHEIISHIKDSVLEL TANAEGPPAMLPYYTVNGSWVVP EPRPSFFSISPQDCQFALGGRGQKPE LQMLTVSEELPFDNVDGGVWRQGF DISYDPHDWDAEDLQVFVPHSHN DPGWIKTFDKYYTEQTQHILNSMVS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KLQEDPRRRFLWAEVSFFAKWWD NINVQKRAAVRRLVGNGQLEIATG GWVMPDEANSHYFALIDQLIEGHQ WLERNLGATPRSGWAVDPFGYSST MPYLLRRANLTSMLIQRVHYAIKK HFAATHSLEFMWRQTWDSDSSTDI FCHMMPFYSYDVPHTCGDPKICC QDFDKRLPGGRINCPWKVPPRAITE ANVAERAALLLDQYRKKSQLFPSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLDFFNSRPNLHVQAQFGTLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTTSRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSGLAGRYPLSDFTLTEARRTLG LFQHHDAITGTAKEAVVDYGVRL LRSLVNLKQVIIHAAHYLVLDKET YHFDPEAPFLQVDDTRLSDALPER TVIQLDSSPRFVVLFPLEQERFSMV SLLVNSPRVRVLSEEGQPLAVQISA HWSSATEAVPDVYQVSVPVRLPAL GLGVLQLQLGLDGHRTLPSVRIYL HGRQLSVSRHEAFPLRVIDSGTSDF ALSNRYMQVWFSGLTGLLKSGSLC FLASIRRVDEEHEQQVDMQVLVYG TRTSKDKSGAYLFLPDGEA\SPTSPR SPPSCVSLKALSSQRWLRTMSTFTR RSGFTICQGWGCLWTYHPWWTS GTTSTRSWPCTSIQTSTAR/VIFFTDL NGFQVQPRRYLKKLPLQANFYMP VMAIYQDAQKRLTLHTAALGVSS LKDGQLEVILDRRLMQDDNRGLGQ GLKDNKRTCNRFRLLLRRTVGSE VQDSHSTSYPSLLSHLTSMYLNAPA LALPVARMQLPGLRSLFHLPLASSL PCDFHLLNLRTLQAEEDTLPSAETA LILHRKGFDCGLEAKNLGFNCTTSQ GKVALGSLFHGLDVVFLQPTSLTLL YPLASPSNSTDVYLEPMEIATFRLRL G |
| 4542 | 10039 | A | 4839 | 2 | 438 | FVPAKVAGAAEPDEDGGRSRLRDC GDYTPSERLGPKGAMLWFQGAIPA AIATAKRSGAVFVVFVASDDEQSTQ MAASWEDDKVTEASSNSFVAIKIDT K/QMHLLKSETSVANGSQSESSVST PSASFEPNNTCENSQSRNAELCEI |
| 4543 | 10040 | A | 4840 | 1 | 1608 | |
| 4544 | 10041 | A | 4841 | 1 | 3117 | MAPEWRPGTTASLPSGPGARSVCSL RSPEAGSASVFVRLCGPRNLGWFGP HLRLRTSAHARQRHPKTRASAREN TSRHSRNPSVSVPODLLSLASRCAG SIPITLESCLPVGLSKDVWPLTIEPKV KVFIFNLKLPDCPSTMKNPASLLFSL FEGEWAI AEVLSDIWCTGVLAINK DQVLTIGFDINEFLSCSSSSKKSMSC SLTGSLALQPDQQQDHETDSSPAS AYQRIWEAFANQSRERAFLQDT FPEGFLWGASTGAFNVEGGWAVG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GRGVQPKHVKEAFRLLNKSIIRVET PDVNLDQEEIQMEVDEGAGGING HADSPAPVNGINGYNEDINQESAPK ASLRLGFSEYCRISNLIVLHLRKVEE EEDSALKRSELVNWYLKEIESEIDS EELINKKRJIEKVIHRLTHYVEYFSS LHASQITHYKVFLSWAQLLPAGSTQ NPDEKTVQCYRRLKALKTARLQP MVILHHQTLPASTLRRTEAFADLFA DYATFAFHSFGDLVGIWFTFSDFEE VIKELPHQESRASQLQTLSDAHRKA YEIYHESYAFQGWLAFTHMSQTLA NKIRVRGMAQESCSHGSSVGYLQH PGSEQVQFPRTTSPCSSQQLQGHQC TAGPPPPPGGGMVMMQLSVNNPQ SCAHSPQWKQNKYYCDHQRGQK CVEFSSVDNIVQTSLNCTDPVVCVP SSFFVIGDSGIPLEVIAGSVSADELVT RIHKVRQMHLKSETSVANGSQSES SVSTPSASFEPNNTCENSQSRNAEL CEIPTSDTKSDTATGGESAGHATFL FREPSGCSDQRPADLNIRVERLTK K\LEERREEKRKEEQREIKKEIERR KTGKEMLDYKRKQEEELTKRMLEE RNREKAEDRAARERIKQIALDRAE RAARFAKTKEEVEAAKAAALLAKQ AEMEVKRESYARERSTVARIQFRLP DGSSFTNQFSPDAPLEEARQFAAQT SVRVTSSEPPNPASSSKSEKREPVRK RVLEKRGDDFKKEGKIYRLRTQDD GEDENNTWNGNSTQQM |
| 4545 | 10042 | A | 4842 | 3 | 790 | GARGTPFLSPASVESSVLLCLLVPHF VLSRGPPASPPSSYHPSLGPGG/GGQ *PLPEYGLESSEQN*GLSPGEDPGNP GGPFWGSG\PAAGSLMEA*GNKRDA PPPPG\DPSCSAPC/GDPPGMQGIQDS LPCHTASQKGGAFPFGPMAPGRVL HQQGPL*GPSRLSQESPSAGPPMPQ LPSWVLCQVRPRAWGCWEPKGPPG TQFPPRFPDPSGTPCPGYLEIFLLDP IPPRNWLAPLAAAAQ**/PWGRWE MPMALPRGGLPLYT |
| 4546 | 10043 | A | 4843 | 1 | 1026 | |
| 4547 | 10044 | A | 4844 | 1 | 722 | MALEQRLKGGSGAALRSKAFPAEG TAGAKALGQESDWSIGGAVSKPVF VQSVRELVADPCASNPCHHGNCSSS SSSSSDGYLCICNEGYEGPNCEQAL PSLPATGWTE/CHGTPTASACSCYS GA*Q/QSCLALRQR*HCLPGSRKQG\ KSCRNEMGSSGGDPYCLWECQF* QLCGWPPGIL*SATEHLSQDSARCH CLTDFALEGHGHRIPTVLPHRWTKC DPPSGFRGTGPPGGDARLGE |
| 4548 | 10045 | A | 4845 | 2 | 2028 | CSPAAPRRPVRSCCPRWCCCCCSE RGPEAAPWPTRCPRPCL/LPGPCAA QPCRNGGVCTSRPEPDQHPAPAGE PGYSCTCPAGISGANCLVADPCAS NPCHHGNCSSSSSSSDGYLCICNEG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YEGPNCEQALPSLPATGWT/AIHGT PTASACSCYSGA*QNPASLSGNGDT AYLAAENRAESCRNEMGSSGGDPR YCLWECQF*QLCGWPPGIL*SATEH LSQDSARCHCLTDFALEGHGHRIPT VLPHRWTKCDPPSGFRGTGPPGGD ARLGE*SLY\CFVNDVTKS/NCGFA LNSGGEVSTCVPGESHANDLECSG KGKCTTKPSEATFSCTCEEQYVGT CEEYDACQRKPCQNNASCIDANEK QDGSNFTCVCLPGY\NGELCQSKID YCILDPCRNGATCISSLSGFTCQCPE GYFGSACEEKVDPACASSP\CQNNGT CYVDGVHFTCNCSPGFTGPTCAQLI DFCALSPCAHGTCRSVGTSYKCLCD PGYHGLYCEEEYNECLSAPCLNAA TCRDLVNGYECVCLA EYKGTHCEL YKDPCA\KSACLNGATCDSGLNG TCICAPGFTG*ECDIDINEC/ATVTP CHHGG\SCLGDQPNGYTCHCPHW VGANCEIHLHWEVPGTWAESLTNM PRHFPLTFIHWEFPLRGPFHPYADHP DRGDLPHQPH |
| 4549 | 10046 | A | 4846 | 1 | 703 | TISCPA VRSRRPRRISCLSCPGGGGA ASGLQRAAGGTGLSWVPAGLRVCC SQRSWRPAKEEQPVQTPRRTGKGG EISDMEKPYNKNEGNLENEGKPEDE V*PDDEGKSY*EEKPYA*GNTECEG KLKADGEPGDEGQLEDNGSQEKQG KSECEGKPQGEKGPASQAKPESQPR AAEKRPA*RLCGPGKAKK/NKPDQ GDRITFPQGLSGGLTGKASEQ*GDD ERMWRCVKGSRGA |
| 4550 | 10047 | A | 4847 | 180 | 866 | GAYVHGGRGGLCVQSLFQGVSSSDF CPPIPTLVPTLRPRAPCLWCTQDPAR PPCQSQRRLGPFQVAGLKPSGGLL PNILLPESPSKRNFHNGQLVPVQTVFG GGSRGPPLLVPPLPLFVFPFCGCF LSQPRGHRSPSP*EEG*STPLLSVC HSHTDLWGLSWAVPAGWTGPSALF SPQAVNRLPITRPAPTHPHSFPREAP GRW*TPLPTSYSQSLLFYGDLPVK |
| 4551 | 10048 | A | 4848 | 112 | 679 | KI*NMWCYS DTGQFN VV KLSVLL*I IYIFNKILSSFLVKTGKLSLKS VN/NK QOSRITKTSKENKRGGM R*DIKTF YVFAVIKSVLYMQI*ID*WKIESSET DLHISHLIFDKDNKMEKSLKK\WDI VYSSHRKIINLDL*HIPYVNINMIWN IDLKIKRFF*IAT/ENIFVTFSNVGND FLKYQLKSKIKKLKMRMVVYQMV P |
| 4552 | 10049 | A | 4849 | 33 | 394 | GSVWHHPFEGALRGPIPGAAGKPG LGTPSHPGLSHPAACAACPRLPGL CSCAPGSAPLPRLRP*/PAPCGSSDS VPRTP/GRRGLGSPGPAPAPKAE* LLQGGEFFSDPQPLAPEPRQLR |
| 4553 | 10050 | A | 4850 | 2 | 269 | LSGVCTVHIRGVCVWAGGNPSGTE LPGPLPPRPSASPPHPPQ*GVALP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PVLFCFLVLPHPPTPNLIYPPCTVPFS PLPAPFAFFCW |
| 4554 | 10051 | A | 4851 | 1 | 543 | LLSKWIIITPSGAGSGDPPPAASPRR KQRMKIMKTTRSQTTPGRAPAASA SSPTL*TPGRDLESRLRP*PTNLPVR TPPGTAAVCPLLHRPAPQKAPVLGP ARV*ERGE/DANATPKREGLKRA/PP NDTLDFLWLGTSPSTKJKWTRPPAV EPLLVLHPTPTLPPLPVVPIVTQRVE YQGRFF |
| 4555 | 10052 | A | 4852 | 831 | 1301 | FFVFTFKYKNTILLCVINQGPSSKNL FFFQGRDIHQFILSFVFRAGHLVPSQ ASPTSKRPKPFSLIPNPYLLS*FPLLE KLVINFLKKKFPTTRASP*PNQSTSR SSPFSYPGRRVPPLQTSSVPELRTPY WTGAPPLNGSSGYVSPTLPPPLMH |
| 4556 | 10053 | A | 4853 | 1 | 1222 | |
| 4557 | 10054 | A | 4854 | 2 | 563 | AHVIIYRFSMH*VITDVIPMLEVRSV YEINDVGTPEGEQTPPLPTPVGGSN PQPIPAQSHPTSSSSSDGLRDNPVW LKVKN SPLKQSPGYQTELVIQLVW VGGEPPQIASLAVNSSYGLVDFGN CNGIAMVDYLQKAVLLNLGTIELY GSNDPYRREPRSPRKS RQPSGAGLC DISEGLVPSKA |
| 4558 | 10055 | A | 4855 | 648 | 1377 | EYLHGGWEHLQKRSLSPATGGGQG QLGAEGGP/GPGGGAAPAHPL LAPN QACGVGLIDWRPRWTRGGTAAAG ARTPNLNP GAALTP/GRHSCVSVKK GSELELSRRR/TLPVVSPPGGGGCE MLRPDPASSPSSQTP*PVP GAE AQT LALSCPPNSCPAKEVGAAGF*APLH LLSPSVGEGGGASGSTPKVSSFPLPF GGPLHSP*Y*PGPENWEGGGDEGPL SHPARVPAAQSETECVPTESPFQ |
| 4559 | 10056 | A | 4856 | 3 | 394 | SQAPS/GVAAHTPPLS*AWTQPWNS IHMALASTRPNMPLRSGPAICMPQL QLQELFTRSLVESELRIAPSEYPDES PIEQLEERRQLLEQPISLDVMLEPYI LRRSKLDLLYTDSDSLQLYKEQGE GQGDR |
| 4560 | 10057 | A | 4857 | 3 | 666 | SLLPKIFIGCLRRASSGPGAGNMLGS PSPQPLVSILGIAESWSTLPQGQPPA NPEAWAGPAGAKTDKSKT*GHFTP ETLPNVPKKDPLQLGA*KPGGSKPS EE/VWSQ/SPGPWLRNSGFFPPSLNP RWGPFPTLWERF*NCSQPFRALRN PPVPL*GVL RASNWP PPHPHTHPA NMPPAPPRVRLRSSSTSAPPPWGCT QGPRGARAGA*AGAASS*SRGR |
| 4561 | 10058 | A | 4858 | 3 | 361 | FFFFRKWVNIFANYM*KKLILKIYQ QL*KLNHKVQ*LDL*MNKQNFHQK TTQM/AKKHLTGCTKLLICREMKK KTQ*QRNHLTPIRMATYFLKNAN/C W**CNKNETHVGCWWKTKM*SLF |
| 4562 | 10059 | A | 4859 | 3 | 397 | DQPTDIILDEQ*LELFHLRTGIRRG PVSSLPFN/IRAIRQEK*IKGIQLGKEI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KLALFADMILYLENPEDS/AQKL/LR LINNFSQVSGYKINAQKLGAFLYTN NVQAE/SQIKNPIPTVAIKKLKYLKI HLAKE |
| 4563 | 10060 | A | 4860 | 2 | 328 | AHIDAVNEAMRLLEHGFHAPTMSW PVSGTLMVEPIETEDHA*LDRFWDA LINLLQGIADIEDGRICPRVNPLKMS PHSLTCVTSSHWDRA\YSEKGAAFP LPFVKPENK |
| 4564 | 10061 | A | 4861 | 13 | 410 | NKMRRQATDRDKMLAKDTFDK\GT LEIYNQFLKFNNKKMSIPIK*WAKN L/NSHLTREDIQVANKPMKRCSTSY FIKEMQIKAMTRSRCADIKMAKIQT TDDIKC*RTCTRSTNFPFPALHLFYQ LTFRKSSISH |
| 4565 | 10062 | A | 4862 | 3 | 293 | DKGLKGFRGFPTFTSFGQPTWLGLG LDLPEPGN*GPGFGCGP/NSRVGPTL SNLGPGERGPPGPPGLGV*ALKGK RADKKGGASFFPGF*KFPVGLP |
| 4566 | 10063 | A | 4863 | 125 | 366 | GIPGERRLEPPG/PKGPPGLSPQIKGN NGPGPQN*VFFGGFKTKVPFGAQG GS/GNPGPKPIFPPGPPKGRKYRVGP MAPPLQ |
| 4567 | 10064 | A | 4864 | 79 | 336 | HIATFNALSYVQASKRDKKFFACAP NYSYAVLCECLSSSIHLSSACSHVH C*RHDDDDALLWQPHGSIRDDMR*HI ATFNALSYVQASKRDKKFFACAPN YSYAVLCECHRRVFIYRQPAPMST VFYNRKDCLQ/TVDRMLIHKVASLK TNDPILSIQAPK |
| 4568 | 10065 | A | 4865 | 2 | 512 | KIQIASIRNEIGH/LLTDATYIQRRLR E*CGQLQANKFDNLNGRDKFPGRH KLPKLIQKEMEAGRSGPLSPRVLG LQA*ATVSGLTGKFKYKTCKEEIPIIL TILFQKTEKGTLO\SS*EETSTILIPNQ EGKKNFQNGCLSMDDPGTGKVPLTK ILVNQIQQSVIHKDNISI |
| 4569 | 10066 | A | 4866 | 466 | 1451 | EVCGLKKARISLFFF*DGVSLLCCPG WSAVAQSRLTATSASRVK*FSCLSL LSSWDYKRPPRPANFLHF**RQGF TMLARLV SIS/WIS*SVPPWPPKVLE L*AKAGDSLEPGSSRLQ |
| 4570 | 10067 | A | 4867 | 3 | 379 | NKSCQGPRTSFASAGWALKNPRWQ EQKEGLGKAGRPSGMNSSASSPTPG RKRELGMGSPSLSRSP*CE\GRSDR LG*PP*GGQGGGGH GAPSTPGPGG\ GPGDFHSKPPDPSLVPRPTEARGSP GP |
| 4571 | 10068 | A | 4868 | 2 | 1718 | SEGAPRRGAWGGPPARSHTLAPT PLPP/GPLSLCFACKWLGV D/HRDG AG*LGSQKAGGRGHPGMGQGKGT PPAHAW*PTGWCTGKP*KLGFLCPF HIPVSLACFLLSCAASDFSVL TWQ LWGP*EPTEGGHSPFPSCRC/HRQE EGFLPVWQSPRQRPRMRPDSAPPST SARASKVGPGRGLPLL NFG/QRPNL TPYGPAPALALS*PPQRWEELAEGA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PGPQPPVASKGPFSS*PKVLREPAVE TSSCASAPLAVFVRGVHTCIGG*AP GLSGGHPLTVSF*IGGIEGLDCLSPQ *AWGPGLGLEVCCGSHQASPPGPG VLGAPCPPPPCPPQGG/PAQPVGPS/P SHHGGERE*RGRPHSKLPLPPGVWG GC*RIHSRGPPGLSQPLFCF*PRRLS\ PAQPA*SKGGSRLVLSFCFLLPGS* GTRASGRGHSPSLKPGPGRAGRQIG ETRGS\GSPGE*GCWSQNWDRGPA GQPWATSRVSIVRGWRVPGVAGAG FLAVLPWAPPSEARWQEADQNPSA FGPKEWEAAFLPNLPCQGQQRGSPSP PPPPGCRNGDPSQGLGAGAEYSLGP LPYT |
| 4572 | 10069 | A | 4869 | 253 | 451 | RWKA WFGREIKGNNPRCKRGGGK HGTG/EEIKGNNPRWKRGGGKHGT GGK/YKGNNPRWKRGGGKHGTGG K/YKGNNPRWKRGGGKHGTGGKL K/SNNPRW*REGGKHGSGGK/YKGN NPRCKRGGGKHGTGGKLK/SNNPR WKRAGGKHGSGGKFKEIPDGSVK VESMER |
| 4573 | 10070 | A | 4870 | 2 | 269 | EGGLGLNRFP PPPGPPRRPAAACMS AP*PQR/HWPP/SPREEKASLNEPGG PGRGRGRGSGQLHGEGGPRGGE/R GNWP GGMEGEGGIDAPAS |
| 4574 | 10071 | A | 4871 | 20 | 312 | SVMNGTSICKCRANDETGLSPSPAG PKSRSRRLS*LWRPSAATDSGSPPT* PVPTSPPPAPTPARPGSRAPSSPGLA PTLTGPGG\PLRPPPPPAEEP |
| 4575 | 10072 | A | 4872 | 299 | 472 | KSISVATANPGKCLSCTNSTFTFTTC RILHPSDITQVTPR*/GVPGKSGASLL SSAVFS |
| 4576 | 10073 | A | 4873 | 1 | 3454 | MKHTLIPRIKNACLQMSSLAVPVNS LVCLGKILEYLDKWL VLDGILPFLQ QIPSKESAVLMGILGIYKCTFTHKLG ITKEQLTGKVLPHLIPLSIENNLNQF NSFISIIKEMLNRLSEHKTKLEQLHI MQEQQKSLDIGNQMNVSSEETKVTN IGNQQIDKVFSHIGADLLTGSDSEN KEDGALNVPPAGAKPTQQRPTDMS ALNNLFGPQKPKVSMNQLSQQKPN QWLNQFVPPQVSPATGSSVMGTQM NMIGQSAFDVCSNEDLPEVELVSL EEQLPQYRLKVDTLFLYENQDWTQ SPHQRQHASDALSPVLAEEETFRYMI LGTDRVEQMTKTYNDIDMVTHLLA ERDRDLELAARIGQALLKRNHVLSE QNESLEEQLGQAFDQVNQLQHELC KKDELLRIVSIASEESETDSSCSTPLR FNESFSLSQGLLQLEMLQEKLKELE EENMALRSKACHIKTETVTYEEKEQ QLVSDCVKELRETNAQMSRMTEEL SGKSDELIRYQEELSSLLSQIVDLQH KLKEHVIEKEELKLHLQASKDAQR QLTMELHELQDRNMECLGMLHESQ EEIKELRSRSGPTAHL YFSQSYGAFT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GESLAAEIEGTMRKLSLDEESSLF KQKAQQRVFDTVRIANDTRGRSIS FPALLPIPGSNRSSVIMTAKPFESGL QQTEDKSLLNQGSSEEVAGSSQK MGQPGPSGDSDLATALHRLSLRRQ NYLSEKQFFAEWQRKIQVLADQK EGVSGCVTPTESLASLCTTQSEITDL SSASCLRGFMPEKLQIVKPLEGSQT LYHWQQLAQPNLGTILDPRPGVITK GFTQLPGDAIYHISDLEEDDEEGITF QVQQPLEVEEKLSTSKPVTGIFLPI TSAGGPVTVATANPGK\CLSCTNST F/TLFTTCR/IYLHPSDIT\QVTPSSGV PFHLSCG\SSGSSFHSNTAVNSPALS YRLSIGESITNRRDSNYNLSVGTME VGPKFLQER\GIS\AKVYHSP\SENPL QPLPKISLAIPSTPPNSPSHSPCPSPL PFEPRVHLSENFLASRPAETFLQEM YGLRPSRNPPDVGQLKMNLVDRLK RLGIARVVKNPGAQENGRCQEAIEG PQKPD\SAVYLN\SGSSLLGGLRRNQ LPVIMGSFAAPVCTSSPKMGVLKED |
| 4577 | 10074 | A | 4875 | 1 | 638 | LAWGGKGKGASSDSGGLVDSISTL TPTPGDTNT/HSDLIVRGGAYGGQW AHGVLAQVQPSVGAETP*PQMGE *TDVCGSQSPHICSLTLRVGATML GKAR\WKPLG*TLPR\KIV\NSKATC SPGGTAKVSAAIRGLGRCRVVTPTA ASFHSS*\WLVWKTGGSRRKKDSES WVNLTRTPIATAVPDMTTDSLQIQ SIPGHPVLQPIDPGESL |
| 4578 | 10075 | A | 4876 | 31 | 448 | PKSLLSLVKINYGYPK*QATKAK LDNWDYIKLQSFCTTKIMNRVRRQ PAE*ENIFANQTSKGLISKIYKELK QLNSKKANNLIKWNWSDDLNR/HFSN EDIQMASRYMKK\STSQIIREMQIK TTMRYHFMPIRMTT |
| 4579 | 10076 | A | 4877 | 3 | 286 | KFTFKRHHHLQLLKRK*DS*V*T*Q MFMEQIKEDLSKQRDN\SCS*IGKLSI AKNIYVS\NPG*FDAIPIKIPARFFYA FGLYCRNSVSLSPRLN |
| 4580 | 10077 | A | 4878 | 3 | 236 | ATHSTLPSFQGPVSLASMTVVGIDG KASRPLQTP\VCQLDQHSFLHS/FLV IPTCPVPLL*GILTKLSASLTIPRLQ P |
| 4581 | 10078 | C | 4879 | 206 | 262 | MVAIGTGYRRPGLRTFLN* |
| 4582 | 10079 | A | 4880 | 2 | 756 | LTSSRGARPAPLRAPAR/LDPAFRAN PLRSYGSGLPTFPYLHCSNMPKAC SPWRPAADMGT\PGARFTPSPPDFQ GPARAPPDAAGTATLSKARAPLSGR NPFQGRPCPSQRKENS\PRSSRRTSPG SRRVTD\TGRLAGAPCSATPD\SGI*T RLPFRIGRGAPEAIAPSLRNGARPSL RTD*PMFQLLGYNWN\PSVVRPSKV LRLNICYYTP\SHAPAAAPP\GPADFQ GPARAHRTPEPRRFPRHGPLSRGE P |
| 4583 | 10080 | A | 4881 | 3 | 322 | MGSVTGPLYSGYKEEVV\CTLVEV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FPSLLQVSRNPRMPFDLGLIFCLG GQGFPRATTVSGHWPE*LSQSSSSP KLRPPTL*SKPAHPGAAEALKAVPR TSAGAR |
| 4584 | 10081 | C | 4882 | 240 | 500 | MQNGLSGAYFPSVWAAKDSQERR RSPATGRNDSPRAPLPRSSARRPSK ANLHTLGQLKLSSRCRAPRLRRAA RTRSXSQXWRRXTT* |
| 4585 | 10082 | A | 4883 | 22 | 696 | CTFGSFPFGLSAWSFRASLPPAPAP GPNERFRSPGAGGFWGVDAAGQPA PAEVLGTALRASAAPGCAD*NPKKI KWHPG/SFCSPGEGMEILQQVCSKQ LPPCNLSKEDLLQNPYFSKLLNLS QHVDSEGLSLTLAKEQAQAWKEVR LHKTTWLRSEILHRVIQELLVDYYV KIQDTNVTSEDKKFHETLEQRLVT ELMRLSPSQEREIPPLGLEKADLL E |
| 4586 | 10083 | A | 4884 | 1 | 594 | AVVHFRLPLPGPFILCLSGPRFPQP AAPGPNERFRSPGAGGFWGVDAAG QPSPAEVLGTALRAPAAPGLQVCF KGSAGGASGKRSSGRVIPA/MWPET VVALGNPWTVQTEGKVGAGEPVL HFDSSRAL*GSVSCENNL*NQFNRS SCSV*RQALRI*KTPSEHLKCLGPC SSVFNTSECRRVENRSLNCPFTPCNL |
| 4587 | 10084 | A | 4885 | 2 | 326 | VKTAEFVNKWQKNSTKLWNSQAQI DSSSLVNQINDLRQTEIWMGDRIMN LESRIQMCDWNTSDFCVTPQYNE TEH*WKKVKRHLEGREENLT*IVK LKEQDFEASQ |
| 4588 | 10085 | A | 4886 | 2 | 373 | VLLTPEERTVVIALWRKVNVAALC R*GAWA**L*AYPWTHRFFESFGDI DSSDAVMGKPIVNAHGKNVLGAFS DGQSHLDNLLGTYSQSELHCDKL HVDPENFKLLGNVLCVLARNFGK EF |
| 4589 | 10086 | A | 4887 | 3 | 332 | HLSIINLVNQLNSPLKAYTLPVWIP SSVRGPTICCLQEIHFAKNTYKLKV KELSSSFQANEKEKHADKTGFKPK L*REKNGHYIMIKRSVQKENTYIYM FLIADPDIC |
| 4590 | 10087 | A | 4889 | 1 | 304 | HSCSSMRMPPLPTPPP/IVLCPPHPSP LIKALVSSKPP*VPSAETWPVAAL GA*VPAVLGWPLHTENVLPVPPLPL EMPRIQWHFMLCSFPQRSRADEST |
| 4591 | 10088 | A | 4890 | 1 | 254 | RPRRQFGIEGSFLNQIKNIYKKSTAN VILYVDRLNAFSLISGSSSSSSSSSS SSSS*LPVNIIRQ/EKVI*GMQIVKEE LNLSL |
| 4592 | 10089 | A | 4891 | 310 | 415 | SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRSL/DSVAQAGVQWRDLGS LQRPPPGFTPFSCSLPSSWDYRRPP PRLANFFVFSVETGFTVSARMVSIS *PRDPPASASQSAGDTGVSQAPV |
| 4593 | 10090 | A | 4892 | 2583 | 3580 | DRVSLLLPRLECNGAILAHCNLCLS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFFC\RD TVSLCYPGWSRVA*SRITATSA\PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRYPPA SASQSAEIIGVSHHTWPQEVFLFLNL FIYLRWSL\DSVAQARVQRRDLGSL QAPPPRFKPFSCLSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFIYLFYFHRDEGSLCCPGWS* TPELK |
| 4594 | 10091 | C | 4893 | 40 | 180 | MSFEAEIVLSPDRTTALHPGLQIETL SHIIIIILISTISFHQLLH* |
| 4595 | 10092 | C | 4894 | 4827 | 5060 | MWIYFWTLNSVPVIYMSTLMSIPHY FDYCCFIVSDIMLPEITFSTFILLMV ALAIRGPLHFRRHFRJNLSIATKNA* |
| 4596 | 10093 | A | 4895 | 2 | 311 | FILHVC DKLILFVSGDTFQTVSPRFL APRTFLAPLQNP*PLSPCAVHISFSRP LPARSPLPP/PRPPPPPTCSTAIPATH NPILTTHTSTPPPTLPTINLTSSP |
| 4597 | 10094 | A | 4896 | 2 | 374 | DLTPKV*SRKGKIGKLD FIRT KTFW SAKDHVKRLKRQTTDWEKIFLNHIS NK/GLLSRIYK*LQTQY*KTPSNPI/K KTA KD VKEHFTEEDIQMACNPMKR CSTSLAVRELQIKTTVRYLKIEFNF |
| 4598 | 10095 | A | 4897 | 1 | 684 | |
| 4599 | 10096 | A | 4898 | 1 | 1349 | |
| 4600 | 10097 | A | 4899 | 1 | 821 | MLQTSWGYDNPRVTQKVPPFQLNC LPMTVVLLILYAEVATDWNRVGLT QGQLLHSLRLDPWSGLTQRTFPTGA MEISPDYLPPEFIVENTERIDEREKG REQPPKKTENKAWPKMLKGKKA KGKKVAPAPAVVKKQEAKKVNP LFEERPKNFGIGQDIQPKRDLTRFVK WPRYIRLQQQRAILYKRLKVPPAIN QFTQALDRQTATQLLKLAKHYRPE T\SKRRLLAQAEKKAAGKG/VRPT KR/PPVL*AGVNTVTTLVENKEAQL DLYCAI |
| 4601 | 10098 | A | 4900 | 1 | 868 | GTRPKMPKGKKAKGKKVAPAPAV VKKQEG\AKKVVNPLFEKRPKNFG IGQDIQPKRDLTRFVK\WPRYIRLQR \QRAILYKRLKVPPAINQFTQALGP RKQATQLA*AWPTKYRPRDKAREG SRDLFGPGPRKKAAPKGTFTKRP PVPSKQ\G*TTVTTLGGGPRKASAG WWIAHDVDF\LELGLSFLA\ALCRK NGGSPY\CIKKGKQDWGRL\VNKK TCTTGRLSHR*TS\ED/NKALLKLVE AIRTNYNDRYDEIRRH\WG\GNVLP KSVARIAKLEKAKAKELATKLG |
| 4602 | 10099 | A | 4901 | 145 | 745 | RRRG\TQSCNLITTVNHISEITVIMFIE CSLCIKVIRLFHILILLDFSSKPAPPPP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PCGAPGL*TATLLSRLRTARDLGTR L*ASPASPLCAVPSPAAAAFL/SLPLP LCPSSSSARELSPTPGLSGQPAPAA SPGPG/PAG/PPPPPPLAVRPRFAPHL QLCPGPPFSRPSVLPASSRCQPGLSA PSLPSSPRPPPLRGLGRS |
| 4603 | 10100 | A | 4902 | 94 | 432 | TFLFFLIFSSEYWKFKKKQYSLEKSL FVAYNHKDG*THFLKGNNQFIFSLA/ LFTLGDIYCKDIFGRLGLQP/TDISSS DSPFLSFSSSIYILTWGQARWLTPVI PAFWEAKAG |
| 4604 | 10101 | A | 4903 | 109 | 422 | FFEDGVLSRSVAQAGV\QWRNLS LQPLPPRFK*FSCFSLRSRWDRHA PPCPAFFVFLVET\GVTLARMVLIS *PRDPPASASQSAGITGVSHCAPSRH SLS |
| 4605 | 10102 | A | 4904 | 3 | 364 | HEETAYDINILS**TQTFNMARLE*N CCNTIKSISEK/PTANSIR*AKKQEGF FQISGIRQGCLLSSFLFIILEVLARGN R*DKN/GIQIGKKKVELSLFSETMRF NIWKRLWKPHITTRANK |
| 4606 | 10103 | A | 4905 | 50 | 394 | LSYSWHSIHLMLMKIISWHFDGQFSA LVIL*LSVAVDADYSHFLETASLL DFEFTVLSWFSSYL/DMFLFTLVFS LPFSIQLLNIGISQGSVLSPLLYAS ASGYMSLNIMYRH |
| 4607 | 10104 | A | 4906 | 49 | 366 | SGSSLAAVFWGPKGPAQAP\GPWAP WASPSGPDLPRLHPADPQRQRLST VPLPLSRPPALSLIAPMALSHSCSNIP P*TPPPASLRPELTPARS/PPTR*SHS PPP |
| 4608 | 10105 | A | 4907 | 119 | 246 | FCFHHLNLPFLIF/NVCLCV*QSHS VTQAGEQWRNLGSLQPPPPRFKPF CLSLPSS*DYRHAPPQLADFCISSRD GVSPCWPGWSQTPDLR |
| 4609 | 10106 | A | 4908 | 1 | 280 | ESRSVAQAGVLWRDLCSLQPPPPVF K*FSCSLPSSWNYRCAPPCPASFFV FLVE\QGFTMLARLVLS*PQ/CDPP TSASQSAGITGMSHCTWP |
| 4610 | 10107 | A | 4909 | 406 | 661 | SQTPDLR*SAHLSLPKCWDYRR/AA TAPGQNISFKLPNPWEKAKHLMKS T*RLKHFTNFALFV*NCIDD/WMEF ALVAQAGMQWHDLGSLQPLPPQFK WFSC/PASPKCWDYRREPPCPANFF FFLYF**RLGFTMLARVVSNS*PQ/C DPPTSASQSAGITGMSHCAWPFFFF LFFSFFETGSHCVAQAGLK/PLKLG RSSCLGLRKCWDYRREPLRLAPSW TFRM |
| 4611 | 10108 | A | 4910 | 3 | 459 | ELRDGEKVLDLCAAPGGKLIALLQC ACPGYLHCNEYDSLRLRWLRQTLE SFIPQPLINVIKVELDGRKMGDAQP EMFDKVL\DAPCSNDRSWLFSSDS QKAS/W*DKSKEEFAFFYRLGC*GL QLRPLRPGGILVYSTCTLSKAENPR CDQ |
| 4612 | 10109 | A | 4911 | 1 | 95 | TPKVHASWQK/MAD*SGQCPVLQIP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LSSLMMQ |
| 4613 | 10110 | A | 4912 | 253 | 1531 | SWKLAEKVWEAQLPGFPSPQCSV RCGRGQRSRQVRCVGNNGDEVSEQ ECASSPPQPPSREACDMGPCTTAWF HSDWSSKCSAECGTGIQRRSVVCLG SGAALGPGQGEAGAGTGQSCPTGS RPPDMRACSLGPCERTWRWYTG WGECSSECCSGTQRRDIICVSKLGT EFNVTSPSNCSHLPRPPALQPCQGG ACQDRWFSTPWSPCSRSCQGGTQT REVQ/CA*APTRPSAPDALLNCGPPG SAPVNSQPC/MPAP**SMARDSSSTF APWVGTGPGFCVLPLLTQPPVCRSL RTCPGSGLPRIPPERGPGHLHGFLCH HRSPIGLGPLWNPLGSSSLFPGLOQ GMSSR*TEGVGKVNGTQSDFSGT GQAHVGGCDGVCCTYCLRCCFWG LHGICVWSNVYHFSKRRLHRTLEG TRPVFLEDFS |
| 4614 | 10111 | A | 4913 | 131 | 355 | STADTLP**TPKLSPQLMDTILPSQS VAMFHT*DHSAPTG/TGAPPHHTPS RPLNTRGPTEEFSPRPPPQHRPSSC |
| 4615 | 10112 | A | 4914 | 3 | 420 | QQPTRLD*GPKQLMPHSPHNPHTI* NPAVLSLPPQTKLLGPPVVRGPLLIR *SPQLLPACLPL*RSTRPGTLKPKAT PA/PPPTTVHKPVASLRSHLRADGPG APPHTTPSRPLNTRGPTEEFSPRPPP QHRPSPPTK |
| 4616 | 10113 | A | 4915 | 11 | 375 | |
| 4617 | 10114 | A | 4916 | 3 | 260 | |
| 4618 | 10115 | A | 4917 | 3 | 208 | |
| 4619 | 10116 | A | 4918 | 1 | 422 | |
| 4620 | 10117 | A | 4919 | 127 | 4348 | GASISDIQTETTEEDSVLLMHTLLAA TKDSLAMDPPVVNRPKKSKTKKAPI KTTTKAAPAAPPVPAANEIATNPKI TWQALNLPVITQISQALPTTEVTNT QASSVTAQPKKANKMKRVTA QGSQSPTGHEGGTIQLKSPLQVLKL PVISQNIHAPIANESASSQALITSIKP KKASKAKKAANKAIAASATEVSLAA TATHTATTQGQITNETASIHTTAASI RTKKASKARKTIAKVINTDTEHIEA LNVTDAAATRQIEASVVAIRPKKSKG KKAASRGPNVSEISEAPLATQIVTN QALAATLRVKRGSRARKAATKARA TESQTPNADQGAQAKIASAQTNVS ALETQVAAAVQALADDYLAQLSLE PTTRTRGKRNRKSKHLNGDERSGS NYRRIPWGRRPAPPRDVAILQERAN KLVKYLKVKDQTKIPIKRSMDLRDV IQEYDEYFPEIHERASYTLEKMFRVN LKEIDKQSSLEVLISTQESSAGILGTT KDTPKLGLLMVILSVIFMNGNKASE AVIWEVLRKLGLRPGVRHSLFGEV RKLITDEFVKQKYLEYKRVPNRPP EYEFFWGLRSYHETSKMKVLKFAC RVQKKDPKDWAVQYREAVEMEVSQ AAAVAVAEAEARAEARAQMIGEE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AVAGPWNWDDMDIDCLTREELGD DAQAWSRFSFEIARAQENADAST NVNFSRGASTRAGFSDGASISFNGA PSSSGGFSGGPGITFGVAPSTSASF NTASISFGGTLSTSSSFSSAASISFGC AHSTSTSFSSSEASISFGGMPCTSAF GGVSSSFSGPLSTSAFSGGASSGFG GTLSTTAGFSGVLSTSTSFSGAPTTS TVFSSALSTSTGFGGILSTSVCFGG PSSSGSFGGTLSTSICFGGSPCTSTGF GGTLSTSVSFGGSSSTSANFGGTLST SICFDGSPSTGAGFGGALNTSASF VLNTSTGFGGAMSTSAFSGGTLST VCFGGSPGTSVSFGSALNTNAGYG GAVSTNTDFGGTLSTSVCFGGSPST SAGFGGALNTNASFGCAVSTSASF GAVSTSACFSGAPITNPGFGGAFST AGFGGALSTAADFGGTPSNSIGFGA APSTSVSFGGAHGTSLCFGGAPST LCFGSASNTNLCFGGPPSTSAFSG ATSPSFCGDPSTSTGFSFGNGLSTNA GFGGGLNTSAGFGGGLGTSAGFSG GLSTSSGFDGGLGTSAGFGGGPGTS TGFGGGLGTSAGFSGGLGTSAGFG GGLVTSDFGGGLGTNASFGSTLGT SAGFSGGLSTSDGFGSRPNASFDRG LSTHGFSGSNTSTGFTGEPSTSTGF SSGPSSIVGFGGPGSTGVGFCSPST SGFSGGPSTGAGFGGGPNTGAGFG GGPSTSAFGSGAA\SLGACGFSYG |
| 4621 | 10118 | A | 4920 | 3 | 1380 | NMLGKYL*VKDQTKIPIKRSHMLR DVIQEYDEYFPKIIERASYTLEKKFR VNLKEIDKHSSSYILISTQESSAGILG TTKDTPKLGLLMVILSVIFMNGNKA SEAVIWEVLRKLGL/RPGV*LGSLSA CCPCCPLAREDPRIASVWWSGGT GWGAGLGRGPRVLTVCVDDGQMV KLSAVSLLNVLCF*A*MLDRPSRIP DKEGIWVLNCLLLVAMCSLLSSLH* DCPMC*ERSPSMLGKWPLALNLGQ FLICGSWGLIFPNCQG*GIHSFGGSE GKLIT\DEFVKQKYL\EYKRVPNR P\EY\EFFWGLALPTTETSKMKVLK FACRVQKKDPKDWAVQYREAVEM EVQAAAVAVAEAEARAWEFQHQH WLYLANPAPSNAGSSSGPKFYCW PAVDPSTGVGFCSPKHQVASSGGP STGAGFGGGPNTGAGFGGGPEHQC WLWQVEPPVLPVAF |
| 4622 | 10119 | A | 4921 | 1 | 412 | TRMGLPDASRRRTCRMDPEGWQE AMSSA*GRITLQRLSTG\PEGQGGRE KVGPEGGSENPPQPKAAGVLSKHL PGAPAQPPQRPPSSPPPLAGPLTERV EKVCDFLDAAGDYLN/GTPG*PSPG ESPAAQDPPVPPWPP |
| 4623 | 10120 | A | 4922 | 117 | 295 | |
| 4624 | 10121 | A | 4923 | 1 | 3564 | |
| 4625 | 10122 | A | 4924 | 1 | 355 | LPGIEVLWQGPVVSKVIPVESIEEV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | CKSIKRAPVIWDTIHVN/DF*SALTP YQIVTTKFYFRIKKIVHWGPFPHSSQ KILSICEKYQWLSVPLTHNLTKFLSII VNYSRYHCHIKPQLV |
| 4626 | 10123 | A | 4925 | 3 | 3145 | AAAEGLGAWRGNSGRPKIIGRAA EAENEDRTLGRLLPGNERSQPRSPL MLLAPQLKAEAAADKGLAPVPPPF SSGHSGPCEREGERGQRGRGRSRRG AHLELKPSPLRAGAPTDRGRGGP AEVAAAGGRRMVQKESQATLEERE SELSSNPAASAGASLEPPAAPAPGE DNPAGAGGA AVAGAAGGARRFLC GVVEGFYGRP WVMEQRKELFRRLO KWELNTYLYAPKDDYKHRMFWR MYSVEEAEQLMTLISAAREYEIEFIY AISPGLDITFSNPKEVSTLKRKLDQV SQFGCRSFALLFDDIDHNMCAADK EVFSSFAHAQVSITNEIYQYLGE PET FLFCPT EYCGTFCYPNVSQSPYLRT VGEKLLPGIEVLWTGPKVVSKEIPV ESIEEVSKIIRAPVIWDNIHANDYD QKRLFLGPYKGRSTELIPRLKGVLT NPNCFEANYVAIHTLATWYKSNM NG\VRKDVVMTDSEDSTVSIQIKLE NEGSDEDIETDVL YSPQMAKLALT EWLQEFVPHQYSSRQVAHSGAKA SVVDGTPLV AAPSLNATTVVTTVY QEPIMSQGAALS GEPTTLTKEEEKK QPDEEPM DMVVEKQEETHKNDN QILSEIVEAKMAEELKPM DTDKESI AESKSP ESMQEDCISDIAPMQTDE QTNKEQFVPGPNEKPLYTAEPVTLE DLQLLADLFYLPYEHGPKGAQMLR EFQWLRANSSVSVNCKGKDSEKI EEWRSRAAKFEEMCGLVMGMFTR LSNCANRTILYDMYSYVWDIKSIMS MVKS FVQWLGC RSHSSAQFLIGDQ EPWAFRGGLAGEFQRLLPIDGANDL FFQPPPLTPTSKVYTIRPYFPKDEAS VYKICREMYDDGVGLPFQSQPD LIG DKLVGGLLSLSLDYCFVLEDEDGIC GYALGTVDVTPFIKKCKISWIPFMQ EKYTKPNGDKELSEA EKIMLSFHEE QEVLPETFLANFP SLIKMDIHKKVT DPSVAKSMMACLLSSLKANGSRGA FCEVRPDDKRILEFY SKLGC FEIAK MEGF PKDVVILGRSL |
| 4627 | 10124 | A | 4926 | 3 | 251 | HERHELQMLVDAPCSDLAQELRQS CATVQRLQHTLQQVLD/Q/REEVRQ SKQLLQLYLLALYNEVSLLS*QDIF NVALDVCMCRS |
| 4628 | 10125 | A | 4927 | 1 | 408 | GTSLNSLSKTKAKDLFIGDVIHNAG PHRDKKLKYIPEVVYSGLYPPYAG GG\GFLYSGHLALRLNHIADSVQF*P R*DPYTVR*LLKPSSAGYDPTFVLLI GTDGIYTYTPSSCENGLGSCEEPHL MSFRSYFHG |
| 4629 | 10126 | A | 4928 | 187 | 378 | LCQKTM SLFTHSFCFSVGRNMEGV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LMDVDCESVYPIV*ASN*GLASAEV GGSFEPRLRPAT |
| 4630 | 10127 | A | 4929 | 26 | 121 | PDRTMGG\REQRQSPGAQRTFFQLL LSFFVES |
| 4631 | 10128 | A | 4930 | 3 | 867 | |
| 4632 | 10129 | A | 4931 | 1 | 558 | EV RVKCVKALKG\LYGIPDLTACL KLFTGRFKDWMVSMIMDREYSVA VEAVRLILILKKNMEGLMDVDCE SVYPIV*ASI*GLASAVGEFLYWKL FYPECEIRTMGGREQRQSPGAQRTF FQLL\SFFVESKSHFVTQGGGSGQF SAHRNLCLPGSGNFHVSASRVAGIA GAPHTWLIYVFFS |
| 4633 | 10130 | B | 4932 | 1 | 1617 | MKNGVQWAE LAGHDYVLDLVSDL ELLRDFPRQKSYFIVGTEGPAASRG GPKVVFNGNSWDSDEDMSTRPQPQE HMPKVLDSDGYSSHNDGTNGETE AQRGTATHQGQPTMAAVSESDSLG EPAVPHKGLDCYLDLDFPVL SYGD ADLEKPTAIA YRMKGGGQPGGGSS SGTEDTPRRPPEPKPIGLDASTLAL QQAFIHKQAVLLAREMTLQATALQ QQPLSAALRSLPAEKPPAPEAQPTS VGTGPPAKPVLLRATPKPLRPAPLA KAPRIPIKPVAAPVLAQDQASPETSL HRDAATVTQMHLTGQGRLLSLD DSSLHLWEIVHHNGCAHLEELSFQ LPSRPGFDGASAPLSLTRVTVLLV AAGDIAALGTEGSSVFFLDVTTLTL LEGQTLAPGEVLRSPDDYRCGKA LGPVESLQGHLDPTKILIGYSRGLL VIWNQASQCVDHIFLGNQQLESCL WGRDSSTVSSHSDGSYAVWSVDA GSFPTLQPTVATTPYGRACTPVAHD HIDELVRGAVFSEKHFCIEDL* |
| 4634 | 10131 | A | 4933 | 1 | 811 | HASAGAGCWHLPGIIEGAAQ GKGR GRQVIAVARTADVIMMLDATKGE VQSLLEKELESVGIRLNKHKPNIFY KPKKGGGISFNSTVTLTQCSEKL VQ LILHEYKIFNAEVLFRDCSPDEFID VIVG\NRVYMPCLYVYNKIDQISM E EVDRL\ARKPNSVGSSSCG\MKLN L\ DYLL\EMLWEYL\ALT\CILHQGRR RDRRARFSQDAILRK GASVEHVCH RIHR\SLASQFQVTPWVWGAPAPSY SPQAGGALTH\TMEHEDVIQIVKK |
| 4635 | 10132 | A | 4934 | 1 | 431 | QRFPAAFPG\PGARRDAPPHSPPAEC RAHAATWRLKPRPHRPHSLTAPLP VHWAGTTEPLSPRPATGTESARRC ISGDTQSFLRLARPCRQPGPS*DRC RPGVVSCLDREEKNAGHWLSMAFS LLWVLATQHCLHPEESLTM |
| 4636 | 10133 | A | 4935 | 56 | 252 | GAQERGCPREKHGNAELAEGLVIL RGRGKPPSASLAGRE*1*SRGPEWK VTVNQTAKAKERTGP |
| 4637 | 10134 | A | 4936 | 81 | 896 | CGLVTPACLDPWVGIAPLPDTLIVL RGGGSALLPAPIPPVTLEEKQTLTRL LAARGATIQELNTRKALSQ LNGGG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LAQAAYPAQVVSLILSDVAGDPVE VIASGPTVASSHNVQDCLHILNRYG LRAALPRSVKTVLSRADSDPHGPHT CGHVLNVIIGSNVLALAEAPAAAGR TG\YQAVVLSAAMQGWGTPAAHR DDRYQCHGHPPLVPAASVMA*VTF WEFRGGLQGQGQMAEQARLADGG FPLPLRMRTSPSASSAFPCFSLGQPL S |
| 4638 | 10135 | A | 4937 | 100 | 332 | NKPQPQLLYRIKLTSTPFHPIQKVGL RQMIDLNIPPRIIKLLEENIK*YLS DLGV\TK*KLTKFNFLKIKHFCSPSSC |
| 4639 | 10136 | A | 4938 | 692 | 900 | NKLLWLGAVTPACNPSTLGG*GGQI MRSGVRDQPVQHGETWSLLKIQKL AGHGWPAAGSPSCLAGLRQE |
| 4640 | 10137 | A | 4939 | 87 | 322 | ARLVQNTGAQLKEVQYKLFFGFLF FE*/QSHSVAQAGYSAVIAHCNLSL LGSSDPFFSAS*VAGTTGMCQHA WLIFDR |
| 4641 | 10138 | A | 4940 | 91 | 356 | GHAFLFGGYSSSHWPSTYPPHAPV PPPPPS\PPYPSLPPFHSLPPIKPFPLPP \SPSPSPSL*SPPTPPPTLLIPSPSPPP ASPPLQ |
| 4642 | 10139 | A | 4941 | 2 | 332 | CGGPPGSPDTRGGSLIPQGV*AA\GP MEQVPLVAPSSAIPAVPGSLSGTPSH QPVLGTHTPSCPGITYIPPESEL PCPAPGRQRPCPGQTPLTPCPSFI FSKQRA |
| 4643 | 10140 | A | 4942 | 637 | 1560 | VWQLDKSMRAAQPWAPAGGAAGS EWAGLKR\RLPLGWSSFSPAAAQSP ELLGHPQSPWPSEAPWKACQVSF QGT/RVAASYHNAQHGTQHS SSC*GLGS*/CNSPTWARLSTHCPQ/HSR NTPRTQHCPHYPPRGLAKRWLCGE GPNPYSHPLREGPLRRRVGRGMGK EVHLFYRAWHSGIHFPS/TPSRTSHQ DSPHLEN*TSPLIDLTPTWAPPMCK RIL*KCTCNLSLPQKPSMALQCI*NEI NKTSTTSPT\CLAPH*APATLACSPF LQPAELLPISGTLHVIFHPPRTLFPKS RTGSFLSSPQVSV |
| 4644 | 10141 | A | 4943 | 2 | 335 | ALHPTLTLDLYFTIYTKIHST*IVDL DVKPKTLKCLEESIR/VKLCDLRLSK ISWILKAQSIEEQTDWDLKT*NNY SSNGTVKRIKRQVED\WHKVFARRI SDTGLVSRISC |
| 4645 | 10142 | A | 4944 | 2 | 345 | FFFFFFETESRSVAQAGVQWRDLSS LQAPPPG\SRHSLASAS*VAGTTGVC HHARLIFVFLVETGFHHVSQDGLN LLTS*SAGLGLPKCWDSEKLFFFG DKSFRFCCPGWSTMV |
| 4646 | 10143 | A | 4945 | 178 | 388 | RREPLHPANLLLFFFFFFEMESPSVA QAGVQWRDLSSLQAPPP\GSCHSPT SLS*VAGRLRNKNCLNPDAW |
| 4647 | 10144 | A | 4946 | 546 | 850 | FSVLFFFESESCSVLQAGVQWRDL GSLQPPPP\GSSHSPTSAS*VAGTTGT CHHTQLIFFLVETGFHHIGQASLKL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LTS*FAHLGLPKFWDYRCEPPHPA |
| 4648 | 10145 | A | 4947 | 169 | 358 | GNGFLFCTQVEVQGAFL*YLNLLAP GVK\LFSCLTLLKPWDSGTFPTFSFN FFIYLAEKGFNG |
| 4649 | 10146 | A | 4948 | 1 | 145 | ANSAAMP SLGCSASSGLVFWPQGL YLLGVVSVSPLPPTPTTVTFPEQI*LL SPQVSSSPVSEGSSQH\PA*SLRPFHV PRS/SPVSSLQPFAPAKSPGPSATCAF SAPSL SLLTLLASGDSSFWGPGPIQM SAGGSIVMCS*GLVFWPQGLYLLG VVSVSPLPPTPTTVTFPEQI |
| 4650 | 10147 | A | 4949 | 1 | 295 | GTSSRLRLHRTDELTA PSIYRSTKST LDGSLAANEREPFTLGKKPPFSDKP SIPAGRSLGEHL PKIQKPPLPPTTER HDWSRRLAGKKPPVPKHGWVP*/R EDDNE*DELTA PSIYRSTKSTLDGSL AANEREPFTLGKKPPFSDKPSIPAGR SLGEHL PKIQKPPLPPTTERHDWSR RLAGKKPPVPKHGWVP |
| 4651 | 10148 | A | 4950 | 119 | 1036 | HASCLKTQALQECSVGVGGGLPVS PAGPPRCFCPALPAAALALQGTFPA TGG*AWGLSSPDWTFSTKKLVMS ARSHGEGGAQGPATLTGPPGEGAL RASQ/PGTAGSELRHRARGPAQICST RTR\ PAPWWT*SLPPPGHSRAVGFD RCGPASP\GVPVNAAVALPPSTCGE ESRLPQEEGGIHMA/PGTPLCSGDCI CCED*PQSRSGQFGADSL*RAKGGT LPSGPSARRRSPL*ASESASCCRRAS S\GPPAAQGERADSRALGTAPPGEG LALRPTPGGIGTPPAGGSEDISREVD PAKRHGLGA |
| 4652 | 10149 | A | 4951 | 2 | 1262 | GSAAGSTYEPSSMRLEALQVLTLLA RGYFSMTQAYLMELGEVICKCMGE ADPSIQLHGAKLLEELGTGLIQQYK PDSTAAPDQRAPVFLVVMFWTMM LNGPFSRFSADSEHPTLQASACDAL SSILPEAFSNLPNDRQMLCITVLLGL NDSKNRLVKAATSRALGVYVLFPC LRQDVIFVADAANAILMSLEDKSLN VRAKAAWSLGNLTDTLIVNMETPD PSFQEEFSGLLLLKMLRSAIEASKDK DKLSTISIYYFNGQENRKEKNWNER EYKLEIPYELCTEVD AINKWTAPWT SQAYNALTSVVTSCKNFKVRIRSA ALSVP GKREQYGSVDQYARIWNAL VTA\ LQKSEDTIDFLEFNTVSSLRTQ ICQ\ALIHLLKLG/RSASDLPLMKET LELSGNMVQSYILQSLKRSIGR |
| 4653 | 10150 | A | 4952 | 52 | 730 | KSACDALSSILPEAFRNLPNDRQML CITVLLGLNDSKNRLVKAATSR\AL GVYVLFPCLRQDVIFVADAANAMV MSLEDKSLN VRAKAAWSLGNLTD LIVNMETPDPSFQGRVLWSPAENG YDQALEASKDKDKVKRHA\VRAL GNLLHFLQPSHI/GKTPHLQKFI*GSL SRALNLLF*QKLAMKVRWNACYA MGNVFKNPALPLGTAPWTSQAYNA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LTSVVTS |
| 4654 | 10151 | A | 4953 | 3 | 363 | HELEFEIKNTIPFILAP/N/NIKYLGIT/ LTKYVLYLN/DLYAENYKTLMK*IR DLNGDPLSCKVKNLIKINKYMKÆIL CSRIGKDSNIV*VSLLPQLACRLNAI PIKIPANHFVEVN*LILKFI |
| 4655 | 10152 | A | 4954 | 179 | 438 | ENIMSKTSTENCTKQCHFVHVNI*Y SIFFFFLRQSL/DSVTQAGVQWRHLG SLQAPPPGFTPFSTRFSLPSSWDYRCP PTSLANFFCILVETGFTVLARMVISIS *PRAPPASAS*SARCKLHLP GSHRSP ASASPVAGTTGARQQAWLIFFVF |
| 4656 | 10153 | A | 4955 | 1 | 264 | QFPKPSPRGP/TPTKSLFHILSPPNQ*I SPPP*QLPPSLYQIPPTIRLSPLPLAES PSPLSVGLGGPLGWVGQLLCLSFPG GPKHVEV |
| 4657 | 10154 | A | 4956 | 3 | 369 | HERHEL VKEFNK VSGYKINAHKSV ALLYTN/DDQAENQIKSSTPFTIAAK SVK/YLGIYLTKEVKDLYKENYKTL LKEIVDNTNKRKHIP*P*MGRINIVK MTTLPKAIYKFNSMPIKISPSHFG |
| 4658 | 10155 | A | 4957 | 2 | 338 | GCWDN*ISTCKRMKLD CSLMLHMK INSM/WIKDVNIKSSSYEKNIGVNLP DNVLGNGFINMMPKAQASKEKIIN WDSAKLK/IRK*RQLTEWEKLCANP IYSHLIPVLCYLYLV |
| 4659 | 10156 | A | 4958 | 42 | 447 | IELVTVLQFYRAFYLFERYAGFLFY YYFLFFVEIRFHYIFQAGLS/ELLGSS DPPTSGLPKCWDYRR/DHRTWPDM QDFLMFHIFPKLFSFPDMCFLASE*P SANTWLLL VVQSSFSLLSHTYHPPG KASTLWFS A |
| 4660 | 10157 | A | 4959 | 377 | 1220 | FRKV VPLAESH PAVPG\GKVRTSRS PKSPPRALPT*/PGLFNPGCQRETPSP LG/PPGQHP/VPGQLNSKRKQIPHNE LVEQTLRSGLTSAQPAHPTGGYSCS KLRPGPLPNPNGLCRCSDGRIPGDR EPLALSRT*IHLRACTGPDAAAQVL PGLLPCPPHLPPHLSGMFDSWLAPP LPDPCQRPTPPQAPSSEANNQRSQA PGCGPHSLRDSELQGQCPGPAQAFC RGSGLFQLTQLTGPLHGTR*RLSPK NSQALKPHM*AVGRILHWPPAARP GNSGRYPDD |
| 4661 | 10158 | A | 4960 | 3 | 353 | HEVPAKGPRPHLTD CPTTQDFLPGF SPRPASGPPPSLSLRLFQQPG*TVW SPGPPCPVVPDCTSASGQVPFLPPAF RFKNVF*PSRPSPGTRGGP/PP*VCTS R/PLP*TSEPQQPG |
| 4662 | 10159 | A | 4961 | 301 | 343 | TRMAHFWS*STKPSPMGPIQWSHM PGAFSE\SSSCHSHSAFLPPYFSHGPS NRPPIRALCRNLPLPLPNKPRAPSAA DEDNSL NVEWYVPYITRPQA*AALI KINQDGTFLVRDSSKK |
| 4663 | 10160 | A | 4962 | 2 | 319 | ARGPGPSGKSGARSGLGNTPRRGG AGLGRVPWSLCY*EGVESGRPEGA GPGTSPGVGFIGAYHGRGVTKVGG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LPG/GQACGVWSDPKSPGEPVEPIPG GSWPPQREP |
| 4664 | 10161 | C | 4963 | 109 | 372 | MQA WINIRKSVYVIHCVNLIKXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XKLRRELPQPVKGHLQKPMADIPN GKKLKASTTKIMNKTSS* |
| 4665 | 10162 | A | 4964 | 3 | 990 | RTLRECYK/HI*ANELNNLDEMSKL KDA/TLLQLTQEEIETLKYNNEIE*I M/NKLPTKKSPGPHGFTG*FYQMFG EEFTPILSRL**KIKEEGTVPNLLYEV /SIIMIPKPKDKDITRPVSLMIIGAKIFK QNI*HTQVYAHHRIVYHDHNGFM QAWFNI*KSVYVIHCVNRIKDKNH MIVSIGA/EKAFDKIQHPFMVKTKT QERTF/FILLKGIY/NKPMADIPNGKK LKA/LPLRSGTRRVPDRFWKWQ/CP LPLLFSIVLEVLARAVRQEKEIKGM QIRKVVKLFTDGMILYVEKSKESTI KTSKLINRFNKGSEYKANIKK*VVF L*SSNQQT |
| 4666 | 10163 | A | 4965 | 3 | 314 | HENDSNPETDNRQEGPSQENIGRVS D/MAFVPSAWTASGGVAWGNPGES GSRTGGVRAETLAPRLQV*PAHLIG HPRSNRGQGRPPWKAGKLGKCQEV LFRFAAF |
| 4667 | 10164 | A | 4966 | 2 | 329 | ARGEERKAFRCIYDCVIHE/CEECR KAFRCIYDCVIHERIHNGEKLIEC*E CETSLSSNSVLIQHQRHTAEKPYEC NECGKAFHRTSVFLQHQRFTGEQ LYKCNCEWKTFRCSSRFIVHQRHN G*KPYECNECGKAFHRTSVFLQHQ RFHTGEQLYKCNCEWKTFRCSSRFI VHQRHNG |
| 4668 | 10165 | A | 4967 | 61 | 533 | WTEPVRHPDIHSQKREPSLMPPTVT GPGTTNMLFQPHRGPEKSRVPLHSS SSSSSSSSSSSSSSSPKTF/FGAPK/LP PSAPTSPDLAQAS*GLKSWKPWSGE RRFGCSKQRRALPTAS*FQGQSHAA PETPSYVGQDQSPSPGG*RPSTSPEG DSCFP |
| 4669 | 10166 | A | 4968 | 22 | 482 | GKGP GPPGGVCKSTLPPAKPWRGPP HLPLPLGL*EKALPRALGQWEGRES FWDQPGKLPLQN/PPRSLGVAMGT QAVEIPDGRLPDLSPTPAHSFSFLAL KPLLGEARVHFRASAWPLPTRAWT LDLPQLGWGFWDCLMALESRSSG ESPSLL |
| 4670 | 10167 | A | 4969 | 146 | 1299 | GAPGPWPTGTTWLPGAAGAVPDPG FLLPSSAALSRTAS*FSQPPPVPPAL TVPWPRCGC*TSCPAVPQSP/GLPR TLVPACRGLPLSSVPSSPASRPKLPL HSPSSWSIPPEGSWGPLPTTLPLPWG L/PRLQSREHKPALSAATWQGLVVD PSPHPLLAFLLSAQVHF*PGLRSW VGPFGLRKQP*HTGLSSLTTGCCP AWLTSWPRISQSERKAHP*CLPL*Q ALSPPISYFNLTVDLNRNDYHSASSS SSSSSSSSSSSSSRRLSWSPKHHPL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LPSFILSWPQGIPRGLKNPGKTRGGL GWWKKGFLANWLSKKPRRKKGPS FPPLVL*FQGPRALPVPRNPHPKLG ASSQSPSPWWGKRPKPKSPGNGTS WLPPK |
| 4671 | 10168 | A | 4970 | 298 | 954 | QVQGHEDFLGARNTTLCSSFSCPGP GILGAEILETVGWCEKVCMLRAEK GSPHCFVIPGPEPCSPRNPNLAGAGP ESKPWWVEAKQKP*SGLLLPLVVS VPRS*NCEPGVGERSGRG\HLGFLQP GYP*PHQGFWEILQGQLSRLFPNSSL PPH/MPLKPQOKSHSSHKQKGRGKN EEKTLCQVICRQRMGLVP*QHPTPC GAPPSPHHPQTPPKQVPYL |
| 4672 | 10169 | A | 4971 | 4 | 410 | PIERPHELKHRLPHVQKLVEDVGDG VIPAALEEGQAGWSHGFLVFLVEIK SAEGP/PGPADSRVRGVRPQRSQSA GPA*RAGRQDGVCRSLGQGRGGGR ATSLVLHPPGYPGCWFSVGVPSLPQ YTGIRSSSPRTRG |
| 4673 | 10170 | A | 4972 | 148 | 268 | LQPR*PLTCAPPPCPVQTQTHPISVS QTLLGLEFCCSLSL |
| 4674 | 10171 | A | 4973 | 397 | 1449 | RSHPSGTGRRTSRLESWFLGVSCCK SKVREGPLGPA**AG*RGVRPQRSQ SAGPA*RAGKRQDGG/SPEPRAGVG GEVGTQSP/GPSGASGYPGMLVSKP VGGTSASWLPAGCIPS*LS*QRSQG SPSSCLIGHLLALWAAFGLGVTSLP QYTGIRSSSPTA*ATVQGD SGHKGG TGGTGLGRGRNTQPDAAACGRGHR SPTR/RPHGNPNNGNTGCAEGGQARS LLPKLAPKLPGWPVSVPAVGP FGWRQAQYQSSLWDLSSPRNTLGR SATSAGPAPPALLGAGSGRSSGTSP AAPGCSSRCHCWASAPAGVSGGPG\ GRGAEAPPSPTLAQRGSPPG\AAIFP PACGIPP |
| 4675 | 10172 | A | 4974 | 2 | 637 | ARAKEV*DLYTERTK/PLLKEIKEDR NKWKHTSCLWIARLNIVKMSILCKL VHRLSAITIKI/PCWLCLAEIDKLILK/ FIWKFK/RSRVAKTVLKKRKRVRRL TLNFKTYFRVTVIKIEWLWQKD KYIDQWNRIKSLEINSYICGLLIFYK SAKTIS*ENSVSWYLDNWPTCERM KLAPYIYKKIK\WIKDLNIRAITVKL IKENIGPGARL |
| 4676 | 10173 | A | 4975 | 254 | 590 | KARYILPDLMIGLDFFFFLGETKFP FAPQPGGHQGD LG*LKLTPPRDFP/C LTPPRSGNYRLGPPPLNFFVF*KKR GGPHVGQTGFELLT*KDPPPLASQR AEITGGTHHA |
| 4677 | 10174 | A | 4976 | 103 | 378 | CFLYSICRGADTQRRFKLSDLINST ECLHVHCRGLEISLADCAYT*ILTK GNHNPLS*YTFMRNNAKQPVN*YHR CTETFSLTRMELLVSV |
| 4678 | 10175 | A | 4977 | 2 | 327 | RQCLALWPRLECSGVIIAHHSLHLL GSSDPPTSAS*VAGTTGMHHHAQLI/ LFWVLIDTG*CYVAQTGLEPLNSGH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PPTSASQSAGIIGLRHRAQPCVFQSS QKRGPELF |
| 4679 | 10176 | A | 4978 | 19 | 1009 | KTTQQQQNLFFSSAHETFTNTDHI GHETSFDMF*HIQVI*STFLYHNVIK LEVNSRKISGKCPNMWKLNNNTVLS NTKIINFLDNKQNETIKI/RAETNELE NR/RTEKIN*TKM*FFEMINTIDKSL AR*SRGKRHKLLISGMTNVVSHCVS LPTLFLFQSCFDYILTTLHFLINF/QN RFNNLYKMIRGY*QLYKN*FDKLH EMKNFL*/RY*LPILTQEEI/S/HLNSPI YILKIEIVVLNLPNTKTYW*TLKF/EE MIPIVHRLFQKQETLPNPFYEVSITPI PKI/QD/D*TKENFRPISL\VDKIPSK NLSNYICSRLNASHPQRSTDPNLQ NF |
| 4680 | 10177 | A | 4979 | 3 | 358 | STSNA YHSNSLHQIQIKEKKNHTILSI DAEKAFYKIQEPLLAITL*NRNSGN/ FLNMLMTTY**PKVNVILIGNTIPY* YFAFLP*KLRTQSRSLSSLFNIVLK NPANVTVISINIKRK |
| 4681 | 10178 | A | 4980 | 3 | 341 | FFETESNSVAQAGVQWHDLGSLQP PSPGSSNSPASASRVAGITGACPNV QLISVGFLFFVFWFFETESLSVAQA TGVQWVRWAYCNLRLPGSGRFLC LCLPSSWGLQGVR |
| 4682 | 10179 | A | 4981 | 658 | 1001 | LILSARPPKGEKGSFLLAEFSSYFHS GLFSSARSFFFFFFFETESHCAVAQA GVQWLDLGSLOPPPGSSNSPASAS QVAGTTGVCHHAQLIFVLLVETGF HHVGQAGLELLTS |
| 4683 | 10180 | A | 4982 | 53 | 394 | PQQSGFWFIYFSKQGCFFVNILNIC SFVLFFFETESCSVAQAGVQWHDL GSLQPPPPGSSDSPASASRVAGITG ACHQTWLIFVFLVDMGFRHVGQAS LKLLTSGFKKWVT |
| 4684 | 10181 | A | 4983 | 66 | 516 | HFYQFFPHFSGRMDLWSSLLCHFF MTSQFVTFVFLLYFIFVYILSV*LD F*MRKQT*LISG*ASI*YRYV*LQNL YVLKLYITPLSL*AHVLIYL/CYLKS ESHVSTQAGVQSHNLSSLPPRFK*FP CLSLPNG*DYRNVPPHPANFCIS |
| 4685 | 10182 | A | 4984 | 3 | 324 | HENRMKYEISINMWKLNNIFLNKL WVKEITSRLQKYFECSENKTTTYQK L*DAKIKMNQCQGYLWVFMAISA* ISKRKRLINYL SFYLSKLEK*EPTK PKASSRKVV |
| 4686 | 10183 | A | 4985 | 108 | 277 | ARVIRANFCIFGKDRVSPCCPG/W/ SPELPGLKRSPSLSLPKCWDYP*AT APGQHPYS |
| 4687 | 10184 | A | 4986 | 29 | 454 | |
| 4688 | 10185 | A | 4987 | 116 | 424 | |
| 4689 | 10186 | A | 4988 | 1 | 1217 | PPTTCTPACQGLSGAAMKSLVLLC LAQLWGWHSAPHGPGLIYRQPNCD DPETEEAALVAIDYINQNLPGYK HTLNQIDEVKVWPQQPSGELFEIED TLETTCHVLDPTPVARCSVRQLKEH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AVEGDCDFQLLKLDGKFSVVYAKC D\SSQDSAEDVRKVCQDCPLLAPLN\ DTRVAHAEKAALAAFNAQNNGS\ FQLEEISR\AQLVPL\PPS\TYV\EFTV SG\TDCVAK\EATEAAKCNLLAEKA IMAFVKATLK*ESLGGGRRLQLTCT VF\QTQPCDLHSPNPEGANEAVPTP VV\DPDAPPSPPLG\APG\LPP\AGSP PELPCFYWAAPPG\HQLHR\AHY\D LR\HTFHGVWVFIGGHPSGRKCSHP PGKHGTVGSSLVFWCCCCCLGPVVP SIVPGRIRHFKVLG |
| 4690 | 10187 | A | 4989 | 1 | 443 | KKFVIPDFEFTGHVGRIFEDVKELT GGKVAAYIPQLAKSNPDLWGVSLC TVDGQRHSVGH TKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAIIVS SLIKMDCNKA EKFD FVLQHLNKK |
| 4691 | 10188 | A | 4990 | 3 | 217 | ATKRKKKMKDKDKA\KLEAMGTS KTNEEDKRRGLDKRTPDQAAFEKM QEKRD FSRHLD TLTEHYDIPKVHH |
| 4692 | 10189 | A | 4991 | 3 | 475 | AASTESGMVAYYQVQKGPLKLKG VAKLGVT K/RVRPEGPRDSVFIPLKP FLGTPGDPPTRRLLMFFSRKKKKK DKDKAK\LEAMGT SKKN EEEKR RGL\DKRTPAQA AFEKMQEKRHME RILMKA\SKTHKQ RVEDFN RHLGTL \TEHY\ DIPKV\TWTK |
| 4693 | 10190 | A | 4992 | 783 | 5158 | PDKSGRRRDVEGGVCCFLSLRNSR YLLSTHILERGKKASLCHPGWNAL VPSPLTAASASWVQVILLPLSLPSG WDYSLHLLEELTGESPTSERAFNYH PTTCLRRKILQDSEHTASTRGPM TL DRPGEGATMLKTFTVLLFCIRMSLG MTSIVMDPQPELWIESNYPQAPWE NTTLWCRSPSRIS SKFLLLKDKTQMT WIRPSHKTFQVSFLIGALTESNAGL YRCCYWKETGWSKPSKVLELEAPG QLPKPIFWIQAETPALPGCNVNILCH GWLQDLVFMLFKEGYAEPVDYQV PTGTMAIFSIDNLTPEDEGVYICRTH IQILPTLWSEPSNPLKL VVAGLYPK PTLTAHPGPIMAPGESLNLRCQGP IY GMTFALMRVEDLEKS FYHKKTIKN EANFFFQSLKIQDTGHYLCFYDAS YRGSLLSDVLKIWVTDTFPKTWLL ARPSAVVQMGQNVSLRCRGPVDG VGLALYKKGEDKPLQFLDATSIDD NTSFFLNNTYSDTGIYSCHYLLTW KTSIRMP SHNTVELMVVDKPPKPSL SAWPSTVFKLGKAITLQCRVSHPV L EFSLEWEERETFQRFSVNGDFIISNV DGKGTGTYSYRVETHPNMWSHR SEPLKLMGPAGYLTWNYVLNEAIR LSLIMQLVALLLVVLWIRWKCRR L RIREAWLLGTAQGVTMLFIVTALLC CGLCNGVLIETEIVMPTPKPELWA ETNFPLAPWKNLTLWCRSPSGSTKE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FVLLKDGTGWIATRPASEQVRAAFP LGALTQSHTGSYHCHSWEEMAVSE PSEALELVGTDILPKPVISASPTIRGQ ELQLRCKGWLAGMGFALYKEGEQ EPVQQLGAVGREAFFTIQRMEDKD EGNYSCRTHTEKLPFKWSEPLE LVIKEMYPKPFFKTWASPVVTPGAR VTFNCSTPHQHMSFILYKDGSEIASS DRSWASPGASAAHFLISVGIGDGG NYSCRYYDFSIWSESPDPVELVVTE FYPKPTLLAQPGPVVFPGKSVILRC QGTFQGMRFALLQEGAHVPLQFRS VSGNSADFLHTVGAEDSGNYSCIY YETTMSNRGSYLSMPLMIWVTDTF PKPWLFAPSSVVPMGQNVTLWCR GPVHGVGYILHKEGEATSMQLWGS TSNDGAFPITNISGTSMGRYSCCYH PDWTSSIKIQPSNTLELLVTGLLPKP SLLAQPGPMVAPGENMTLQCQGEL PDSTFVLLKEGAQEPLEQQRPSGYR ADFWMPAVRGEDSGIYSCVYYLDS TPFAASNHSDSLEIWVTDKPPKPSLS AWPSTMFKLGKDITLQCRGPLPGVE FVLEHDGEEAPQQFSEDGDFVINNV EGKGIGNYSCSYRLQAYPDIWSEPS DPLELVGAAGPVAQECTVGNIVRSS LIVVVVALGVVLAIEWKKWPRLR TRGSETDGRDQTIALEECNQEGEPG TPANSPSSSTSQRISVELPVI |
| 4694 | 10191 | A | 4993 | 1 | 369 | GTFQLPKPIFWIEAETPALPGCNVNI LCHGWLQDLVFMLFKEGYAKPVD YQVPTGVTMAIFSIDNLTPEDGVYI CRTHIQMLPTLWSEPSNPL\KLVA GGCGLWLLASGNCCPRYHGWLS |
| 4695 | 10192 | A | 4994 | 183 | 429 | ISIKSMKLISDYKYCIYTRYHRDVI RLGIIDYSVLHPTSAQYTFSSLHGT LTTRDNILGHKTLNKFKEIRQYL FSDQ |
| 4696 | 10193 | A | 4995 | 2 | 270 | TSGCLOGSCCVTGPPGAVGRASRSR PSTRPPSRARPLGSPGCSARAQDAA DLPLPPPPPPCCSPSSAGCRCSLGC RRCPLRSSRRSRF |
| 4697 | 10194 | A | 4996 | 1 | 428 | NPCLSERQGCCEKLPLERSSTPQDS AGHPVT/HAHCSLPSPVDLCPLLLAT HRISCWHCQDEVQGGTD\SADTGD LEALSLLAGHGD TDGHILDVPDGA PYPQRTKAGIDHLHQKILKIEQITIE HEARDDNAPDYPKLANN |
| 4698 | 10195 | A | 4997 | 131 | 412 | RKWLKLLPCSFFSSKNIAETFSPCV CIRVCIHVCVYTCVYTCVCIHVCSC PC/VGQASALKSVSLCQLHCILVLTP MLTLRFDKKFFTQDSHF |
| 4699 | 10196 | A | 4998 | 2 | 175 | KFTWKHKGPRIARNILKRKIKVEGF TLPNFKTYKAAVTETVWYWHKD SGLDHFVLL |
| 4700 | 10197 | A | 4999 | 2 | 175 | KFTWNHKGPRRIARNNLEKEN\KVEG FTLPNFKSYKAAVTETVWYWHK DSGLDHFVLL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4701 | 10198 | A | 5000 | 1 | 909 | MVLEVSVS DRDA VWRL WRAPIGES QQRSLGFWSKVLPYSADNYFPFER QLLACYWALLETDRLTVGHQVTLQ PELPIMNWVLSDPSSHKVGHVHQH SIKWKWYIRDQTRAGPEGTTTPVIT Q/WDAHEQSGLSGRDGKQGRFVLT GVDTYSGYWFAYPAHNASAKTSY GFTECLIHCHGIPHSIASDQGTFTA KEVWQWAHAHGIHWSYHIPHHPIA AGLIEWWNGLLKSQQLCQLGDNTL QGWGKDLQKAMYSLNQRLIYSTVS PISRIHGSRNQRVEVEVAPLTITLSD PLAKFFFLP |
| 4702 | 10199 | A | 5001 | 1 | 1014 | |
| 4703 | 10200 | A | 5002 | 349 | 718 | AGPEGTTTAECPI/CQQQRPILSLRY GTISWG/DQSATWWQVDYIRTLIS WKWQSASAKTTIHGLTKCLIHHDIP HSIASD*GTCFMAKEVWQWYCFSH SQDSRVQESRGGIGSCTTHHPCSF PN |
| 4704 | 10201 | A | 5003 | 1 | 558 | |
| 4705 | 10202 | A | 5004 | 1 | 2205 | MGAVFEALWQYSPPELPAKASVMVQ EASKAIGQCQSSAAKLRRSGKESVT EPWARVLGALEMAARLYKVTSGH CHGIHTPSWRCLCFSTGGKERHAH DLPHVTAQSQGHQGGKISRTALK EPTVHKVTASLSPVATSPQPMLP SDFPPLSEEINPMLPEATVIASPEIA RQDNVDSPQEPPPTPQFSSRPITRLK SQWAPRGPECVIGIDILSSWQNPFIG SLTGRVRAIMVGKAKWKPLELPLP RKIVNQKQYHILGGTVEISATIKDLK DTEAVTPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAVPD V/VSLLEQINTSPGTWFEWSPKKAL QQVQAAVQAALPFGPYDPADPMVL EVSVADRDAIWSLWNAAGESQRR PLGFWSKALLSSADNYSPPFERQLLA SYWALVETERLTVGHQVTLRPELPI MNWVLSDPSSHKVSGAQQRSIIKLK WYIHDWVRAGPEGTTTSVITQWAH EQSGHGGRDGGHAWAQHGLPLT KADLATATARIHRSRNQGVKVEVA PLTITPSDPLAKFLLLISATSTSLEVT VPEGEMLPPRDTTKIATFGTQTGFL ALQLADGLLWDLVIIPGKGKPSRDL VESPSPYSTYEGIDGWPDEPAPTAT KPPVMPAPALPPDTRSGSKAPTVP PYPQMEHHQVQLASNNSENTEALGH LSPQSSWVQTPGQNSGPAIPNHLGK DMISPPQMAPAGVKWESQKY |
| 4706 | 10203 | A | 5005 | 155 | 531 | GNLWSVDLRPGTPLRQNFRTIRQQ HSRFTKNHCSQTPLLIPRQTGSGVD LSKLQQTCS*GSCLVCTIDLANAFFS IPVHKA/HQKQFAFSWQYTFVTLPR LTWLQPC*VPNLPAAEINTEPSNGT |
| 4707 | 10204 | A | 5006 | 1 | 518 | MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VHKAQQKQFAFSWQGGQQYTFTVLP QWYINSPALCHNLIRRDLCFSLPL DITLVHYIDDIMLIGSTIKWVVHSS/ DSIIKWVYVHDWARAGPEGTTN GLAG*SGTCKKHEWKTGDKGIRGR G |
| 4708 | 10205 | A | 5007 | 1 | 2592 | MVRKAKWKPLQLPLPRKIVNQKQH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCRMTVDYC KLTQVMTPIAAVVPDVVSLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEKAQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYSPPFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLS DPSR HKVGHAQQHSIIKLKWIYCDQARA VPEGTC*LNKEVAQMP/MGTTRKW TAAALQSLSGISLKDSGEGKSSQWT ELQAVHLVVHFAWKEKWPGTWKK HDWKTGDNEIWGRGIWMDCEWS KTVKIFVSHAHEPSGHGGRDGGYA WAQHELSFTKADLATGIVECPICQ QQRPTLSPRYGTIPQGQTFILTGINT YSIYGFAYPAHNASAKITIRGLTECL IHHHGIPHS/IVSD*GTHFTAKDVET RIHRPRNQGVVEVAPLTITRSDTL AKFLLPVPTTFRSANLEVLLLEGGT LPPGDPTTIPLNWKRLRPRGHFGLPL PLSQQAKKGVSVLAGVTDLDYQDE FSLLLHNRVTAAPFSLHSSFAILD NMIEKANKCHVEGVVDHVSDPAQRR ECDRHTGSSCHLLRGPPQLQSQLVS GPRSPKSDSGESCLAWDPTFKAES PLAQGSPRNSVQEPSRPTGSPKSLG ALIALWPSWYLSSDPDPQGSNSRNL EISACQKYLSPAFGNSDYSTAEDFN SDYTLKSPENSIGYARLEKHRRLYG GDGGDGGGDDVRGGKRGDDASR KGVTERV |
| 4709 | 10206 | A | 5008 | 1 | 942 | MVGKAKWKPLELPLPRKIVNQKQH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSRMTVDYCK LNQVVTPIAAAVPDVVSLFEEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFTVLPQDYINSLA L*HNLIWRDLDFLLQDITLVHYI DDIMLIGSNDHKVGGAAQQHSIIKW LYIHDQAQTGPEGTTTSVIAQWAHE QSGPGSRDGGYAWAQHGLPLTK ADLATTAECPVCQQQRPTLSPRYG TIPSLPLTKALTQLKKCSSGPMLM EFTGLAMFPIILKQLD |
| 4710 | 10207 | A | 5009 | 1 | 1795 | MRKCGKPQFKLGQTNKANSRIQEE LIHSKSLIEQEGEKPVQFSAHRMW QPADSQCDIIDSADIWADPLVRHREI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | ITGSGGINRRRTRGGRGRGGEAAGG AENCGSREERERAGVGTAVTQLQN LNTIGIIGSRGGRGQVAAINHQKQG GHSYCKGQQKQNSNQNSVTHVEL WHWLNHSVPRSEIDRKPTTFLNL YKQKTSRDLWPFTRVTLHRGKRND QTFQGLLDTGSELMLIPEDTKHHCG PPVKVEAYGGQVINGVLAQIQLTV GPVGSNGTHPVVIYPVPECIIGILSS WQNP HIGSLTSRKT DGSWRMTVHY HKL NQMVTPIAAAIPDVVSLLEQVN TSPGSWYAAIDLANAFFIPVHKAH QKQFAFSWQGGQYTFTVLPQGETL VNFSLPQDITLFHYIDDIMQIGSSDQ EVANTDLLPRKSTTPSG/LYGFWR QHIS/HLGLLLTPY*VTQKAA/SFEW GLEQEKALQQVQATVQASLPLGVY DPADPMVIEM/SLSDPSSHKVGCAQ QHSIIKWKRYVCDQA*ASPEGTS*L YCTSFIMEKEEVC/LSLEQTLTDMG LPILHAMLLWIHLWIHGLPYPSWY STQQCL |
| 4711 | 10208 | A | 5010 | 3 | 169 | DFQPFTRTVTHWGKGNQDQTRGLL DTGSELTLPKDPKHGYPVVKVG/ AYGAQLL |
| 4712 | 10209 | A | 5011 | 1 | 562 | |
| 4713 | 10210 | A | 5012 | 3 | 591 | DPADPMVLEVSEADRDA\VPISQ QRPLGFWSKALPSSANNYSFFKRQL LACYWVLVEIEHLMGHQVTMRPE LPIINCVLSDPCSHKVGHAQQHSIIK WRWYIHDWAEGTSKLHEEVAQIPM VSTPSLPQAPMASWEVPYDQLTEE EKTRAWFTDGSARHAGATQKQWTA VALQPLSGTSLQDSSEEKSSQWTEI |
| 4714 | 10211 | A | 5013 | 2 | 586 | |
| 4715 | 10212 | A | 5014 | 3 | 514 | |
| 4716 | 10213 | A | 5015 | 1 | 994 | MVRKAKWKPLQLPLPRKIVNQKQH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCRMTVDYC KLTVMTPIAAVVPDVVSLKQINT YPGTCKFLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEKALQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYS PFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLSDP SRHKVGHAAQQHSIIKLKWIYCDQARA VPEGTC*LNKEVAQMMPM |
| 4717 | 10214 | A | 5016 | 1 | 643 | MVGKAKWKPLELPLPRKIVNQKQH HIPEGIAELAITKDLKDAGVVIPTTS PFNSPIWPVQKTDGSRMTVDYCK LNQVVTPIAAVVPDVVSLFLEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFTVLPQDYINSLA L*HNLIWRDLDFLLQLDITLVHYI DDIMLIGSNDHKVGGAAQQHSIIKWK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LYIHDQAQTGPEGT |
| 4718 | 10215 | A | 5017 | 3 | 1074 | VTASLSPVVATSPQPMLPSDFPPLS EEINPMLPEATVIASPKEIARQDNVD SPQEPPPTPQFSSRPITRLKSQWAPR GPECVIGIDILSSWQNP HIGSLTGRV RAIMVGKAKWKPLELPLPRKIVNQ KQYHILGGTVEISATIKDLKDTEAV TPTTSPFNSPIWPVQKTDGSWRMTV DYCKLNQVVTPIAAAVPDV/VSLLE QINTSPGTWFEWSPK\KALQQVQAA VQAALPFGPYDPADPMVLEVSVD RDAIWSLWNAAGESQRRPLGFWS KALLSSADNYSPPERQLLASYSWAL VETERLTVGHQVTLRPELPIMNWV LSDPSSHKVSGAQQRSIIKLKWIH DWVRAGPEGT |
| 4719 | 10216 | A | 5018 | 1 | 1482 | MAPNSRVQELVLGQVAVICQGLLS LQPRTEGYTVGFLTFEVLDLTGSSA CRWPVGLHVSIIILDKVTKEKDEL RDSNSWLQKQILSLKFSKTALSES SCRQRAEIVENQTQGLIMRPLAFHR GNCIGERGMITLFRGYWTEPTLIPED PKHHCSPPVKVRAYEDGSWKMTV DYHKLNQVMIPVTAAVPDVVSLLE KINTSPALFHNLVQRNLDCFSLPQDI TLVHYVDDIMLIGSSEQEVANTLDL LVRRLCAKGWEINLTKIQGPSSLVK FLGVQWCGASQDIPSKVKNKLLHL ALPTTKKEAQCLVGLFGFWKQLIPH LATPIIPQRAHEQSGHGGRRNGGYTW AQQHGLPLTKADLATATAECPICQQ QRENGA/PRYGTIPRGDQPATWWQ VDYVGPLPSWKGGQFVLTRIDTYS AYGFAYPTCNASAKTTIHSLTACLI HRHGIPHSIASDQGSHTAKEVQQW AHAHGIHWSYHVPYYPEATGLIEW |
| 4720 | 10217 | A | 5019 | 1 | 1494 | |
| 4721 | 10218 | A | 5020 | 101 | 304 | |
| 4722 | 10219 | A | 5021 | 1 | 1912 | MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP VHKAQKQKQFAFSWQGGQYTFTVLP QWYINSPALCHNLIRRDLCFSPLPL DITLVHYIDDIMLIGPRQLLACY/W ALVETEHLTISHQVTMRPELPIMNW VLFDPSSHKVGCAGQHSIIKWKWY VHDWARAGPEGTTTPVISQWPHEQ CGHGGRDGGYAWAQQCRLPLTKA DLNTATAKRPICQQQRPTLSPQYGT IPQGDQPATWWWVDYMGSLPSWK GQRFVLTGIDTYSGYGFAYPACNAS AKTAICGLTECLIHHDIPHSIASDQ GTHFMAKEVRQWAHDHGIHWSYH VSHHPEAAGLIEWWNGLLKSQQLQC QLGDNTWQGWGKVLQKVYYALN QHPIYGTVSPIAKIHRSRNQGLEVAP LTITPRDPLAKFLLPFPATLQSAGLE VLVPEEGTLPPGDTMIPLNWKLRP PRHFGLLLPLNQQAQKKGVTVLAV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TLDYKDEITLLHNGGKEEYAWN TGDPLGLLLILPCPMIKVNGKLQQL KPEALVPKGVVFPPGDTTMLSLSW KLRLPSGHVGLLMPLSQQVQKGV VLAGVIDPGHTSAASLVLRSCVWS GSDTIVSPGSQDFRLGINDTTGFPV PD |
| 4723 | 10220 | A | 5022 | 3 | 835 | DLWPFTRVTVH/WGKANDQTFQGL LDTGSELTLPGYPKRHCCPPVKVR VYGGQTDGSRMTVGYHKLNQVV TPIAAAVPDVVSLEQINTPPSTWY GQVAAFAPPTTKKEAQLVGLDF GGNTLLIWVYYSGPLSSDLKGCQFE WDPEQERLCKAFSAHSQWFGCQGL GRSVDWKIDDKKLGRMRMDLSE LGKNREEYWYPVQQAQKGVKVL VVIDQTIKMKSVYYFTMEKTCQRQ ATTAELEPEKNVIGVDETVEGQSYH SSKQKDIPFQGEK |
| 4724 | 10221 | A | 5023 | 2 | 1300 | DLWPFTRVTLHRGKRNDQTFQGLL DTGSELMIPEDTKHHCGRPVPKVEA YGGQVINGVLAQIQLTVGPVGSST HPVVIYPVPECIIGIGILSSWQNPHIG SLTSRKTDGSRMTVHYHKLNQVM VTPIAAAIAPDVVSLEQVNTSPGSW YAAIDLANAFFIPVHKAHQKQFAF SWQQQYTFTVLHQGYINSPALYH NLIWRDLDRFSLPDITLIHYIDDMT LIGSSEQDVANTLDLL/SDLSRGGF* *SSG*DDPFCGHHSASFSPHPCNRP MGP*TK*PWGQGWRLRMGSATCTP THQG*PGYGHC*VNLPAETNTKP SIWHHSSG*SASYQAAG*LYWTSFI MERA-EVRP/TWSTCLLWIWVCLSCT QCFCQDYHLWTHGMPYPLSRYSAQ HCL*PRHSLYS*RSVAVGSCSWNSL VLPCSPSS*SSWI |
| 4725 | 10222 | A | 5024 | 2 | 790 | PRGRNRRRKTFQERRMTLNESPEKI GKWIECYGHPPASKLVEIYHTVFV EDKLSICIRSFNKKADGSRMTVD YCKLNQVVTAIAAAIPDVVSLEQI NTSPDTWYAAIDLANALFSIPVHKG YINSLALCHNVIWRELDLCSLPRDT TLVHYIDDMIGSSVQEVENKLDL LVKDKLLHLAPPTTKEEVQHMVGL FGFWRQHPIHLGVHLHQPIYRVIRKA A/SFEWGPEQEKAQQVQAAVGGK QSENNLGHQRSPGLWFS |
| 4726 | 10223 | A | 5025 | 281 | 1461 | VRVLSPEKELKLWKNTHKLLSYP TVGAAVTQLQNLTAMGVIGSHGAR GQVVALNRQRQGDLPFTRVTVH WGKG/NMQIFGGLDGTGSELTLP DPKHHCGRPVPKVGAYGGQVINGVL AQVQITVGPQTHPVVISPVPECIIGID ILSSWQNPHIGSLTGIMVGKAKWK QLELPLPRKIVNQKPYCIPGGTVEIS ATIKDLKDAGVVIFTTSLFNSPIWPV QKTDGSRMTVGYRRLNQVVTPIA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AAVPDVVSLLEQINTSPGTWYAAID MANAFFSIPVHKAHQKQFAFTWQG QQYAFTVLPQGYINSPALCHNLIWR DPDCFLLLQNITLLVHYVDDIMLIGS SEQEVANALDLLVFSHLAIKWVM HSSIASSSGSGICVIRLKKVLKAQ |
| 4727 | 10224 | A | 5026 | 1 | 3179 | MAEDKEEQVPSYTDGSRQRENEED TRVKTPDKTIRSHETYSLPREQYGG NYAHDSSIHQVPPTTCGNYGSTIQD EIWVGHDHSGYVRPVPVPRSLNSDIS YFGVGGKQAVFFVGQSARMISKPA DSQDVHELVLKEDFEKKEKNKEAI YSGYIRNRKDDYDNHTGIDLVGTH ATIKGSNEEDTDTPFIGKVRTLEFP FVNGSAEIMLMPNQQHKTDEKGR ANLGVFSVFAPRGEHTLQVKAIYN KSIIEGPPIKLMILPDPEKPVRLNVKY DKDASFLAGGLFTAPPLPAQLMSSL SCAWHIESVLNSWRKGCNKLNRQR ALHKKQDRGKLPEDRELQHTKKQT NWAGLLIPAMNNNVDMTARKLQR DLQPFTSVTVHCRKGNDQTFGGPL DAGSELTLIPGDPKHHCPPVKVGA YGGQVINGVLA\HPLIWLQKTDGS /WRMTVDYCKLNQVVIPIAAAVSD VVSLEQINTSPGTWYAAIDLANAF FSIPVHKAQQKQFAFSWQGGQYTF TVLPQWYINSPALCHNLIRRDLCF SLPLDITLVHYIDDIMLIGSSEQEVA NTLDFVRHLRARGWEINPTKIQGP STSVKFLGFQWCGACQAIPSKMRD KLLHLVPPTTKKEAQCL\QLLACY/ WALVETEHLTISHQVTMRPELPIMN WVLFDPSSHKVGCAQQHSIIKWKW YVHDWARAGPEGTT/HPCHFPMAP *TMWPWWQGWRLCMGSAM*TST H*G*PEYSHR*APNLPTAETNTEPSI WHHSSG*STSYLVVG*LYGISSIMER AEVCPHWNRYLLWIWVCLSCMQC FCQDCHLWTHGMPYPPS*YPTQHC L*PRHSLYG*RSAAVGS*SWNSLVL PCFPSS*SSWIDRMVEWPFEVTITVS TR*QYLAGLGQSSPEGRVCSESASNI WYCFSHSQDSQVQESRARS GTTHH HP*GSTSKIFASFSCNITVCWPRGLS SRGRNAATTRHNDSEIKLEVKIATQT LWAPPTFKSTG*EGSYSVGWGD*PG L*R*NHSPTP*WR*GRVCMERYRSI RASLNITMPYD*GQWETTITAQARSS |
| 4728 | 10225 | A | 5027 | 2 | 1284 | CHCGPP/VKVEAYGSQVLKGVLAQ VQLTVGPVGPRTHPVVIFPVPECIIGI DMLSSRQNPHTGSLTGRVWTIMVR KAKWKPLELPLPRKIVNQKQYHIPE GIVEISATIKDLKDAGVVIPTTSPFNS PIWPVQKTDGSRMTVGYCKLNQ VVTPIAAAVPDVVSLLEQINTPPGT WYAAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEINMT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KIQGPSTSVKFLGVQWCGACQDIPS KVKDKLLHLVPPTIKKEAQCLVGLF GFWRQHIFHLGMPLQPIYRVQMA ASFEWGSVEQEKALQQAGQAQAAVQA ALPLGP/HKDPADPLVLEVSVDSDRD AVWRLWQASI/GHKVGHAQQHSIIK WKWYIRDWARADPEGTTKGQGQR RWWQLAERQDSRDREAAIGERQET AVGKTARDGEAVCD |
| 4729 | 10226 | A | 5028 | 422 | 1252 | TTLFSVQIFQWRQLENLYFREKKFS VEVHDPRRASVTRRTFGHSGIAVHT WYACPALIKSIWAMASQHQFYLD RKQSKSKIHAARSLSEIANDLTRTRT LENSKLANMGSKGKIISGSSGSLSS GSGARRHCILLPGSQESDSSQSACK DMLAALKSRQEAEETLRQRLEEL KKLCLREAELTGKLPVEYPLDPGEE PPIVRRRIGPAFKLDEQKILPKGEEA ELERLEREFAIQSQITEADRRLASDP NVSKKLLKQRKTKYINAVKKLQVY |
| 4730 | 10227 | A | 5029 | 1 | 400 | RHEERTTGILTSEGLASDTSLICVIED FFDTALHSRSSSEGKIQMLDSFLLSL GFLVTEKTVNHLLQQEERPCMDTL DCG/LQVAISEALCRLTIKKSRDELV HKWFDDEVIAEAFKEIKDREFETDS RRFLN |
| 4731 | 10228 | A | 5030 | 1 | 612 | |
| 4732 | 10229 | A | 5031 | 64 | 323 | LFPTLWLLDLLGTVEEILPSLSENIS VWGMKDSVPQGVISLKEKLSTSPD EPVPRSHHVVSLLKSTCLYIFTSG/T TGMIOFFWKA |
| 4733 | 10230 | A | 5032 | 287 | 508 | YYSIFLIYYYYYFLRWSFALVAQAV VQWCDLGSLLQPLSPGFKRFS\PSALS SWDYRHEQPRPANFIFLVETGFL |
| 4734 | 10231 | A | 5033 | 1 | 3627 | |
| 4735 | 10232 | A | 5034 | 3 | 3613 | |
| 4736 | 10233 | A | 5035 | 353 | 406 | MLHLQGIILMIVLYSCCRELIHSFLK DSKSMPCWGESDGPVTGARHPSW EEEEDGGVWNTTGSQGSASSHNSA SWGQGGKKQMK/CSLKKE |
| 4737 | 10234 | A | 5036 | 1 | 514 | ECKDCGKSFTVSSSLTEHARIHTGE KPYECKQCGKAFTGRSGLTKHMRT HTGEKPYECKDCGKAYNRVYLLNE HVKTHTEKPFTCTVCRKSFRNSSC LNKHVHIHTGIKPYECKDCGKTFTV SSSLTEHIRTHTGEKPYECKVCGKA FTTSSHLIVHIRTHTGEKPYICK |
| 4738 | 10235 | A | 5037 | 1 | 3222 | |
| 4739 | 10236 | A | 5038 | 1 | 4267 | MGPWAWKLRWTVALLLAAAGTA VGDR CERNEFQCQDGK CISYKWVC DGSAECQDGSDSQETCLSVTCKSG DFSCGGRVNRCPQFWRC DGQVDC DNGSDEQGCPPKTC SQDEF RCHDG KCISRQFVCDSDRDCLDGSDEASCP VLTCGPASFQCNSSTCIPQLWACDN DPDCEDGSDEWPQRCRGLYVFQGD SSPCSAFEFHCLSGECIHSSWRC DG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GPDCKDKSDEENCAVATCRPDEFQ CSDGNCIHGSRQCDREYDCKDMSD EVGCVNVTLCCEGPNKFKCHSGECIT LDKVCNMARDCRDWSDEPIKECGT NECLDNNGGC SHVCNDLKIGYECL CPDGFQLVAQRRCEDIDECQDPDTC SQLCVNLEGGYKQCCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKM TLDREYTS LIPNLRNVVALDTEVA SNRIYWS DLSQRMICSTQLDRAHGV SSYDTVISRDIQAPDGLAVDWIHSNI YWTD SVLGT VSVADTKGVKRKTLF RENGSKPRAIVVDPVHGFMYWTD WGTPAKIKK GGLNGVDIYSLVTENI QWPNGITLDLLSGRLYWVDSKLHSI SSIDVNGGNRKTILEDEKRLAHPFSL AVFEDKVFWTDIINEAIFSANRLTGS DVNLLAENLLSPEDMVL FHNLTQP RGVNWCERTTLSNGGCQYLCLPAP QINPHSPKFTCACPDGM L LARDMRS CLTEAEAAVATQETSTVRLKVVPD KTVRWCAVSEHEATKCQSFRDHM KSVIPSDGPSVACVKKASYLDCIRAI AANEADAVTLDAGLVYDAYLAPN NLKPVVAEFYGSKEDPQTFYYAVA VVKKDSGFQMNQLRGKKSCHTGL GRSAGWNIPIGLLYCDLPEPRKPLE KAVANFFSGSCAPCADGTDFFQLC QLCPGCGCSTLNQYFGYSGAFKCL KDGAGDVA FVKHSTIFENLANKAD RDQYELLCLDNTRKPVDEYKDCHL AQVPSHTVVARSMGGKEDLIWELL NQAQEHFGKDKSKEFQLFSSPHGK DLLFKDSA HGF LKVPQRMDAKMY LGYEYVTAIRNLREGTCPEAPTDEC KPVKWCALSHHERLKCDEWSVNS VGKIECVSAETTEDCIAKIMNGEAD AMSLDGGFVYIAGKCGLVPVLAEN YNKSDNCEDTPEAG\YFAVAVVKK SASDLTWDNLKGKKSCHTAVGRTA GWNIPMGLLYNKINHCRFDEFFSEG CAPGSKKDSSLCKL\CMGSGNLNCE PNNKRGD TTGYTGAFRCLVEKGD V AFC* KHQTVPTGTLGGEKNPDPW A\KDLNEKDY\ELLCLGWVPGKPV\ EEYAN\CHLARAPNHRCGSHGKDK EACVHK\LRSTASHLFG\SNVTD\CS GNFWLVR S\ETKDLLFRDDTV C/LW AKLHDRNTYEKYLGE EYVKA VGN LRK CSTSS LLEACTFRP |
| 4740 | 10237 | A | 5039 | 2 | 342 | LSRVVL SAAATAAPSLRNAA/FLGP GVLQATRTFHTGQPHLVPVPLPEY GGK VRYGLIPEEFFQFLYPKTGVTG PYVLGTGLILYALSKEIYVISAETFT ALSCSAFELFRDHF |
| 4741 | 10238 | A | 5040 | 53 | 940 | DCYLDVSLTMLS RVVLSAAATAPT IIMKNAAFLGPGVLQATRTFHTGQP HLC PMY\PIIPEY G\GK VRYG\LIPE\ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FFQFLY/PLKTGVNTDPNVPPETWG LNLVTVLFQRKYMVEFRRRGPSLA LIKY*GGKWVYGNLKKYGSPLVAG LWLD*TPMEQKLGPT*EE/ARQGGF PSQHIQNAIDYGRSLYQALVQKRH YLFQDVQRNNIAMALEVTYRERLYR VYK\EVKNRLDYHISVQNHDVAVRN GTTNSLLNW\VEKHVRACLFPQA RKEDILPKWHCRPIKLLAKEGSKAQ AQLW |
| 4742 | 10239 | A | 5041 | 2 | 205 | APVTSW/IQPKDGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADML\ VSFSGYSSAPKNQEQ |
| 4743 | 10240 | A | 5042 | 1 | 360 | SPCLSERQFCCEKLPLQRSSRPQDSA GQPVT/HAHCSLASTVDLCPPLLAT HRISCWHCQDEVHGGRD\SVDKGD LEALSLPAGHGD TDGPISLDVDPGA PDPQRTKAAIDHLHHKILKSTE |
| 4744 | 10241 | A | 5043 | 106 | 396 | |
| 4745 | 10242 | A | 5044 | 77 | 4026 | |
| 4746 | 10243 | A | 5045 | 1 | 344 | LDFIQTMLQVVGVSVAVPV/IPWI AIPLVPLGIIFILRRYFLETSRDVKR LESTTRSPVFSHLSSSLQGLWTIRAY KAEERCQELFDAHQDLHSGLSISGN GFKGQDLLLFLA |
| 4747 | 10244 | A | 5047 | 3 | 378 | ERDGA TLPLTPGLPSPPLPP/HTSS QAHYRLSAFGQQFLFNLTANAGFIA PLFTVTLLGTPGVNQTKFYSEEEAE LKHC FYKGYVNTNSEHTAVISLCSG MLGTFRSHDGDYFIEPLQSMDEQE |
| 4748 | 10245 | A | 5049 | 2 | 278 | FVNHGCSQ\TLHFVFKVGNRFQTAR FYRDVLGMKVQAGADRGWRARLE PAPEPALAEGGENGCVVNLSRRVS DLRPCAVFSFRSVASCRWGS |
| 4749 | 10246 | A | 5050 | 1 | 1539 | MRLTPFSLSTGNSFRYSRRLKKNIFG TAPALRVSEMSLRPSSRIFPCFSRNG LDFTIVITLAQPPVPGISFIVAKPRLF PGAGSAGCGLLERLFLSLLGTGLR WCLRGCFPGARFCSTTSPEGHTTFT GLRRSARTQRLAQGPKPGPPAATV ARQTSRVSPAPPCSLRPGLRHESAPS GIGDVTARGALRGLGCTVRVTAAC GGNHGCSQ/LCLHFVFKVGNRLQT AAFHIGTSMGMKVQOHEEFEEG\CK AA\CNGPIYDG\KWSKTMVG/YLGP EDDH FVAELTYNYG\VG DYKLGND FMG\ITLA\SSQAVSNARK\LEWPLT EVAEGVF\ETEAPGGYKFYLQNRSL PQSDPVLKVT LA VSDLQ\SLNYWC NLLGMKIYEKDEEKQRALLGYAGL TSVSLELQGVKGGVDHAAAF\GR\A AFSCPQKE\LPDL\EDLMKRENQKIL TPLVSLDTPGKATVQVVILADPDGH EICFVGDEAFRELSKMDPEGSKLLD DAMAADKSDEWFAKH NKPKASG |
| 4750 | 10247 | A | 5051 | 21 | 223 | HPGSRGCSEPRSGHCTPAWGTVKVK T/SRLNKNKTKQKKEVKDCMSSTPL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AHPPGVWCEWRGLIPSSSP |
| 4751 | 10248 | B | 5052 | 64 | 543 | RGWKRDRDKRDDQDDVSSVRSEG GNIRGSFRGRGRGRGRGRGRGN PRLNFDYSYGYQEHGERTDQPFQTE LNTSMMYYYDDGTGVQVYPVEEA LLKEYIKRQIEYYFSVENLERDFFLR GKMDEQGFLPISLIAGFQRVQALTT NLNLILPPLKDSTE* |
| 4752 | 10249 | A | 5053 | 1 | 567 | AAATSAGA/PGRAVAGAGAGTQRA PGGCPREAPGAAPGVHKARGPGGPF GGEPPPPPPP/LVAVAAVAAGSAGR GRPGR\VAAGPAEKRPPLLPPKGN PWTKKPPQHLSPDTTGPPPPPLETLE AEFGSLKIIKAGKLKTKKSNKASDF SDMENWPTPSELVNTGFQSVLSQG NKKPPNRKEKEEKGEREEQ |
| 4753 | 10250 | A | 5054 | 3 | 763 | SGRPHPVIRESSPSSSLALGGQLGRG RPSGRAAPGRANPSAPAGGPAREGP EFGSLKIIKAGKLKTKKSNKASDFS DMENWPTPSELVNTWISERPQPRK\ KKPQNRKEKEEKVEKRSNSDSKEN RETKLNGPGENRQ/STDEAQSSNQR KRANKHKWVPLHLDVVRSESQERP GSRNSSRCQPEANKPTHNNRRNDT RSW/ESEIEKKE/HDQDDVSSVRSEG GNSRGSFRGRGRGRGRGRGRGRG NPRLNFDYSSC |
| 4754 | 10251 | A | 5055 | 1 | 372 | RHEQGISFLETETFM TDQLVDALT TWQNKTKVGLLWSAAHIRFKPTLS QQQKSPEQHETVLDGNLIIRYDVDR AISGGSITREALIKILDDLIPRDQFN LIVFSTEATQWRPSLVPASAEN |
| 4755 | 10252 | A | 5056 | 1 | 1021 | AQAQYSAAVAKGKSAGLVKATGR NMEQFQVSVSVAPNAKITFELVYEE LLKRRLGVYELLLKVRPQQLVKHL QMDIHIFEPQGISFLETETFM TNQL VDALTTWQNKTKAHIRFKPTLSQQ QKSPEQQETVLDGNLIIRYDVDR AIS GGSIQIENGYFVHYFAPEGLTTPK NVVFVIDKSGSMSGRKIQQTREALI KILDDLSPRDQFN LIVFSTEATQWR PSLVPASAENVNKARSFAAGIQALG GTNINDAMLMAVQLLDSSNQEERL PEGSV\SLIILLTDGDPTVGETNPRSI QNNVREAVSGRYSFLCLGFGFDVS YAFLEKLALDNGGLGRG |
| 4756 | 10253 | A | 5057 | 570 | 831 | HGNYRNV CILLGLFYPHFVGEKKIH IGFFLFFPAIDLKSGSGKVYQGPAG AADTTILSDEYFMEVVLGKLD PQK AFFSGRLKAEG |
| 4757 | 10254 | A | 5058 | 1 | 2229 | MGSPLRFDGRVVLVTGAGAGLGRA YALAF AERGALVVVNDLGGDFKG VGKGS LAADKVVEEIRRRGGKAVA NYDSVEEGEKVVK TALDAFGRIDV VVNNAGILRDRSFARISDEDWDIIH RVHLRGSFQVTRAAWEHMKKQKY GRIIMTSSASGIYGNFGQANYSAK LGLLGLANSLAIEGRKSNHCNTIAP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NAGSRMTQTVMPEDLVEALKPEYV APLVLWLCHESENGGLFEVGAG WIGKLRWERTLGAIVRQKNHPMTP EAVKANWKKICDFENASKPQSIQES TGSIIIEVLISKIDSEGGV SANHTSRAT STATSGFAGAIGQKLPPFSYAYTELE AIMYALGVGASIKDPKDLKFIYEGS SDFSCLPFTGVIIQKSMGGLAEI PGLSINFAKVLHGEQYLELYKPLPR AGKLKCEAVVADVLDKSGSVVIM DVYSYSEKELICHNQFSLFLVGSGG FGGKRTSDKVKVAVAI PNRPDAV LTDTTSLNQAALYRLSGDWNPLHID PNFASLAGFDKPILHGLCTFGFSARR VLQQFADNDVSRFKA IKARFAKPV YPGQTLQTEMWKEGNRIHFQTKIV QETGDIVISNAYVDLAPTSGTQAKT PSEGGKLQITFVFEEIGPRLKDGP VVVK\KVNAVFEWHITKGGNIGAK WTIDLKSGSGKVYQGP\AKGAADT TIH/ILSDEDF/LWEVVLGQA*PSRKA FFSGRLEGQEGNIMLS\QKLQMIL\K DYAKL |
| 4758 | 10255 | A | 5059 | 1 | 7449 | |
| 4759 | 10256 | A | 5060 | 1 | 7458 | MTDSKPITKSKSEANLIPSQEFPFAS DNSGETPQRNGEGHTL/HQDTQPGR ASLPQRPQR\SGRRRNSLPPSHQKPP RNPLSSSDAAPSPELQANGTGTQGL EATDTNGLSSSAR PQGQQAGSPSKE DKKQANIKRQLMTNFILGSFDDYSS DEDSVAGSSRESTRKGSRASLGALS LEAYLTTELLALDFGIFGIRGSLVFA GYPLTLLHTYRQGSNTSSLVFTGLG SGFIELLGCPLRPQQKAAVQRPSMS GLHLVKRGREHKKLDLHRDFTVAS PAEFVTRFGGDRVIEKVLIANNGIA AVKCMRSIRRWAYEMFRNERAIRF VVMVTPEDLKANA EYIKMADHYV PVPGGPNNNNYANVELIVDI AKRIP VQAVWAGWGHASENPKLPELLCK NGVAFLGPPSEAMWALGDKIASTV VAQTLQVPTLPWSGSGLTVEWTE DLQQGKRISVPEDVYDKGCVKDVD EGLEAAERIGFPLMIKASEGGGGKG IRKAESAEDFPILFRQVQSEIPGSPIF LMKLAQHARHLEVQILADQYGNA VSLFGRDCSIQRRHQKIVEEAPATIA PLAIFEFMEQCAIRLAKTVGYVSAG TVEYLYSQDGSFHFLELNPRLQVEH PCTEMIADVNLPAALQGF KPSSGT VQELNFRSSKNVWGYFSVAATGGL HEFADSQFGHCF SWGENREEAISN MVVALKELSIRGDFRTTVEYLINLL ETESFQNNIDITGWLDYLIAEKVQA EKPDIMLGVVCGALNVADAMFRTC MTDFLHSLERGQVLPADSLNLVD VELIYGGVKYILKVARQSLTMFVLI MNGCHIEIDAHRLNDGGLLLSYNG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NSYTTYMKEEVDSYRITIGNKTCVF EKENDPTVLRSPSAGKLTQYTVEDG GHVEAGSSYAEMEVMKMIMTLNV QERGRVKYIKRPGAVLEAGCVVAR LELDDPSKVHPAEPFTGELPAQQTL PILGEKLHQVFHSLVLENLTNVMMSGF CLPEPVFSIKLKEWVQKLMMLTLRH PSLPLELQEIMTSVAGRIPAPVEKS VRRVMAQYASNITSVLCQFPSQQA TILDCHAAATLQRKADREFFINTQSI VQLVQSLGTEQDLVFYEKEKRNQSI LGFEPVNSRHVSHVPETHRYKESHY DKCVINLREQFKPDMSQVLD CIFSH AQVAKKNQLVIMLIDELCGPDPSLS DELISILNELTQLSKSEHCKVALRAR QILASHLPSYELRHNQVESIFLSAID MYGHQFCPENLKKLILSETTIFDVLP TFFYHANKVVCMA SLEVYVRRGYI AYELNSLQHRQLPDGTCVVEFQFM LPSSHPNRMTVPISITNPDLLRHSTE LFMDSGFSPLCQRMGAMVAFRRFE DFTRNFDEVISCFANVPKDTPLFSEA RTSLYSEDDCKSLREEPIHILNVS IQ CADHLEDEALVPILRTFVQSKKNIL VDYGLRRITFLIAQEFAEDRIYRHLE PALAFQLELNRMRNFDLTAVPCAN HKMHLYLGA AKVKEGVEVTDHRF FIRAIIRHSDLITKEASFEYLQNEGER LLEAMDELEVA FNNTSVRTDCNHI FLNFVPTVIMDPFKIEESVRYMVMR YGSRLWKLRVLQAEVKINIRQTTTG SAVPIRLFITNESGY YLDISLYKEVT DSRSGNIMFHSFGNKQGPQHGM L N TPYVTKDLLQAKRFQAQTLGTTYIY DFPEMFRQASPA AQTRVHVHNVQA LFLKLWGSPDKYPKDILTYTELVLDS QGQLVEMNRLPGGNEVGMVAFKM RFKTQEYPEGRDVIVIGNDITFRIGS FGPGEDLLYLRASEMARAE GIPKIY VAANS GARIGMAEEIKHMFHVAW VDPEDPHKKKKTVAFSAGNWIRSL TKVFFKGFKYLYLTPQDYTRIS SLN SVHCKHIEEGGESRYMITDIIGKDD GLGVENLRGSGM IAGESSLA YEEIV TISLVTCRAIGIGAYLVRLGQRVIQV ENSHIILTGASALNKVVEPCTVQDIA NHVVSKQVLGREVYTSNNQLGGV QIMHYNGVSHITVPDDFEGVYTILE WLSYMPKDNHSPVPIITPTDPIDREI EFLPSRAPYDPRWMLAGRPHPTLK GTWQSGFFDHGSFKEIMAPWAQTV VTGRARLGGIPVGVI AVETRTVEVA VPADPANLDSEAKIIQQAGQVWFPD SAYKTAQAVKDFNREKLPLMIFAN WRGFSGGMKDMYDQVLKFGAYIV DGLRQYKQPIL IYIPPYAELRGGSW VVIDATINPLCIEMYADKESRGGVL EPEGTVEIKFRKKDLIKSMRRIDPAY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KKLMEQLGEPDLSKDRKDLEGRL KAREDLLLPYHQVAVQFADFHDTP GRMLEKGVISDILEWKTARTFLYW RLRRLLEDQVKQEILQASGELSHV HIQSMRLRRWFVETEGAVKAYLWD NNQVVVQWLEQHWQAGDGPRSTI RENITYLKHDSVLKTIRGLVEENPE VAVDCVIYLSQHISPAERAQVVHLL STMDSPAST |
| 4760 | 10257 | A | 5061 | 6 | 906 | EQPALLPRYRSGIRGYMKTVVLDLL RRYL RVE TIFSKARDADANTSGMV GGVRSLSFTSVWVLSPPAHYDKCV INLREQFKPDMSQVLD CIFS HAQVA KKNQLVIMLIDELCGPDPSLSDELISI LNELTQLSKSEHCKVALRARQILIAS HLPSYELRHNQVESIFLSAIDMYGH QFCPENLKKLILSETTIFDVLPTFFY HANKVVCMA SLEVYVRRGYIAYEL NSLQHRQLPDGTCVVEFQFMLPSSH PNRMTVPISITNPDLLRHSTELFMD S GFSPLCQRMGAMVAFRRFEDFT |
| 4761 | 10258 | A | 5062 | 2 | 560 | APRLDV SFSQIIHRDIKPENILVSQSG ITKLCDFGFARTLAAPGDIYTDYVA TR*PVDI WALGCM IEMATGNPYLP SSSDLDLLHKIVLKVG NLSPHLQNI F SKSPIFAGV VLPQVQHPKNARKKYP KLNGLLADIVHAWLQIDPADRISS DLLHHEYFTRDGF I*KFMPELKA*L LQEAKSQF |
| 4762 | 10259 | A | 5063 | 1 | 573 | |
| 4763 | 10260 | A | 5064 | 2 | 791 | NLVN LIEVFRQKKKIHLVFEFIDHTV LDELQHYCHGLESKRLRKYLFQILR AIDYLHSNNTV DIWALGCM IEMA TGNPYLPSSSDLDLLHKIVLKVG N SPHLQNI FSKSPIFAGV VLPQVQHPK NARKKYPKLNGLLADIVHEIEKEKK PKEIKVRVIKVKGGRGDISEPKKKE YEGGLGQQDANENVHPTSPDTKL V TIEPPNPINPSTNCNGLKENPHCGGS VTMP PINLTNSNLMAANLSSNLFS P QCEVSCNREEP |
| 4764 | 10261 | A | 5065 | 3 | 524 | TYGPASRGICRVSLGRPRWENAAT WKLAAMASIRLQGLHKPVYHALSD CGDHV VIMNTRHIAFSGNKWEQKV YSSHTGYPGGFRQVTA AQLHLRDP VAIVKLA IYGMLQ/NNLHRRTMME RLHLFPDEYIPEDILKNLVEELPQPR KIPKRLDEYTQEEIDAFRLWTPPED YRL |
| 4765 | 10262 | A | 5066 | 1 | 250 | YSSHTGYPGGFRQVTA AQLHLRDP VAIVKLA IYGMLPKNLHRRTMMER LHLFPDET*RLSAIRE*ELQKITVK*L KLSSDEFL |
| 4766 | 10263 | A | 5067 | 129 | 796 | MGKCSHLANFAALASIRLQGLHKPV YHAPE*L/CGDHV VIMNTRHICIF/H GNKWGTSILFRILAYPGWSLDKVT SLAPAFTLRRSQW/CNL*NLAIYGIP AKKTFTRRTIDWKGLHLFPDELYS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RKIFLKKFS*EELPSTTEKYLNVLDE YTTRNRRLFKIVDSTLKIIGYKRIRI AENNSEVIETFLMSFSNLQDGVKQ LLQFEHLFLCAESLWGKVRKV |
| 4767 | 10264 | A | 5068 | 15 | 350 | GPGSAITVGPQPL/RAQRNHRLPVPS PGLSIVMGLRPVSPGPTGLPGHRQ SSEMRPREAGSLRSSGEKGLPAPVP RPQQSDMTKRTLPRDTPDTPRCPPQ HCPWSRVRGQPQ |
| 4768 | 10265 | A | 5069 | 1 | 2175 | |
| 4769 | 10266 | A | 5070 | 3 | 86 | KNYRGTMS/KTKNGITCQKWSSTSP RRPR |
| 4770 | 10267 | A | 5071 | 2 | 583 | LLLLFLKSGHGEPLDYYVYAQGA SLFSVTNKH LGAGSTEECASQCVED KEFTCGAFQYHSKEQQCAIMAENK KSSIIIRMRDVVLF EK*MYLSECQTG NGKNYRGTMSKTKNGITCSKMGVP LFPHRPRFSPATHPSEGLARNPDNDA QGPWCYT TDPEQRYDYCDIPECEG QEWALGKCFHFCSSPVKINLL |
| 4771 | 10268 | A | 5072 | 844 | 4515 | TVKAPGYSHSHPGALLDLEVGDPN GTNAQLIKCFLPLCPSFPLCPEECM HCSGENYD GKISK TMSGLECAWD SQSPHAHGYIPSKFPNKNLKKNYCR NPDREL RPWCFTTDPNKRWELCDIP RCTTPPPSSGPTYQCLKGTGENYRG NVA VTVSGHTCQHWSAQTPHTHN RTPENFPCKNL DENYCRNPDGKRA PWCHTTNSQVRWEYCKIPSCDSSPV STEQLAPTAPPELTPVVQDCYHGDG QSYRGTSSTTTTGKKCQSWSSMTP HRHQKTPENYPNAGLTMNYCRNPD ADKGPWCFTTDP SVRWEYCNLKKC SGTEASVVAPPPVLLPDVETPSEE DCMFGNGKGYRGKRATTVTGTPC QDWAAQEPHRHSIFTPETNPRAGLE KNATECGGASTELCSTSLCAFTML MDYEGQGEPLDDYVNTQGASLFSV TKKQLGAGSIEECAAKCEE GVEEFTC RAF\QYHSKEQQCVIMAENRKSS\III RMRDVVLF EKKV\YLSECKTGNGK NYRGTMSKTKNGITCQKWSSTSPH RPRFSPATHPSEGLEENYCRNPDND PQGPWCYT TDPEKRYDY\CDILEC *RRECMFAFVGGKLLTGKIFPTMS WDWECQAWGLFRSPHG\HGYIPSK FPNKNLKKNYCRNPDREL RPWCFT TDPNKRWELCDIPRCTTPPPSSGPTY QCLKGTGENYRGNVA VTVSGHTCQ HWSAQTPHTHN RTPENFPCKNLDE NYCRNPDGKRAPWCHTTNSQVRW EYCKIPSCDSSPVSTEQLAPTAPPEL TPVVQDCYHGDGQSYRGTSSTTTT GKKCQSWSSMTPHRHQKTPENYPN AGLTMNYCRNP DADKGPWCFTTDP SVRWEYCNLKKCSGTEASVVAPP VLLPDVETPSEEDCMFGNGKGYR GKRATTVTGTPCQDWAAQEPHRHS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | IFTPETNPRAGLEKKNYCRNPDGDVG GPWCYTTPNPKLYDYCDVPQCAAP SFDCKGKPQVEPKKCPGRVVGCCVA HPHSWPWQVSLRTRFGMHFCGGTL ISPEWVLTAAHCLEKSPRPSSYKVIL GAHQEVNLEPHVQEIEVSRLFLEPT RKDIALLLKSSPAVITDKVIPACLP PNYVVADRTECFVTGWGETQGTFG AGLLKEAQLPVLENKVCNRYEFLNG RVQSTELCAGHLAGGTDSCQGDG GPLVCFEKDKYILQGVTSWGLGCA RPNKPGVYVRVSRFVTWIEGVMRN N |
| 4772 | 10269 | A | 5073 | 9 | 141 | FYRLSLGFKCDWFTMEKRVKLEER YRDMAEENLKKDISISLKL |
| 4773 | 10270 | A | 5074 | 3 | 360 | QTKPKESRKRIIMFRTVEFNETENRI ESSSSSSSSSFSSSSSSYKCLARLTK/ RKK/EKIQIIVRSEKKEITNYRIKRIT KGYIELLYANQLYHLMKCPKFLER HKLLKLTQEETKSGV |
| 4774 | 10271 | A | 5076 | 1 | 245 | AAAYYYTAAARRRQKGERRKKRK EEER\KEEKKRKKKEKKRRRRG GRRTKKEEKEKEKKRRTKKEKKK KKKKKKKVSM |
| 4775 | 10272 | A | 5077 | 68 | 246 | SMAFLTIEDTALKFIQNHKRPQIA\ KPILSKNRAESITLFNSKIHYPMTVI KPLRVST |
| 4776 | 10273 | A | 5078 | 3 | 364 | TSIVAAQMFNVITVMQVRISPQHMT SMWPIMVCELSQTFTQLEEDVKDK VESLRSTNKVNRKVSVDANGPS VGYPQSEL\IMYLSACKFLDAALSIP HYKIPLFKIYRWAFIPEVDTE |
| 4777 | 10274 | A | 5079 | 2 | 1315 | GKDAKILCSNPNTGEVLYELPTNTQ RCFDIQWCPRNPVLSAASFAGRIS VYSIMGGSTDGLRQKQVDKLSSSFG NLDPFGTGQPLPLQIPQQTAAHSIV LPLKKPPKWIRRPVGASFSGGKLV TF\ENVRMPHQGAEEQQQQHHVFI SQVVTEKEFLSRSDQLQQA VQSQGF INRQKKIDASQTELEKNVWPFLPV TFEDDSRGKYLELLGYRKEDLGK/K DCFGL/GTKWMEPMWLLKTLTKYH ITNHEPAG*PPVTNAAATASSSSTA KPVFIPTDTSSRWTALPWRTATSW NRHAPIFFTAQY*RCPRGSYWKYLP ACAVFGNKKNYQETYSR*APHSKD HI*GSYSALPFFSNRPSNQEEAR*CQ QTFGVSV**T*GTDFTNNHQWFTQ HCKEH*NSKLLRRIDHAYPHS*HQQ LQ*DLCFHASSQSCL |
| 4778 | 10275 | A | 5080 | 18 | 3600 | |
| 4779 | 10276 | A | 5081 | 238 | 480 | SIQFYFFSFQDSKGKHSLSVSVIGPQN GWNPPALNRVPKKKKMPENFMPP VPITSPIMNPLGDPQSQMLQQQPSA\ PVPLS |
| 4780 | 10277 | A | 5082 | 352 | 4060 | DYSRRYILRMKLKEVDRTAMQAW SPAQNHPIYLATGTSAQQQLDATFST |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NASLEIFELDLSDPSLDMKSCATFSS SHRYHKLWGPYKMDSKGDVSGVL IAGGENGNILYDPSKIIAGDKEVVI AQNDKHTGPVRALDVNIFQTNLVA SGANESEIYIWDLNNFATPMTPGAK TQPPEDISCIAWNRQVQHILASASPS GRATVWDLRKNEPIIKVSDHSNRM HCSGLAWHPDVATQMVLASEDDR LPVIQMWDLRFASSPLRVLENHAR GILAIWSMADPELLSCGKDAKIL CSNPNTGEVLYELPTNTQWCFDIQ WCPRNPAVLSAASFDGRISVYSIMG GSTDGLRQKQVDKLSSSFGNLDPFQ TGQPLPPLQIPQQTAAHSIVLPLKKP PKWIRRPVGASFSGGKLVTFENVR MPSHQGAEEQQQQHHVFISQVVTE KEFLSRSDQLQQA VQSQGFNYCQK KIDASQTEFEKNVWSFLKVNFEEDS RGKYLELLGYRKEDLGKKIALALN KVDGANVALKDSQVAQSDGEESP AAEEQLLGEHIKEEKEESEFLPSSGG TFNISVSGDIDGLITQALLTGNFESA VDLCLHDNRMAAILAIAGGQELL ARTQKKYFAKSQSKITRLITAVVMK NWKEIVESC DLKNWREALAAVLTY AKPDEFSALCDLLGTRLENEGDSLL QTQACLCYICAGNVEKLVACWTKA QDGSHP LSLQDLIEKVILRKA VQL TQAMDTSTVGVLLAAKMSQYANL LAAQGSIAAALAFDPDNTNQPNIMQ LRDRLCRAQGEPVAGHESPKIPYEK QQLPKGRPGPVAGHHQMPRVQTQ QYYPHGENPPPPGFIMHGNVNPNA AGQLPTSPGHMHTQVPPYPQPQPY QPAQPYPFGTGGSAMYRPQQPVAP PTSNAYPNTPYISSASSYTGQSQLYA AQHQASSPTSSPATSFPPPPSSGASF QHGGPGAPPSSSAYALPPGTTGTLF AASELPASQRTGPQNG\WNDPPALD \KVPKKKKMPENFMPPVPITSPIMN RLGDPQSQMLQQQPSAPVPLSSQSS FPQPHLP GG\QPF PWGYSKPF GFKQ GMATIFFQSPNIEGAPGAPIG\NTFQ HVQSLPTKKITKKPI\PD\EHLILKTT FEDLIQRCLSSATDPQTKRKLDDAS KRLEFLYDKLR\DRTFSPITTSGLHNI ARSIETRNYSEGLTMHTHIVSTSNFS ETSAFMPVLKVVL TQANKLGV |
| 4781 | 10278 | A | 5084 | 121 | 419 | DLCFTTPKAGRRQEITKIRAE LNKV EVQETIQKISEKRSWLFNIINKIARLL TRLIQKKDAQINTVRNDKGDITTYPT EIQKTLRDYYEHL YACRVENLQ |
| 4782 | 10279 | A | 5085 | 1 | 279 | TMDSNNTV\DQLDL\TDIYRTLHLTS AAYTFFSSAHLRCSR\DLRLSHKTS LNKFKKIVIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL |
| 4783 | 10280 | A | 5086 | 1 | 279 | TMDSNNTV\DQLDL\TDIYRTLHLTS AAYTFFSSAHLRCSR\DLRLSHKTS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LNKFKKIVIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL |
| 4784 | 10281 | A | 5087 | 1 | 1915 | MAILPLLLCLLPLAPASSPPQSATPS PCPRRCRCQTQSLPLSVLCPGAGLL FVPPSL\DRRAAELRLADNFIA SVRR RDLANMTGLLHLSLSRNTIRHVAA GAFADLRALRALHLDGNRLTSLGE GQLRGLVNLRHLILSNNQLAALAA GALDDCAETLEDLDSYNNLEQLP WEALGRLG\NVNTLGLDHNLLASV PAGAFSPLHKLARLDMTSNRLTTIP PDPLFSRLPLLARPRGSPASALVLA GGNPLHCNCELVWLRLAREDDLE ACASPPALGGRYFWAVGEEEFVCE PPVVTHRSPLAVPAGRPAALRCRA VGDP EPRVRWVSPQGRLLGNSSRA RAFPNGTLELLVTEPGDGGIFT CIAA NAAGEATAA VELTVGPPPPPQLANS TSCDPP/PGRGLPDALTPPSAASASA KVADTGPTDRGVQVTEHGATAA LVQWPDQRPIPGIRMYQIQYNSSA DDILVYRMIPAESRSFLLTDLASGRT YDLCVLAVYEDSATGLTATRPVGC ARFSTEP\SLRPCGAPHAPFLGGTMII ALGGVIVASVLVFIFVLLMRYKVHG GQPPGKAKIPAPVSSVCSQTN\GAL GPTPTPAPPAPPAALRAHTVVQLD CRALGARPRTCGTLARRPPL |
| 4785 | 10282 | A | 5088 | 1387 | 1567 | GKNLLPLFFFFFFFETVSQSVAQAG VQWRHLGSPKPLPPAGSSDSPASVSQ AAETTGTCHH |
| 4786 | 10283 | A | 5089 | 96 | 408 | SPRK RKTRHSTNPPLECHVGWVMD SRDHGPGTSSSVSTSNASPSEGAPLA GRYGCTPH\SF PKFQNP SHELLKEN GFTQQVYHKYRRRCLSERKRLGIG QSQEMNT |
| 4787 | 10284 | A | 5090 | 390 | 665 | PLNIHYCFLGGKYL VFGFSVAANKT SGAP\GNSPVSAIRAFGDAHPDLVT PGTF\IPYCSMAHAQLCFHGH RDAV KFFVA VPGQVISPOSSSS |
| 4788 | 10285 | A | 5091 | 185 | 386 | WEASKKKPRGAQISNAITTYKYL PK VG\KNYQTEALYKPIQTGKIGHPV FFQKPPLLGDGQNYDTPP |
| 4789 | 10286 | A | 5093 | 3 | 330 | GTGLKARKSASSLPETFPTRTRHGE AALPLSPTWKMTGPVGNPMIPRQR SMSLLTAVSGQPHFQDSALSQASSS PDLL/LHLSPR\SCPGRVQETLKATD RPPRCPAGCG |
| 4790 | 10287 | A | 5094 | 2 | 349 | PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLKKGENPPNSFYGAIP RIPNPNMDLPSSSPT/RPVSGRNMEA KIFTKFLAGHFKQSF GREIHHDQREF IPGIQGGFNIGN |
| 4791 | 10288 | A | 5095 | 2 | 353 | PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLASSSSSSSSSSSSSSSS SSPPNMDLPSSSPT/RPVSGRNIEAKI FTKFLPGHFQQSFGRVTHLDQRELI LGNQGGSTICKS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4792 | 10289 | A | 5096 | 1 | 262 | RGRAGGEPLPATTGAAPPPGRRRLH/ RQLPDRRGLASMPREEKASLNEPG GPGRGRRRGSVQLHGEGGPRGEE GTGREEWNEKAEFTL |
| 4793 | 10290 | A | 5097 | 116 | 177 | LGEHGVYSGVGTGGRLLSS*KKGKP WFK*KKLKGGPIPI*RDPRGFSRFSV |
| 4794 | 10291 | C | 5098 | 231 | 347 | MGLGPHLKFFYLKHGLPFFKELNPL KVKIWPRNPWIKKI* |
| 4795 | 10292 | A | 5099 | 518 | 931 | ATRHSMLSCTIYTYTYIKHTHTHVFI YIYTYTYIHTHIYTYTYICIHTHIHIYI YIYIHTHFFFFFFFETESRSVTQAGV QWHDLGSLQAASWGHA/DSPASTS QAAGTTGAHHHAQ/LIFFFFVFLVET GPHRASQDS |
| 4796 | 10293 | A | 5100 | 2 | 1109 | DAEMLVMAPRTVLLLLSAALALTE TWAGSHSMRYFDTAMSRPGRGEPR FISVGYVDDTQFVRFDSDAASPREE PRAPWIEQEGPEYWDRNTQIFKTNT QTDRESLRNLRGYYNQSEAGSHTL QSMYGCDVGPDRLLRGHNQYAY DGKDIALNEDLRSWTAADTAAQI TQRKWEAARVAEQDRAYLEGTCV EWLRRYLENGKDTLERADPPKTHV THHPISDHEATLRCWALGFYPAEIT LTWQRDGEDQTQDTELVEPTRPAGD RTFQKWAAVVVPSGEEQRYTCHVQ HEGLPKPLTLRWEPSSTVPVIGIV AGLAVLVTVAVVAVVAAMCRR KSSGGKGGSYSQAASSDSAQGS DV SLTA*KA |
| 4797 | 10294 | A | 5101 | 3 | 1145 | SDSPQTPRMRVMAPRTLILLLSGAL ALTETWACSHSMRYFYTA VSRPGR GEPRFIAVGYVDDTQFVRFDSDAAS PRGEPRAPWVEQEGPEYWDRETQ KYKRQAQTDRVSLRNLRGYYNQSE AGSHTLQWMYGCDLGPDRLLRG YDQSA YDGKDIALNEHLRSCTAA DTAAQITQRKWEAARAAEQQRAYL EGTCVEWLRRYLENGKETLQRAEH PKTHVTHHLVSDHEATLRCWALGF YPAEITLTWQRDGEDQTQDTELVE TRPAGDGTQFQKWAAVVVPSGEEQRY TCHVQHEGLPEPLTLRWEPSSTQPTIP IVGIVSGPAVLAVLAVLAVLAVLGA VVA AVIHRRKSSGGKGGSCSQAAS SNSAQGSDES LIACKA |
| 4798 | 10295 | A | 5102 | 3 | 242 | GFWAPRVCKDIDKWHLSEPEALWF GEGGSPGGCRWGGWLCQGNRA AGGVGAEGACLGLLSATGLLWMT GLQEPREPQV |
| 4799 | 10296 | A | 5103 | 1 | 138 | FPLIPKPGKDPFN/ENFRPIFLMAKN AKILKKILANLIFQPLKKIL |
| 4800 | 10297 | A | 5104 | 59 | 337 | IPYPALPFTSVEAPNSHVKA VMKTS VLLSWEIPENYNSAMPFKILYDDGK MVEEVDGRATQKLIVILNPEKSYSF ELTYRGNCAGGLELMVT |
| 4801 | 10298 | A | 5105 | 54 | 226 | TKAETENLNRPVT/EIKSVI/NSLPTK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KSPGLDGFIAKFFQTYKREIPTLLK LLQKLKW |
| 4802 | 10299 | A | 5106 | 2 | 265 | ETVKLLEENI/GQKLFDIGLGSDFLDI TPKAQETKINKWDFIKLSFCTVKE TIKMKRQSVEWEKILVSHVSDKWFI SKIQGIYITQYQ |
| 4803 | 10300 | A | 5107 | 1 | 296 | GREKEEGESGEDWGRV\GREKEGG EGREEEGEGGREEEGEGGRKEEGE GGREEEGEGGREEEGEGGREEEGE/ GREEEGEGGRQEEGEGGRRREGRG GRS |
| 4804 | 10301 | A | 5108 | 1 | 253 | |
| 4805 | 10302 | A | 5109 | 190 | 472 | |
| 4806 | 10303 | A | 5110 | 1 | 314 | HNVPVPHVFMQLQKEITKKNSTFRVHI KAVFYN/HDIYCMPLLNRYRKTDFV IVIDPPWQSKSVKRSNRYSLPLQI KQIPKLAAPNCLLVTWLTNTQKH LRFIK |
| 4807 | 10304 | A | 5111 | 3 | 362 | FFFFFETESLSVPQAGVQ*HDLSSLQ PP/PPGFTPFSCSLSPSSWDYRCPPPR PA/NIFFVFLVETGFHHVSQDGLDLL T/S/GDPPASASQSAGITGVSHRARPP PPQFFIQLPLYNIHTLEGR |
| 4808 | 10305 | A | 5112 | 3 | 385 | FFFETESRSVAQAGGQWHDLSLQ APTPGFTPFSCSLSPSSWDYRCPPPC PANFFVFLVETGFHHVSRDGLDFLT SDPPTSASQSVGITGVSHCARARPF FKKKKKKKTSILSSSSLSFSHKQRSFG F |
| 4809 | 10306 | A | 5113 | 1 | 390 | SKAVKV/YRLITRNSYEREMFDKAS LKLGLDKAVLQSMGRDGNITGIQ QFSKKEIEDVLRKGAYAAIMEEDDE GSKFCEEDIDQILLRRTTTITIESEGK GSTFAKASFVASGNRTDISLDDPNF WQKWA |
| 4810 | 10307 | A | 5114 | 2 | 214 | GRVDIERAHLVQTGQQALEPA\YRL RRAPYPCHTSDLFLNNVGFFFLIM MLTWMVSVASMRPLVSQQE |
| 4811 | 10308 | A | 5115 | 30 | 379 | KRSVNSPGRALSELCVSTELGFLRC VSVVCSLSQEYFLFTLLYFGL/LPF ACLLSSSPVFFVFRCSVPLFFCFLFC VSLCLPFLGFFHVLFFHRLLPVFSF MEGFYWAWCLVFFCL |
| 4812 | 10309 | A | 5116 | 1 | 304 | GTRETVGLGDTNLAHQCSRLTMVN NDNHSEAYNNLAVLEMKGHVQQ ARALLQTASALSPHMYET\DFNFATI CDMTGYLHRSYVDAQKSEAALSEH VDTQH |
| 4813 | 10310 | A | 5117 | 119 | 264 | |
| 4814 | 10311 | A | 5118 | 720 | 2798 | VYWPHSFLGCPSNYPLYLGAETRQ GGRARPPFLPLSFPPRFRPNSPFQN VLETQRISYSFPLLADTSNTRATSGH AQQPAPILPLREVAGAEDIIRVHVPF SLSDLSQIAKRLGSFSSDPDTYKEF KYLTQSYELTWHDLYHLSSTLLPEK KERVWLAAQAHANDLHRQDPTKPI GAAAVPLEEPPWKYQPTDPGRASR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NHMITCLIAGLNKAAHKAVNFEKL KEISQRADENPAEFLSRFTEALQKY TRVDPTSREETIVLNNHFISQSAPNI QHKLKKAEDGPQTPQQDLLNLTFK VFNNREEQIKLDKAQRDCAKYQLL AVAIHQPSHSTQGHKKPNGSNPPGP CFKCSKEVTYLGVLSPGAQAMTP AQATLINSPLPSSKNEILSFLRLEGF FRIWIPNFALLAQPLYEAAKGPLNE PLSPIHNILPSFCKLQTALITAPALSL PDLSQPFVLYTTKNQGIALGVLGQQ KGNPPSFDPVAYLCKQLDNTVKGQ PTCLKASSAVAVLPLESKKLTFGQS TTIHSPHNLQDLLSSWALSSLSPSQI QSLYALFIKNPEFSLAKSAPLNLASL LPISSPPTHSCDILDHLQPQFPNISS KPLTNPDDQLFIDDSSSRAPGSPKIV GYAVVTLNHVIEAKPLPPETSSQKA ELVALTRALTLSKDKQHWLISEPVQ RPPSSVHST |
| 4815 | 10312 | A | 5119 | 2 | 697 | HGRLLLLLLLLLPCCEKTTEGEAM KEITAGLPVKVVVDVLRQASKACV VKREFKKAELIKHAVYLARDHFG SKHPKYSDTLDDYGFYLLNVDNICQ SVAIYQAALDIRQSVFGGKNIHVAT AHEDLAYSSYVHQYSSGKFDNALF HAERAIGIITHILPEDHLLLAASSKRV KALILEEIAIDCHNKETEQRLLQEAH VDVHLSLHLASKSYGDLAVVVLVH MSLLKSY |
| 4816 | 10313 | A | 5120 | 3 | 277 | EEEEAPPPGRERARGKGGDRPRGG NPEHQCGGTPRAEGSSTA/A/PPTCT SSSRTPASTVGPEPCGAGSAATAPG PELSGQNQMGRGPPVEDTE |
| 4817 | 10314 | A | 5121 | 1 | 337 | GTSSCVREVQAMGKKKVLVKVH LKDKFVIDVDKNISISDVTSSLVVL RNDSTLHKILPNKVHSLVSLMMV NTVPY/STNETIVSLDGPMVTILFSD KLSFTAPQLYIFTG |
| 4818 | 10315 | A | 5122 | 2 | 302 | ARGLPFFTRNDFS VWTIA/RNKC VG LELSKITMPIAFIQPLIFLHRITEYME HVYLIHRAFCQPQPLERMQVGLKG ARQEFVMKVMPLACLATQSWGPR HL |
| 4819 | 10316 | A | 5123 | 3 | 346 | HENWKKLLPCSSKAGLSVLLKADR LFHTSYHSQAVHIRPVCRNARCT SIS WELRQTL SVVFDAFITGQGKKDWS LF/RMFSRTLTEPCPLASESRVYVDI TTYNQDNETLEVHPPP |
| 4820 | 10317 | A | 5124 | 213 | 425 | QNSQGKLFSSGCLPFCGSNTKGILK YIQNH/KKPQIAKATLSKKNKAGSIT LPDFKIYYKALKPKITWYWH |
| 4821 | 10318 | A | 5125 | 1 | 356 | GTSTRIIFYRDGVSEGQRQQGLHHE MLAIREACIKLQKDYQPGITFIVVH NIHHTRLLCSDKNHPLGKRGNSPTG SNCGTKITHPTFEFDYLR RHAGIQG TSRPSYYHVLWD\DNRRFFS |
| 4822 | 10319 | A | 5126 | 1 | 238 | HMHSHHMHSHTPHA/HHTHHMHS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HHMHSHTTHMHSHHMHSHPHAL TPHACTHTTHMHSHHMHSHHMHA LTPHACTHTPH |
| 4823 | 10320 | A | 5127 | 180 | 405 | IWGEQDTFHSMKWIHLNVNHKT VKLLDDNIG/IKRGDLG/VDNEFLGT TPKAQSMEETIDKLDFIKMKNFCSV KDG |
| 4824 | 10321 | A | 5128 | 61 | 85 | PS*NYPP*KGITFGPLNKK |
| 4825 | 10322 | A | 5129 | 3 | 2004 | RRRRRPASPPAGLALAPRSPSASPEP REGETLSPSMQREEGFNTKMADGP DEYDTEAGCVPLLHPPEIKPQSHYN HGYGEPLGRKTHIDDYSTWDIVKA TQYGIYERCRELVEAGYDVRQPDK ENVTLHWAANNRIDL VKYYISKG AIVDQLGGDLNSTPLHWATRQGH SMVVQLMKYGADPSLIDGEGCSCI HLAAQFGHTSIVAYLIAKGQDMD MDQNGMTPLMWAA YRTHSVDPTR LLLTFNVSVNLGDKYHKNTALHWA VLGNTTVISLLEAGANVDAQNI KGESAPDLAKQRKIVWIINHLQEAR PAKGYDNPSLPRKLKADKEFRQKV MLGTPFLVIWLVGFIADLNIDSWLI KGLMYGGVWATVQFLSKSFFDHS MHSALPLGIYLATKFWMYVTWFF WFWNDLNFLFIHLPFLANSVALFYN FGKSWKSDPGIHKATEEQKKKTIVE LAETGSLDLSIFCSTCLIRKPVRSKH CGVCNRCIAKFDHHCPWVGNCVG AGNHRYFMGYLFFLLFMICWMIYG CISYWGLHCETTYTKDGFWTYITQI ATCSPWMFWMFLNSVFHFMWVAV LLMCQMYQISCLGITTNERMNARR YKHFKVTTTSIESPFNHGCVRNIDF FEFRCCGLFRPVVDWTRQYTIEYD QISGSGYQLV |
| 4826 | 10323 | A | 5130 | 3 | 144 | HEKYHKNTALHWAVLAGNTTVIS LLEAGANVDAQNIKAILRCHMAL |
| 4827 | 10324 | A | 5131 | 148 | 325 | RQGKECKIHCKKKLSPGIRSYPVEN/ F/VDTMYDYLPAYYKLNDLTNAD PCAVRYLLFDQN |
| 4828 | 10325 | A | 5132 | 175 | 405 | NILNSQFSTFLNDYVEFFVVKIFNFI IIIF*DRVSICCPGWSIMVQSWLTAA LTFGR*SSNLSLPSSWDYRRVP |
| 4829 | 10326 | A | 5133 | 14 | 26 | YSPHEVGWKGRNREKMFCSEINV FPDSVCQEMGFHHVAPAGLELMSS SDSPASASQSAGITSVSHHSCLYTSK GVE*FTGIIFSS |
| 4830 | 10327 | A | 5134 | 177 | 454 | PLLERAKIGPRPEKPMETRQGWGPF SPKVPGQKKFWG*LAPIPSGMHPN PILGPMV*EGGP*PPGILGPP*PYGKP LF*RKRGSNGGPYLQ |
| 4831 | 10328 | A | 5135 | 3 | 92 | NAWRTATEEWWTEDWNEDCSEP* HFTYVI |
| 4832 | 10329 | A | 5136 | 1 | 442 | PLIMNSIKSFSDDHAQCGR\EFDRQED DIHLVTLCVTELNDREENENHFPVI YGLAVNIKTAEIYRASFQDRGPPEQL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RAARTLAGGPMISYDAETEQLRNG PYSWTPFPHVDFWLHQDDKQIFEN LSTSPLAEPHFVEHIRSYLD |
| 4833 | 10330 | A | 5137 | 177 | 566 | EPFWSLSYLSLRRGGRNVRLCRLSA LVFCQFKAMLLTLTAGNNKTAIEY RASFQDRGPPEQLRAARTLAGGPMI SIYDAKTEQLRIGPYSWTPFPHVDF WLHQNDKQILKGRVYRLGKS*ISAP WPHL |
| 4834 | 10331 | A | 5138 | 1 | 981 | PLLVEGR*VRLPQSAGDLVRAHPPL EERARLLRGQSVQQVGPQGLLYVQ QRELA VTSPKDGSIILGSDDATTCH IVVLRHTGNGATCLTHCDGTDTKA EVPLIMNSIKSFSDDHAQCGRLEVHL VGGFSD\DRQLSQKST\HHFLIEFDR QEDDIHLVTLCVTELNDREENENH FPVIYGI\AVILLSLTAVNIKTAIEYR\ ASFQSRSGVREEQA/LRAARKL*AGG PMISYDAETETTS**DPYFLGHPFP HVGF\WLHQD\DKQILDESFFRPL AEPHF\VEHIRSTLMVF*KNTPSA \NTLFPGNKALLYKKNEDGLWEKIS SPGS |
| 4835 | 10332 | A | 5139 | 1 | 405 | AYVTVCNQCGRSKLLSKFYEL NIQGHKQLTDCISEFLKEEK*GDN RYFCENCQSKQNA TRKIRLLSLPCT LNLQLMRFVFDRTGHTKKLNTYI GFSEILDMEPYVEHKVW*PTSLNSM LSLKLGGMCMLT |
| 4836 | 10333 | A | 5142 | 2 | 204 | ETGFCHVVQAGLKLGGSSDLPASAP QSAGITGMCHCAQPTKVS VASKVF KGSHKD*ILT*GYANKGA |
| 4837 | 10334 | A | 5143 | 1 | 360 | QQLTVLVAHLGVTLMQDQRGYHWL LKSLMTQYQGLLYENP*ITLIVNTL NPGTLLPNESVPGSALHCRVDVHE MLSIQRDLTDHTLRDSIEYFIDRS FILGGDPLSGVCSSDFGLST |
| 4838 | 10335 | A | 5144 | 36 | 380 | FVALMGHKMSHNKFKIEIIRSMFSN HNRSQ*SK*IKEIYKCGN*HTSK**M H*GKKSLAKLENNEMNENESTT*Q NLWDAAKTALNEQFML*MPILKKG *MSQINKPTFHLKTIK |
| 4839 | 10336 | A | 5145 | 1 | 362 | ELNLPAPELPRKRTENLFLQLAEYV AHSLNVT*YVCEGTTMGD*WPWE TQELEPTDPVPDIIPVQKAQTSNFW VLKTSINGQYCIPRKGKDFITPVGRL N*LGQKLYKSITGTQGQSPG |
| 4840 | 10337 | A | 5146 | 2 | 428 | MFLLVVINLHILFVF*FKLFSWS*AF L*FLF*FMSESENIYYAEIGHITIVT LKSLIATYCINPSSHCKVYLVLSY LYCIIVNFDIYFLLCVPFCYFSLIISL SPLFLLIYMIFLYIHFILLFVIFYTFIP FSFY |
| 4841 | 10338 | A | 5147 | 3 | 361 | TLFQL*DLRKQRLEDLSTLIPRIYPG WKCRTHFLLMKKSQIVAGWYRRY AQHKRNQPTKSTVLVLQSYIRGRK ARKILRELKHQKRCTEAVTTIAAY |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | WHGTHALTETERLKEEARRKH |
| 4842 | 10339 | A | 5148 | 1 | 424 | VHLTADDDKVIAGLWSIVNAQDAV GETLGRLLQGVYPWIQRFFGSFGNLS SASAI VNP KVT AHGKNVLTSLVD AITHLV DLMGTFAQLRELH*DKLYE DPENLHTLGHVLT VLV LVIHFGT*FT AEVQASWLMMDTERANAL |
| 4843 | 10340 | A | 5149 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGGKVLTS LGDAI KHLDDLKGTF AQLSELHCDKLHVD PENFKLLGNVLT VLV LAIHFGKEFTP EVQASWQKMVTG VASALSSRYH |
| 4844 | 10341 | A | 5150 | 38 | 501 | APSPDAMGHFTEEDKATNTSLWGK VNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAH GKKVLTSLGDAIKHLD\DLKGTFA QA*SELH\CDKLHVDPENFKAPGG NVAGDPFLAIPFSAKEFHPLKVARL SWAERWVTW |
| 4845 | 10342 | A | 5151 | 2 | 198 | KVRPPPLKKTFFDSVDYRVLSEVD ERFAELPEFRPEDDLSSFS*PFLSPP CMSTALAHGDFSL |
| 4846 | 10343 | A | 5152 | 1 | 119 | DIMTGPHDEVA AKNIQLTNEIQTLE TE*HEATKEFQVLS |
| 4847 | 10344 | A | 5153 | 3 | 83 | RMVLRMLPLSTDEALCFHAMFQPF LDMIHEAQQAMDIHFHSPDFQHPPT EFIREGDDDR TVLREMHHI*TG*LR VKWRCEEWR*I |
| 4848 | 10345 | A | 5154 | 2 | 370 | GAARLDERTKEGSDDDEDSG*GARA ELEGNKEGESEGQYKAKGERSAWS KLRTEIRQKAESIDGIKVDDPS*IS MKATYTTMKIS*RQIRKIRQREKKN TAKGEGQERQNKNL SHKRHDISC |
| 4849 | 10346 | A | 5155 | 106 | 344 | RPCQQMQINVIHPINRMDKKHVIPI DTSDKI*HPFMIQTLNTLCI**MYLSI IKAIYDPYTADILTG*TFNAFFSTI |
| 4850 | 10347 | A | 5156 | 198 | 474 | |
| 4851 | 10348 | A | 5157 | 1 | 131 | PQEV PQSFGPPGDKAGC*GAGKMS PRERGGFLKCAEGGHPAPA |
| 4852 | 10349 | A | 5158 | 104 | 440 | FSKIYHFLLC CCFVLSKNCPILLHFL KIYLLALGNINISYFYSYHSKTLATG LKLTD DSQHISHGTSGSRFKCLLS KAVLMSSLP AVYS*LLKLLDVREVS NMVHDTLGIL |
| 4853 | 10350 | A | 5159 | 2 | 393 | EVWPRGLMGYVTVTEPSAVLVVRG VRDRLVITYPHEHHALTSSRLYLLM LFVGDPSGSGSNGSPDS*GLLLFRN DQA HIDL FVCFSVILSCFFLFLSLCEL LWNAKQAMDQRQEQRRLQEMTK MARRPF |
| 4854 | 10351 | A | 5160 | 2 | 154 | FRDGVSLHCSGWS*TPGLK*SSCLS LPKCWDYRHEPPLL FPLWRAIGNIY |
| 4855 | 10352 | A | 5161 | 142 | 399 | HLLTYSEMFLGGVRYFLQSTLPADL SKHAYLYAP*LRLFA*RYTSAFTEW THSANKTVCLMPKLYELTYVGIDTL ATPVIKRYCYCS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4856 | 10353 | A | 5162 | 3 | 410 | HEG*PTFSSILHPPHGAWAQLQ*PSQ ATTALFTLISVA*QQAGCSPQPGAG NTPPPPPNSGTLTPSPACAHWAQC* ANKDEFSVPGPQCLWPR*GPSYAS LPQALRARPSQMTRVPQAPPPTGPG PVVSPCANTN |
| 4857 | 10354 | A | 5163 | 168 | 435 | IIAQ*N*FLKNNFQ*TI*K*NKTILFTT RSK**I*QKQQKNLYLEKYKTLLKEI KDLNKWKNISCSWIGTLSIDKLVT SKLNYRVNVI |
| 4858 | 10355 | A | 5164 | 2 | 427 | QIFRYLIMEKEQEHTYRGFKTVNR WTDAYDYAQHYSEASVASKDVS W*FHDYLGMSRHPDVLQA*QETLQ RHGAGSGGSRNLSGTRNCHVELEH ELADLHLKDSSLIFSFCFIANDCTLF TLAKILPGREIHS DACQHAFM |
| 4859 | 10356 | A | 5165 | 11 | 1232 | MAGAATGSRTPGRSELVEGCGWRC PEHGDRVAELFCRRRCRCVCALCP VLGAHRGHPVGLALEAAVHVQKLS QECLKQLAIKKQQHIDNITQIEDATE KLKANAESSKTWLKGKFTLRLL DEEEALAKKFIDKNTQLTLQVYREQ ADSCREQLDIMNDLSNRVWSISQEP DPVQRLQAYTATEQEMQQQMSLG ELCHPVPLSFEPVKSFFKGLVEAVES TLQTPDIRLKESINCQLSDPSSTKP GTLLKTSPSPERSLLLKYARTPTLDP DTMHARLR\MSADRLTVRCGLLGS\ LGPVPVLRFDALWQVLARDCFATG RHY\WEVDVQEAGAGWWVGAAY ASLRRRGASAAARLGCNRQSWCLK RYDLEYWAFHDGQRSACGPATTST GSASSWTTTRPASSPSTT |
| 4860 | 10357 | A | 5166 | 115 | 447 | MSSWARLCESPVVWYF*HVL FVCL HKLRLISQQFLTGINCQLSDPSSTK PGTLLKTSPSPERSLLLKCKTPGSGD RVETVEMVGCWVEEDHGNGGPSFF LIRIYLF IYLF |
| 4861 | 10358 | A | 5167 | 1 | 423 | ADMKAHLLHSGGMGFSCECSTGF VKHS*LIEHIRTHTGEKPFQCPKCDK SFRLKAQLLSHHGLLTGDRPFHCPE CDKNLRERGHMLRHQRIHRPERPF ACGYCGKGFYKSKLAHIRVHTKS CPAANELDIKKMLHPLV |
| 4862 | 10359 | A | 5168 | 481 | 908 | EGSQWEAQKALAIQPVPCGAVRVP WTTSSIPASIPKQSVGKGCDCRL*L GDFAPARGEACECHTEPFRNSRGV GGAWARPGYL VLSLLSLQCPDSAC NQDLLAYLQRIALYCHQLNICKSVK AEVQNLGGELVVS GVSIS |
| 4863 | 10360 | A | 5169 | 2 | 2799 | EMTAVHAGNINFKWDPKSLEIRTLA VERLLEPLVTQVTTLVNTNSKGPSN KKRGRSKKAHVLAASVEQATENFL EKGDKIAKESQFLKEELVVAVEDV RKQGDLMKAAAGEFADDPCCSSVKR GNMVRAAPALLSAVTRLLILADMA DVYKLLVQLKVVEDGILKLRNAGN EQDLGNQYKALKPEVDKLNIMAAK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RQQELKDVGHRDQMAAARGILQSN VPILYTASQACLOHPDVAAYKANR DLIYKQLQQA VTGISNAAQATASD DASQHQQGGGGGELAYALNNFDKQI IVDPLSFSEERFRPSLEERLESIIISGA ALMADSSCTRDDRERIVAECNAV RQACRTC VSEYMGNAGRKERSDAL NSAIDKMTKKTRDLRRQLRKA VMD HVSDSFLETNVPLLVLIEAAKNGNE KEVKEYAQVFREHANKLIEVANLA CSISNNEEGVKLVRMSASQLEAGCP QVINAATWALAPKPQSKLAQENMD LFKEQWEKQVRVLTDAVDDITSIDD FLAVSENHILEDVNKCVIALQEKDV DGLDRTAGAIRGRAARVIHVVTSE MDNYEPGVYTEKVLEATKLLSNTV MPRFTEQVEAAVEALSSDPAQPM ENEFIDASRLVYDGIRDIRKAVLMIR TPEELDDSDFETEDFDVRSETSVQT EDDQLIAGQSARAIMAQLPQEQKA KIREQVASFQEEKSKLDAEVSKWD DSGNDIIVLAKQVMCMIMMEMTDFT RGKGPLKNTSDVISAACKIAEAGSR MDKLGR TIADHCPDSACKQGLVA YLQGIALYCHQLNICKSVKAEVQNL GGELVVS GNC DTCGALQGLKGWPP PLCLATHWVDSAMSLIQA AKNL MN AVVQTVKASYVASTKYQKSQGM SLNLP AVSMKMKAP EKKPLVKREK QDETQTKIKRASQKKHVN PVQALS EFKAMDSI |
| 4864 | 10361 | A | 5170 | 25 | 458 | |
| 4865 | 10362 | A | 5171 | 3 | 764 | GPLCIALALQEFGTRRRWACRSLSS SGRRSLFRRMGSVKAVKNKAYFKR YQVKFRRRIRKGKTDYYAR*RLVIQ DKNKYNTPRYRMIVRV TNRDIICQI AYARIEGDMIVCATYAH*LPKYGV KVGLTNYAAAYCTGLLLARRLLNR FGMDKIYEGQVEVTGDEYNVESID GQPGAFTCYLDAGLARTTTGNKVF GALKGAVDGGLSIPRSTKRFPGYDS ESKEFNAEVHRKHIMGQNVADYM RYLMQEDEDAS |
| 4866 | 10363 | A | 5172 | 8 | 400 | PLASFD TGDVECALCMRLFYEPDTT PCGHTLCLRCL*RCLYHNAKCPLCK DGLSQ**ASIKYSYNVIVEELIAKFL PEELKEREKLYE*EMEELYNLNNNV PILMCTMAYANVTCPLHMFEP CYR LMIRIW |
| 4867 | 10364 | A | 5173 | 2 | 400 | SLPLASFNTCNVECALCMRLFYEPV TTPCGHTFCLKCLERCLDHNAKCPL CKDGLSQCLASRKYIKNVIMEELIA KFLPE*LNERMKLYEYEMEELS NLN NNVPIFVCTMAYPTDPCPLHIFEP CY RLMIRIC |
| 4868 | 10365 | A | 5174 | 1 | 216 | AGRTGRPEERAPESKSGSGSESEPSS RGGSLRRGGEACGTSDGGSPF*GS SVVSFTLLSYLGYYSYLLSTV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4869 | 10366 | A | 5175 | 301 | 446 | SYFSYIILIIRGNESEGGFFEN*YFCL LINGGSWSGEPPIRRNSHTFNC |
| 4870 | 10367 | A | 5176 | 155 | 404 | AAVPSRILKQYSHPNIVRLIGVCTQK QPIYIVMELVQGERGALSSR*GAQP GQVAALPQEAQQGSSPPAGGDFLTF LRTEGAR |
| 4871 | 10368 | A | 5177 | 172 | 443 | TGMIRGPWTKVGPAGIEKPPVGDGK VPNGCPKSLGNRQPCF*VLEVNEPY VPKKFKAEPFPFHANICPLSEKERQF RKQ TALVDL*KPKPR |
| 4872 | 10369 | A | 5178 | 3 | 428 | PDQTLCCCAEMGSHCVAQAGLEL LGLSDLPILASQSAITGVGHACPV VLGS*RPSQMLCPFPWWLLSATFY LAVPHLLPCLLFQPHSLRCSRSSSSA NLPVVFSPGAGCLSLLSCMECSSFP AKVLVIPFSPERPPCS |
| 4873 | 10370 | A | 5179 | 2 | 432 | NIVSQNNDLPQTVIWMGDCIISLETR IQMQCDWNTSDFCVTPHS*NETEH HWEIKCHLVGREENLTLDIVKVKE QVFEASQAHLTLLPGTDIFSEAANG LSAINSLKWIKTTGNSTLVN FVLIHC LFLAAAFSPEAASASVD |
| 4874 | 10371 | A | 5180 | 163 | 585 | VEVRAHPKKRQRKKKEKKKSDRYS SSSSSSSDSSSSSSDSEDEDKKKENR RKKKKNRSHKSSSESSMSETESDSKD SLKKKKKSKDGTEKEKDIKGLSKK RKMYSEDKPLSSESLSESEYIEEVQA KKKKSSSEEREKATEK |
| 4875 | 10372 | A | 5181 | 18 | 566 | AEQSGEAAARGPVAGPLRPSLWPGFP RRATVCSVQHHGEAGQSGWPYMN PNSNGEIKGSQSQSSGPTIQDYLNRP RPTWEEVKEQLEKKKKGSKALAEF EEKNE*ELEERTGKTQGEIVKWK*E LIQKKDRERKKKRRNLVGSSSDSED EDKKQGKRRKKKKNRSHKSSSESSM SETESDSKDSL |
| 4876 | 10373 | A | 5182 | 27 | 382 | SVILSFFFFFFYIAWATVRLCLKQTN ENNDKRDLTSLKVVRK*TLNLHPSI KAMIIRLYFEQLYDNRLANLDEMDI FLATQKLPKLAQEEVKNFRCVTM DYVNNQNL*TNKGPEPDD |
| 4877 | 10374 | A | 5183 | 2 | 342 | GRSCDPKSVGQTLCVALLSVPLPGD PGQRKLPSQNSEEEL*SQKCGPNPM CCSFPVPLAGGPGHSRRSTQSRTR*L KPQLPGWRTEKGAPEEIGKMMLQV IDERPGSALSCRC |
| 4878 | 10375 | A | 5184 | 2 | 147 | AETGFHHASQDGLDLLTS*STRGLGL PKCWDYRREPQRPADTWFLKSTT |
| 4879 | 10376 | A | 5185 | 8780 | 9035 | LALQVHTMTPSKFFIFLVETGFHH VSQDGLDLLTF*STRGLPKCWDYR SEPPRPAYFYIFLRRSLSPRAGVA VSRDHATAL |
| 4880 | 10377 | A | 5186 | 75 | 355 | SNKNPSISCPRTWGECVCQATSRST WFLYPMPSYAPIKPTPGDVPGTAPS GRPDSTPS**HRLQGTLPKPAPLLG VFPKPLLAPLFPEGPGP |
| 4881 | 10378 | A | 5187 | 262 | 354 | VWSPPLTWCLVCQCRY*PGLLM |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MCFILPT |
| 4882 | 10379 | A | 5188 | 1 | 104 | ESETLPGGVAHACNPITLGG*GGRIT RSGV*DQP |
| 4883 | 10380 | A | 5189 | 1 | 144 | RDKVFALSHRLECSGAIHAHYNLQL LG*NNHRVSDSPVAGMAGVCHHT |
| 4884 | 10381 | A | 5190 | 99 | 241 | CFPGA WVR LQLTQASDGPWQCSSS QRLHHAPHVVTLYLCCAFSPCSPVK LRDFESA VNNFEKALERAKLVHNN EAQQAII SALDDANKGIIRLKTNY VENLKEKSEGEASLYEDRIITREKD MRRVRDEPEKVVKQWDHSEDEKE TDEDDEAFGEALQSPASGKQSVEA GKARSDLGAVAKGLSGELGTRSGE TGRKLEAGRRESREIYRRPSGELE QRLSGEFSRQEPEELKKLSEVGRRE PEELGKTQFGEIGETKKTGNEMEKE YE*SHR*R*GSSVLVLDGDIAQEHG GKDGAELSDASLGP GSDYSSHL LMGP GSARVARGSIMHHTLSHSTC VVP SPLALQ |
| 4885 | 10382 | A | 5191 | 303 | 427 | IVLFEKKIFFFFETGSCSVPKAGVQ WCGHSSLQP*PTGLM |
| 4886 | 10383 | A | 5192 | 82 | 352 | RVPERVLPRPIPPASCPVSPASRPL* GTPRAAPETRRRPRTARDPRGLRW QTQPAAPLLASPGPGVAPVASGAPI SRNDFQLCKARMLL |
| 4887 | 10384 | A | 5193 | 1 | 248 | QKLKKLARHGGACACGHKLLGWL RW*DHMSLRGQGCSSES*SCRCTPA WTTE*DPVYQHKILSL*DFLI*KASS NRSSVIYEL |
| 4888 | 10385 | A | 5194 | 3 | 370 | AQWRVDS DGAPKRIADSATSPKLL YVDRVVQEILETERTYVQDLKSIV* DYLD CIRDQTKLPLGTEERSALFGNI QDIYHFNSELLQDLENCENDPVAIA ECFVSKSEEFHIYTQYCTNYPR |
| 4889 | 10386 | A | 5195 | 28 | 183 | YDRKRPVGKEKIGKLD CMKT*NFC ASKNTIKEMKRQRTVWEKIFAHYIS ERK |
| 4890 | 10387 | A | 5196 | 1 | 681 | MHPIGIALSKVPVESKEG DIMSHTG GSVPYLDNLNKASVCRGQSCR VFQ VKEMVTQVESEN NQEEQKQVRLPE SRLTPWEVWFIGKEKEERDRLQLK ALEFKEDWKLLKRRVTKKSGSVSV SISSQGNLTVCDCCESFLLTKPVSC KHLIKSHSCPALAVAS/CQRPEGYW SDCGTRSHSDYADEEDSFVSDSSDQ VSSRRTVTHSYAPPQSOPHHRHTQT GTTATYL |
| 4891 | 10388 | A | 5197 | 1 | 2862 | MPGPLGLLCFLALGLLGSAGPSGAA PPLCAAPCSCDGD RRVD CSGKGLT AVPEGLSAFTQALDISMNNITQLPE DAFKNFPFLEELQLAGNDLSFIHPK ALSGLKELKVLTLQNNQLKTVPSEA IRGLSALQSLRLDANHITSVPEDSFE GLVQLRHLWLD DNSLTEVPVHPLS NLPTLQALTLALNKISSIPDFAFTNL SSLVVLHLHNNKIRSLSQHCFDGLD |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NLETLDLNYNNLGEFPQAIKALPSL KELGFHSNSISVIPDGAFDGNPLLRT IHL YDNPLSFVGNSAFHNLSDLHSL VIRGASMVQQFPNLTGTVHLESLTL TGTKISSIPNNLCQEQKMLRTL DLS YNNIRDLP SFNGCHALEEISLQRNQI YQIKEGTFQGLISLRILDVSRNLIHEI HSRAFATLGPITNLDVSFNELTSFPT EGLNGLNQLKL VGNFKLKEALAAK DFVNLRSLSVPYAYQCCAFWGCDS YANLNTENNSLQDHSVAQEKG TAD AANVTSTLENEEHSQIIHCTPSTGA FKPCEYLLGSWMIRLTVWFIFLVAL FFNLLVILTTFASCTSLPSSKLFGLIS VSNLFMGIYTGILTFLDVSWGRFA EFGIWWETGSGCKVAGFLAVFSSES AIFLLMLATVERSLSAKDIMKNGKS NHLKQFRVAALLAFLGATVAGCFP LFHRGEYSASPLCLPFPTGETPSLGF TVTLVLLNSLAFLLM AVIYTKLYC NLEKEDLSENSQSSMIKHVAWLIFT NCIFFCPVAFFSFAPLITAISISPEIMK SVTLIFFPLPACLN PVLYVFFNPKFK EDWKLKRRVTKKSGSVSVSISSQG GCLEQDFYYDCGMYSHLQGNLTVC DCCES\FLLTKPV SCKHLIKSHSCPA LAVASCQRPEGYWSDCGTQSAHSD YADEEDSFVSDSSDQVQACGRAC FYQSRGFPLVRYAYNLPRVKD |
| 4892 | 10389 | A | 5198 | 2 | 413 | VDFFFLRRSLATVAQAGVQWRDL GSLQAPPPGFTPFSCLSLPSSWDYRR PPRPANFFVFFF**RWGFTVLAR MISIS*PRDPPTSASQSAGITGVSDRT RLDFKKKKKYCGKKDIMYRKVYTS LIQLTKKSLIH |
| 4893 | 10390 | A | 5199 | 1 | 142 | RKMFGNGRARS GVIVLPCGKGYQS **GGQAVGSGSASCLPLSLCTFP |
| 4894 | 10391 | A | 5200 | 1 | 375 | GEATMNP SHEAEVVCDVPTWWPP VSTR*MGGRE*RKERA EKGRGKGG MEKEGAGERRGKEKNGDSRERGRE GKSVTDNST*GAAAGLPQSPCPIQA RGVQSPRPQAMSRGEPEYSGIGGW GSGEA |
| 4895 | 10392 | A | 5201 | 109 | 331 | PLYCSPGASYMTLTALGPTQTQVPE QRLFVTCILCQEEQEVKVESRAMVL AAFVQRSSVLSKNRCKFI*DPGKS |
| 4896 | 10393 | A | 5203 | 2 | 168 | FFLDSTLKA*AIKAKINKWNDVKLK SFFKTKETINKM*QPMVWENIFANH LSDKG |
| 4897 | 10394 | A | 5204 | 107 | 357 | DLRWYSSFLWMCCIPGAKWHPING SSCVMMGMIKYDFTGHWIVKHIGL AADLDSFYEYLLKSYILFGE*DDL* MFNAAYQSIQ |
| 4898 | 10395 | A | 5205 | 3 | 376 | CQSQVPTDHGGQPPGSHPGWKPGP DLPPRFPDPEPSRPGN*GLLGPALCP SDLYAFGPQGISVNQGLPQWRPGW GHPWRLPEPDS*APAIPQPLAEPVL WGWGGQRPRVPQQLPTAERCCSDF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | S |
| 4899 | 10396 | A | 5206 | 1 | 262 | QNIFLHLFFCSFTAQKYPMVHLLQK SDNSFNQELLKSMVKSIMNDVYG PMSQILETLNKCPhFKRQR*VLLLD EYIVLLGRFILFA |
| 4900 | 10397 | A | 5207 | 2 | 296 | NGTHASYGAFYLEYSLAEFTLVV KHKLPGVYVQPSYRSALMWVGVL SMWEGG*RQGLVRSTVGLGGAVLS SEDRSWGVSLLSRASAPRLPLAHL RC |
| 4901 | 10398 | A | 5208 | 30 | 280 | FYYAFKEEIPVLYSLFQKIETGGILL NSALLLIPKST*YRRPYKKGKLNRYR PKSFVNINVKILNRILANQIQKCIKRI TYYS |
| 4902 | 10399 | A | 5209 | 1 | 277 | NFSSLLIHGRMHTGEKPYECKNCGK AFTSAKSLQNHGRTHTG*KPCECKQ CGKAFICSSSCQRHEETHSVNMHSV ILIPLKHRKRVGKGPLR |
| 4903 | 10400 | A | 5210 | 220 | 585 | EILVRSLRQDPLRSRRGKRHTGRRW DGSGWRATGARE*RRESRGWEME AREAGRRKPASERRKGSGRRAGDF LEPATRSRSEKEVRTLARNGRP*AS PGSHRSSQ*LQPRVACGGRAATKSS |
| 4904 | 10401 | A | 5211 | 1 | 291 | SFLETLLPRLGCSDAIMAHCSLELLG YMRSCHLSLPS*DYRPTPSRLANSFF LIHGGFFTLWADLQLLGLKQSFRRK SWGLTGVSHHAQPFFPYLY |
| 4905 | 10402 | A | 5212 | 228 | 379 | |
| 4906 | 10403 | A | 5213 | 317 | 534 | ATKEN*INWDLIK*NKQKPFASKDT TKQAKRQHIEWEKKVNNPIYDKAP VSRIKNLLKLNNKNTNNLIVKKK |
| 4907 | 10404 | A | 5214 | 3 | 366 | IGY/NPDTVACV/PILGWNGDNMLE QSANMPWFKGWKVTRKDGNASGT TLLEALDCILPPTPTDKPLRLPLQD VYKIGGIGTVPVGRVETGVLKPGM VVTFAPVNVTTEVKSVEMHHEAQK AK |
| 4908 | 10405 | A | 5215 | 1 | 1254 | |
| 4909 | 10406 | A | 5216 | 33 | 1472 | KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYAWVLDKLKAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVLIVAA GFVEFEAG\SKNGQTREHALLAYT LGVKQLIVGVNKMDSPEPPYS\QKR YEEIVKEGSTYIKKIGYY\PDTLAFEP ISGWNGDDMLEPSANMPWFKGWK VTRKDGNASG\TTLEALDCILPPTR PTDKALRLPLQDVYKIGGIGTVP\VG RVETGVLKPG\MGVTF\APVNVYN GK*KSVEMHHE/AL*SEALSWGNTN GLQLSRNVSVKDVRRGNFAGDSK\ NDPPMEA\AGFTAQVILNHP\AQKN ARHMPLELDCHTAHIACKFAELKE KIDRRSGKKLEDGPKFLKSGDAAIV DIVSG\KPMCVESFSDYPPLGRFAVR DMRQTVAVGVKAVDKKAAGAGK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VTKSAQKAQKAK |
| 4910 | 10407 | A | 5217 | 178 | 566 | KGGATCPESPQDRKRRGNLDMCKL YSENEGMA SNHGKMENE*QPQDQR KPQVTLYSGRQEVRRKRGKDRKQGG NRR*GNV*RIKGKPESEGEAKEGKS EREGESEMEGGSEREGKPEIEGKPE SEGEPL |
| 4911 | 10408 | A | 5218 | 27 | 336 | TNPVQQTLVPIWTSTRLPDTHEDKA FSAPQIEDRGTPGLGSRGPALGPSPT PDCAG*VVAAGPGPAESHPRAPKPT AGMSPGVARLSSPGSGSQGSWQNG ERP |
| 4912 | 10409 | A | 5219 | 2 | 454 | HFNM RDPLTDCPYNKVYKNLKEFS QNGENFCKQVTSVLQQRANLEISY AKGLQKLASKLSKALQNTRKSCVS SAWAWASEGMKSTADLHQKLGKA IELEAIKPTYQVLNVQEKKRKSLDN EVEKTANLVISNWNQKAKKKLM VSTQET*STADLHQKLGKAIK PTYQVLNVQEKKRKSLDNEVEKTA NLVISNWNQKAKKKLMVSTQET |
| 4913 | 10410 | A | 5220 | 26 | 130 | TTWKYQYKNLERNQKEITELKSTIA EIENITRGI*R*FEQTKE*INELEDKI MEIFKDKR*KKGEKSLRGLWPPSRD KEACMPWKLQTEKKKGAERLSEE IMAESFSNLLADMNINS*ELKSTIAEI ENITRGI |
| 4914 | 10411 | A | 5221 | 48 | 394 | SPSMCGSLDPPTLPQTLQVPSMLT HPCPPPPHCPPLAHPSSLPSTHIY H**HLSPYPNPGTQEGHSGVRLRA TDVASPSVLGQFPSYSISVPREGHA ATVAAKGPLECRA |
| 4915 | 10412 | A | 5222 | 3 | 726 | EQEV DYPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCCL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCKKHPEA KRMPCAEDYLSVVLNQLCVLH/EK TPVSDRVTKCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCCL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLRKVGSKCKKHPEA KRMPCAEDYLSRGPEPVMCVA |
| 4916 | 10413 | A | 5223 | 4274 | 5256 | HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECF LQHKDDNP NLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIIDFVLV SNIILPKFNHLCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*LAESLEF GGSGENVVDYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV |
| 4917 | 10414 | A | 5224 | 1 | 332 | RMPCAEDYLSVVLTLQCLVLDKTP VSDIVAKCCSESLVNSQACLSDL*V KDAYVPKEFNTETFTFHADICALSE TERRIMKQTGLDEFVKHKP*ASDER LSAVMDDFAAF |
| 4918 | 10415 | A | 5225 | 7 | 564 | TTRAAGREALSPGQGAGGGEGGAE PRHTATGHAAGREGRGGRGADQG* GWPRGARALHDQAEGRGGLPAGLP VQAERPQREPCSGQVGSEPPCHPA TAGGRKVRPAWPAAAGEAGGHSG TGRAGAAGGAAVGTGGGAAGPGG LPMSGGAGPGGSGAAAPHAAS*VQ PAAGAASAATRNRPKTT |
| 4919 | 10416 | A | 5226 | 132 | 917 | PGLFYLGEEQPGPQPAGGPAAGQG ATAGAEAAAGCPGGAAAPAVLAG GRAGGRSAGWCAGAPGA*PGLFYL GEEQPGPQPAGGPAAGQGATAGAE EAAGCPGGAAAPAVLAGGRAGGRS AGWCAGAPGA*AQP*TTGAAGREA LSPGQGAGGGEGGAEPRHTATGHA AGREGRGGRGADQG*SLSQATDLW TSGPSHKWTDLSLWPYPCCSGCSW GQCL*LRAEGRGGLPAGLPVQAERP QREPCSGQVGSEPPCHPVSHTPKGP VPHCLGASPLLWLATAGGRKVRP AGPAAAGEAGGHSGTGRAGAAGG AAVGTGGCQQRWIR |
| 4920 | 10417 | A | 5227 | 3 | 1245 | AWEFVWHPGGFDRSCPGPQGGEGS EGGEGT*EGSGSLALRPRLSCPRA GPGPGPRLA*ASVYPWNQKRVGGL WRPQRTPARLCDPHAPEHAWAL*G KPGPAGHPAEAA*RQRE*AAGPRGT AAPAGQDRQHHAGPRGRPARGA AAAERQRAPEKGEEQPGPQPAGGP AAGQGAAAGAEAAAGCPGGAAAP AVLAGGRAGGRSAGWCAGAPGA* AQP*TTGAAGREALSPGQGAGGGE GGAEPHTATGHAAGREGRGGRG ADQG*SLSQTTDLWTSGPSHKWTD LSLWPYPCCSGCSWGQCL*LRAEG RGGLPAGLPVQAERPQREPCSGQV GSEPPCHPVSHTPKGPVPHCLGASP GLLWLATAGGRKVRPAGPAAAGE AGGHSGTGRAGAAGGAAVGTGGG AAGPGGLPM |
| 4921 | 10418 | A | 5228 | 612 | 795 | PGFISAIGGLVGLSSYDFYKEYED KPTSPPIAEMNPGYNI*HDLIKSFKM LAFICSISS |
| 4922 | 10419 | A | 5229 | 1 | 345 | SSWSFTLVLTQAGVQWHDLGSLQPL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PSEFKRFSCLSLPSSWDCRRLPPRPA NFLYF**RWGFTILTSLVLSY*PCVS PTSASQSAGITGVSDHARLIVGDFN TPLLITERSSSTQKI |
| 4923 | 10420 | A | 5230 | 1 | 1212 | MPKKRQALVEFEDVLGACNAVNY AADNQIYIAGHPAFVNYSTSQKISRP GDSDDSRSVNSVLLFTILNPIYSITP TRLNVFKNDQDTWDYTNPNLGQGD DPGSNPNKRQRQPPLLDHAPAEYG GPHGGYHSHYHDEGYGPPPPHYEG RRMGPPVGEYGPHADSPVIMVYGL DQSKMNCNDRVFNVFCLYGNVEKV KISLKKQSPGGRPMGEEWLDGYAV DRAITHLNNNFMFGQKLN/CVGA QAREGSRGTGERKGGEWGPAEEHS EAEVLTHTEMGCGSVSKQPAIMPG QSYGLEDGSCSYKDFSESRRNNRST PEQAAKNRIQHPSNVLHFFNAPLEV TEENFFEICDELGVKRPSSVKVFSKG SERSSSGLLEWESKSDALETGFLN HYQMKNPSINLVT |
| 4924 | 10421 | A | 5231 | 1 | 421 | FDPPGCFFTPIGNPFGPFQGNFHRK NGVQAMVEFDSVQSRQAAKASLN GADIYSGCCTLKIEYAKPTRLNVFK NDQDTWDYTNPNLGQGDPGSNPN KRQRGTVISQD*PSLLKNYCTCDF FSCSYICAAHVLCGTFQ |
| 4925 | 10422 | A | 5232 | 2 | 1883 | DEQRRRSGAMVKMAAAGGGGGG GRYYGGGSEGGRAPKRLKTDNAG DQHGGGGGGGGGAGAAGGGGGG ENYDDPHKTPASPVVHIRGLIDGVV EADLVEALQEFGPISYVVVMPKKR QALVEFEDVLGACNAVNYAADNQI YIAGHPAFVNYSTSQKISRIDE*ND YRISVNSVLLFTIVNTINWITDVL TMCNPGCPVQRIVIFRKNGVQAMV VFDSVQSAQRAKASLNGGDIYSGC CTLKIGYAKPTRLNVFKNDQDTWD YTNPNLGQGDPGSNPNKRQRQP LLGDHAPAEYGGPHGGYHSHYHDEG YGPPPPHYEGRRMGPPVGGHRQCP SRYGPQYGHPPPPPPPEYGPHADSP VLMVYGLDQSKMNGDRVFNVFCL YGNVEKVVKFMKSKPGAAMVEMA DGYAVDRAITHLNNNFMFGQKLN CVSKQPAIMPGQSYGLEDGSCSYK DFSESRRNNRSTPEQAAKNRIQHPS NVLHFFNAPLEVTEENFFEICDELG VKRPSSVKVFSKGSRSSSGLLEWE SKSDALETGFLNHYQMKNPNNGPY PYTLKLCFSPAQHAFLIRCLGRVPFE QENISLSFMPFFGFCFCYLQKILGSP FFFFFFFFLKVVEEGFPPP |
| 4926 | 10423 | A | 5233 | 2 | 337 | DMILAERGGVCVMMKTQCCTFIPN TSTTDGSITRALQGLTALSNELANN SGVNDPFTGWLEK*FSKWKGIASIL TSLAAVMGVLLVRCCVIPCLQRLM QRLIKMALTQTS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4927 | 10424 | A | 5234 | 62 | 343 | RQLNRNDPNRNKGKKVGIKQCLRF WNNFILTCLIGVSEIEEKKNGAE*IF EEIMSKNFPKLIKYNPQIQEA**TPS KINTEKTTFRH*IIGKR |
| 4928 | 10425 | A | 5235 | 1 | 359 | TDDDLNWLDHSRTFREQGVDETET CLLRKFSYSDQNVDSRDPVQLNLL YVQARDDILNGSHPVSEKACEFGG FQAQIQFGPHVEHKHKPGFLE*MTF CFSFFSFLSSFSFSFLFLS |
| 4929 | 10426 | A | 5236 | 2 | 264 | SYYPGEISVPFFNICHFFLSCFYNLS RFFCKKSPASPLCFSIKKSPFVKIHL VFSLVTSFLK*FFFYL*FFPESVISF GSFSNSD |
| 4930 | 10427 | A | 5237 | 3 | 246 | LIPRGQGSTVVL PYNPATSI FGNDLN EIKMYGHAKTCIWMFMTSSFIIDRT RKRQ*CSSVREWINKQ*CIQTMELV FGRN |
| 4931 | 10428 | A | 5238 | 78 | 411 | VLNSPICNCLYPILCSFLFLIYFVVC FYTFIPVFYLVYHQEVI*SLTLVFFV CVVKINTRLMVHIFILYICL*LSICNS VYLLHVHIYLEHFL*HILMVVFFKR SDQSS |
| 4932 | 10429 | A | 5239 | 2 | 175 | TKLDFIGIKGFSSVKDNVKGMRQA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN |
| 4933 | 10430 | A | 5240 | 1 | 335 | VTIRGAGIPDESRNVNYSLASFLKR WLTLMDRGFIFNLINDYISGFSPKDP KVLAEYKFEFLQTICNHEHYIPLNLP MAFAKPKLQRV*DSLEYSLSDEY CKHHFLGGLL |
| 4934 | 10431 | A | 5241 | 139 | 354 | SPCLPYCCLLCYRYGDGRIMIGFSC GH*VVISTHTGELGQEIQARNHKD NLTSIAVSQTHIKVATCENNLP |
| 4935 | 10432 | A | 5242 | 2 | 332 | ILAGAII*DNEIKLM*IEKEVVKLFLF TDDMILCVENSKEHTHSHTQLGLI NEFSRASG*KINVQKLFLYTNNVQS KNEIKEPSLCTKASKRIGYLGHLTK EV*DLYSERTKPH*KKNRILRNTFN KRSVRLVQ |
| 4936 | 10433 | A | 5243 | 137 | 290 | GSSDINQTKHVRS*VNRQICSRTTQ QSPEDCDFKKDGLVKRCMGTQTRQ SL |
| 4937 | 10434 | A | 5244 | 1 | 363 | LTCSGDKEQIKDKSHVLKGKGNFE RETS*KKK*SLPPFDDNVEPNLYV EENICSKSDSERPRSASSSSRSSSFT PSQTRQQGPLKSMMNDLHSDDYEE ESDEMEDNGPDFEMGKPVNIR |
| 4938 | 10435 | A | 5245 | 2 | 376 | VHLGWCMLPLRTHTEYVKALSYA* DKQLGA*AGLDRQIFLWDANTLSA LTASNNTVTSSLSGNTDSIYRLAM NQLVTIIVSGSNDKALRVWDPLTCA TLVNLKGHTDNGKALVFNRDGTQC LSR |
| 4939 | 10436 | A | 5246 | 60 | 185 | |
| 4940 | 10437 | A | 5247 | 1 | 146 | RWRDLGSPQPAGFR*FCCLSLSSW DYRHAPLF*QFYLFILLFCKKYF |
| 4941 | 10438 | A | 5248 | 2 | 298 | TFFTPFPVAKPNPRGPKTPAPYFSPQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GPQKIYPPKFLGPPFNFPPLL GKVF RAPNPRV*LPPGARPSSSSSLLPGF* KIPKPLFY*KKIFPTPQKTKK |
| 4942 | 10439 | A | 5249 | 77 | 370 | EYS*SVVFLDLMRRQEELRRMEELH NQE |
| 4943 | 10440 | A | 5250 | 83 | 467 | YSEKSAGLWLNMLEKSLPGHRDTA TQIQHVSPMCQVEPPAKKAATLAE GDKDNDI*PCFVQRQLREGRQGRA ARLWEKWLRWYVEKKAKKTALV VKSSIPLDIKPWDNETNIAQLEACM RFIQLDGLV |
| 4944 | 10441 | A | 5251 | 1 | 359 | KYTLSRLATVPPTLNPAEYNISPDTR RAQVEQLAIRAGLK*EYLLQYNNP NRRGLIEDPALIRWTYARSANVYPN FRPTPKNSLLGALCAFGPLFFWYCV FKTMDMRNQKLIREGKLDQ |
| 4945 | 10442 | A | 5252 | 3 | 349 | SSLATVPANLNPAEYSISPDNRRAQ VEQLAIRAGLK**YLLQYNNPTRIGI IKDPALIRWTYARSANVYPNFRPIPK NSLLGDLCAYGPLFFWYCVFKPDM DRKETLIPEGKLDQ |
| 4946 | 10443 | A | 5254 | 1 | 415 | NAVIQVAHPLVQKQ*VDYIHNGFL VPVMGPALHKTVEEMIASTAYLEL FLRSISEPALLRTLRLFLLLHRHDTH TILDTLVARIGSNSRLCMVSLSLFKT LLNLSCEDVLLQLGLRYLVPCNHV MLSQKPAVRDVL |
| 4947 | 10444 | A | 5255 | 34 | 394 | YRHYTICCIIGFLNTITMMTVSFHKY GEYFPGT*DLRDIDAGKC*YYAVNF PMRDGIDDES YGHIFKPIISKV MEM YQPIAVVLQCDAYS LYGDSLDCFNL TIIRHSTRLYLI*SYHFTS |
| 4948 | 10445 | A | 5256 | 178 | 417 | ILVPPAGGKGPNI*WNP GPPGARG FPGLTPPRGGKKGRAQPPENLVF* EKTGFPIVQRGGLKPPP GPPKGGE*R GGPP |
| 4949 | 10446 | A | 5257 | 749 | 1049 | DGSSLLGPRPGGKGPNTKGNPRPP G*RESPPHPPRRGKKRMAQPPQLI WDFSSSSGFPL*QGGGINPHDP PKG GKKRGEPPEPTTGPSKRGKKQGFG |
| 4950 | 10447 | A | 5258 | 1 | 359 | LFPKVNLSPVTPAKDTGLTAAPQEP KAPKASPVQHALPSSLSVPHTAILV TGAQLCGPAVNLSQIKDTACKSLLG LEEKKHAEAPAAENPHGGPGDSSA PY**GDAPKGHAIRAVEVPD |
| 4951 | 10448 | A | 5259 | 1 | 441 | FFFLNRVLTITQAGVQWCDHGSLQ PRSLGLK*PSHFSLPSS*DYRCAPPH LANFYIFYKDRWGFTMLPRLVWEL LGSSDLSILDSQSAGITGVRHHTWA NFFNFLCVSGIN*RNFY NKFTSWGS HPNSQYYSGISWGQSTNILLGY |
| 4952 | 10449 | A | 5260 | 1 | 553 | FYFYFFFFPLFFFFKPQDDFLVPGDQ NQRPGGSMPLGTAFILFQMKTSLV RRGINQDN*HWRQEDPLIPSPGFPS RIPPLKSEMSLPLSTDGSETRRTQSP FDEIYMAHDASGLRLPDSPPPPAAP GRDPAPSGQRAPGKLRGQCQLKSE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RESRKEERQRSKPGEAAALGGVAC TFHLKSRS |
| 4953 | 10450 | A | 5261 | 1486 | 1695 | GKSCRPNYIFILFSSFLRRSFALVA QAGVQWCDLGS LQPPPPGFK*FSCL SLPSSWDYRYPLCPANFC |
| 4954 | 10451 | A | 5262 | 1 | 334 | RRFVSQETGNLYIAKVE*SDVGNYT CVVTNTVTNHKVLGPPTPLILRNDG VMGEYEPKIEVQFPETVPTAKGATV KLECFALGNPVPTIWRADGKPIA RKARRHEGCEM |
| 4955 | 10452 | A | 5263 | 78 | 313 | KVTYIQKNVYSKCTAGWVFTQAR VGSREPFPAAPSPGPHGGDPPSPQ L G*PLSPLPQAPVRLPSPVMMSE RIL PF |
| 4956 | 10453 | A | 5264 | 3 | 320 | IFSQENL*YSDGSDILGLLALQAEEN LGMVMIFTLVTAVQEKLNEIVDQIK TSSSSSSSSSSSAEEAEKQLFHGTP VTIENVLNWESQGWRRQTFLGKILE KEKG |
| 4957 | 10454 | A | 5265 | 3 | 941 | APPRCLGDLWARARATMTDYGEE QRNELEALESIYPDSFTVDCTLIQPS *QLVFQNINGLS*YHILLQ*CFT*QG PC*VLSENPPSFTITVTSEAGVENDES IHIKLLSCVLA VQTTLKFTYSEKYPD EAPLYEIFLPGKILEDNDVSDILKLL \ALQAEENLGMVMIFTLVTAVHERI NVLDHII TRCEVEMKL*DKEAEE AVKQLFHGTPVTIENFLNWKAR/SF DAELLEIKKKRMKEEEHAGLDKK\S GKQLFETDHNLDTSDIQFLEDAGNN VEVDESLFQEMDDLEDEDDDPD YNPADPESDSAD |
| 4958 | 10455 | A | 5266 | 1 | 332 | LKKHKSTRVP*NVKSGK*NFSPPFKI RPWAQKRAKKKGAREKKAD*EKG EFGKLSSSSSRFRPGKKV*G*PKGFQR NFEKKPVKSQGPVNMGVIPAFEKKP RIPPVAKIPI |
| 4959 | 10456 | A | 5267 | 3 | 375 | SASPQTLQQSLPRSIAPKPLTVRLPM NQIVTSVTIAANMPSNIGAPLISSMG TTMDGSAPSTQVSPSVQTQQHQMQ LSSSSSSSSSQMQMQMQQQQLQQHQ MHQQIQQMQMQQHFQHHMQ*HLQ Q |
| 4960 | 10457 | A | 5268 | 1 | 360 | KGAPKHGQAPLGDP PRAVGGQEH* GPARGRGPGPREPGSGQTSSPWVH VRPGGGKND SGKARP*ILDPKSVSC IPAPSSHRPLSSPTPNPFP*SSYEGSP RSPQPWTLQPQGPWPPSRQA |
| 4961 | 10458 | A | 5269 | 1 | 181 | KKKPQTWEKLV*GLF*KKRNPGWG QRVPPVTPPLWGVKKRGGVFFRGL KPPLKPRENPFF |
| 4962 | 10459 | A | 5270 | 10 | 108 | SHINVPMNQ*VVSLGPGQVTKGW DQGLLMCE |
| 4963 | 10460 | A | 5271 | 1 | 336 | EFLGAVGFCRLWIPNFAVLAKPLYG VTK*GDTELFKWGSQQQ*AFHELK EKLMSAPALGLPDLTKPFTLYVSER EKMAIGVLIQMVGWPWPVAYLSK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ELDGVSKARSEGCE |
| 4964 | 10461 | A | 5272 | 1 | 118 | TEVRHKGKLDSSKWIPIRGN*NIYNP HCLSYKLEHGSDQEIPSDWYPFATV QFSVPDLC |
| 4965 | 10462 | A | 5274 | 2 | 327 | SCLVLVLLCVEYLFPPYLHFQSICVFT GEVSFLQAAYSWMGMFFVFLFILIH SYFL*LLWGLFISLHLWLSLTCEDLF LLFFSRCLIIYIICFVLLFMSFLILWR LLVF |
| 4966 | 10463 | A | 5275 | 171 | 331 | LKTSFRTKTCT*MLTASLFVIAKTW KQPRCPSVGE*LSNL*YVQTMECYS VLK |
| 4967 | 10464 | B | 5276 | 83 | 332 | MGKRDNRVAYMNPAMARSRGPIQ SSGPTIQDYLNRPRTWEEVKEQLE KKKKGSKALAEFEKMNENWKKE LEKHREKLLSGX* |
| 4968 | 10465 | A | 5277 | 76 | 138 | |
| 4969 | 10466 | A | 5278 | 1 | 1050 | |
| 4970 | 10467 | C | 5279 | 146 | 433 | MKKKSNERWDQVYKILKGKSLRPG FPRCATVRAIQHHGEAGQSGGLYEP NSNGEIKGSPVFRANNTGLSESTK AYLGRSKRATRKEKERLQGFG* |
| 4971 | 10468 | A | 5280 | 27 | 264 | NPNHQSLLCRAFCGVLILPVLALL TRLSFGELTYNNHFIYIFKAFFKFI* VFKWTGDNMFFIKGDMDSLAFGGG G |
| 4972 | 10469 | A | 5281 | 135 | 358 | VHSPVL*LISTIPTSRLKFLKETGHGT PMEEIPEEELSEDVEQIDHADRELRR GQNLRCCKGIHRLPTHIQVGQN |
| 4973 | 10470 | A | 5282 | 15 | 196 | KGKIVKLDIFI*NFPSAKDPVNY*K DNYRLRKMTANHISDKEFVSKTYK ECLKLNLKKF |
| 4974 | 10471 | A | 5283 | 307 | 383 | YF*VSLATLCVYFLLDEGNILTATK VFTSMSLFNLRIPLFELPTVISAVVQ TKISLGR |
| 4975 | 10472 | A | 5284 | 3 | 267 | TIVRPYLLKKKTGTIVEERVNAPGW NEDDDVSVSDESELPTSTTLKAFEK STMEQLVEKACFRDYHRLGL*TLSG SCCRS*P*SRRVQ |
| 4976 | 10473 | A | 5285 | 1 | 260 | TAVPSAASMTSTRAASASSVHVPVS ALGAGSAATAASEEMQTIPQATAA KYPRTIHPESSTSASRSLGT/TISSHP VSHKCSFHKSG |
| 4977 | 10474 | A | 5286 | 60 | 292 | VTNFLIFHMRIISKYISIFLTVFFFVSQ IVLLFKHSYFSYLELWKMQRDSK NAT*KRAL*RFHEKSFHEGCMCIKS |
| 4978 | 10475 | A | 5287 | 738 | 1152 | KGRVWSWCSRKRTFCFSGSFSSSDA LTSYITTAIPTTAVGGASATAVPS AASMTSTRAASASSVHVPVSALGA GSAATAASEEMSDKELITCTRQLKR DGCFGQYTNQPGTGNMGKKQPRIT LCPLNKRKVVAVKPN |
| 4979 | 10476 | A | 5288 | 3 | 555 | RKRTFCFSGSFSSSDALTSYITHCCQ SPPAAV*LASATAVPSAASMTSTRA ASASSVHVPVSALGAGSAATAASEE MYVPRVV TSAQQKAGRITITARITGR CDFASKNRISSSLAIMGVSPPHLSC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | CGKTSSQSTVQTHSLKQLPAKYPRTHSIPESSTLSLPRSLGTQISSHPVSHKCSFP |
| 4980 | 10477 | A | 5289 | 94 | 323 | VIGYRNIRCTILTSTITSSLSIL*LNH*PETRLSE*AGV*DKGLVVAQMMWLMDHIFKYTNFGIVSLVHGDDFFIRQ |
| 4981 | 10478 | A | 5290 | 2 | 319 | MVLVTLDDKYAVAALWGKVKVDEVDGEALGRLMVVYPWTQRFWES*GDLSPDADMGNPKVKVHGNKVLGAVSNGQAHVDNLKGTTFATVSEMHCCKLHVAQEPEVL |
| 4982 | 10479 | A | 5291 | 1 | 159 | RDLQHFPSVAM*DQTQNDIASTSNHESILQGIKGQSQL*EEVQLME*APVDC |
| 4983 | 10480 | A | 5292 | 187 | 282 | LRSY*CLLLMISFTRNANLFR LHGTHTDTFKCLEYEKCFNCNSDLIVHHRINMDHNPHTSA*DSGLLLGMHF |
| 4984 | 10481 | A | 5293 | 1 | 156 | SGGVDEQMMREKEELMLWLQDYEKIKKAEREL*EQIKREMKKNQKRKREKK |
| 4985 | 10482 | A | 5294 | 179 | 322 | NKVGGLTLPNCKTYKATIKTVWYWRKKRQIGQ*NRIESPEIDPHKY |
| 4986 | 10483 | A | 5295 | 2 | 395 | RDRESDRDGQRRERERRTRKWSRSRSHYRSPSRCRTKSKSSSFGRIDRDSYSPR*KGRWANDGWRCPRGNDRYRKNDPEKQENARKEKNDIHLDDADDPNSADKHRNDCPNWITEPINCYPDPRTRNPEKL |
| 4987 | 10484 | A | 5296 | 3 | 228 | HELPHPGGLGLKRGCVVLEVAEHVV LGKALLILLPYRFKRNLAMDDKTGMTRNPHFSHNNWIPTFFSTQYFWIIFKVRWPRLKDTTDLRLAPNCLADRLSRHRCNIWQFMQGIRPLVLNFGSCT*PSFQPQQLYTNLFQHPVFLDHL |
| 4988 | 10485 | A | 5297 | 61 | 360 | YVSNKCSNHRK*SLSSSSSSSERESSFVPQVELHGRDLG*LQLWLPFGFKFPGLTPLRNGDDGPRPQPPANLGLLVKTGFSPVAHLGVNLGTLGDCPALP |
| 4989 | 10486 | A | 5298 | 124 | 351 | EREFRFVPQVELHDRDLGSLHPGTPGLRKFSGLTLPRSGDNGPGPPPVNLGFLEETGFSHVAHFGLNFGT*GDCP |
| 4990 | 10487 | A | 5300 | 3 | 388 | HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQRQLLHLNGTFPNTSDADMEPCVDGWVHDHISFSSTIVTE*DLVCDSQSLTSVAKCAFMTG*TADGFLGAHLSHRVRASSNVCMMGGSIVC |
| 4991 | 10488 | C | 5301 | 47 | 269 | MPPLIQSGMSSRTKTRTSSPCWNVHPAPEQYEAPDKDFMIVALDCSAAWPRAWVVTWSSWCPQQHHDIAPVHA* |
| 4992 | 10489 | A | 5302 | 1 | 253 | MYTQ/HPEQYEAPDKDFMIVAL/DL LSGLAEGLGGHVEQL/VARSNIMTL LFQCM/QAEFMPILGTNLNPEF/ISVC NNATWAIGEICMQW |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4993 | 10490 | A | 5304 | 229 | 2984 | PCPCQNFLRCSTSFNFSLPCAMDWQ PDEQGLQQVLQLLKDSQSPNTATH RIVRDKLKQLNQFPDFNNYLIFVLT RLKSEDEPTRSLSGILKNNVKAHY QSFPPPVADFIKQECLNNIGDASSLI RATIGILITTIASKGELQMWPELLPQ LCNLLNSEDYNTCEGAFGALQKICE DSSELLDSDALNRPLNIMIPKFLQFF KHCSPIKIRSHAIGCVNQFIMDRAQA LMDNIDTFIEHLFALAVDDDPEVRK NVCRALVMLLEVRIDRLIPMHSHIQ YMLQRTQDHDENVALEACEFWLTL AEQPICKEVLASHLVQLIPILVNGM KYSEIDIILLKGDVEEDEAVPDSEQD IKPRFHKSRTVTLPHEAERP DGSED AEDDDDDDALSDWNLRKCSAAAL DVLANVFREELLPHLLPLLKGLLFH PEWVVKESGILVLGAIAEGCMQGM VPYLP ELIPHLIQCLSDKKALVRSIA CWTLSTRYAHWVVSQPPDMHLKPL MTELLKRILDGNKKVQEAACIAFAT LEEKACTELVPYLSYILDTLVFAFG KYQHKNLLILYDAIGTLADSVGHHL NQPEYIQKLMPLLIQKWNEKDED KDLFPLLECLSSVATALQSGFLPYC EPVYQCCVTLVQK\TLAQAMMYTQ HPEQYEAPDKDFMIVALDLFSGLA GLGGHVEQLVARSNIMTLLFQCMQ DSMPEVRQSSFAFLGDFTKACSSHV KPCIAEFMPILGTNLNPEFISVCNNA TWAIGEICMQMGAEMQPYVQMV NNLVEIINRPNTPKTLENTGRLTSP SAIPAITIGRLGYVCPQEVAPMLQQF IRPWCTSLRNIQDNEEKDSAFRGIC MMIGVNP GG VVQDFILFCDAVASW VSPKDDL RDMFYKILHGFKDQVGE DNWQQFSEQFPPLLKERLAAFYGV |
| 4994 | 10491 | A | 5305 | 47 | 411 | |
| 4995 | 10492 | A | 5306 | 20 | 1020 | LSLTSRMEEAELVKGR LQAITDKRK IQEEISQKR\RKLGEDKPKA\QPLKT KALAREKWLP RWN PASGKEQEEM KKQNQQDPAPRSQVPRTKYPSGLR KRSQDLEKAELQISTKEEAILKKLKS IERTTEDIIRSVKVEREERAEESIEDI YANIPDLPKSYIPSRLRKEINEEKED DEQNRKALYAMEIKVEKDLKTGES TVLSS IPLPSDYFNVTGIKVYDEGQK SVYAVSSNHSAAYNGTDGLAPVEV EELLRQALERN SKSPTEYHEPVYAN PFYRPTTPQRET VTPGPNFQERITIK TNGLGIGVNESIHNMG NGLSEERGN NFNHISPI |
| 4996 | 10493 | A | 5307 | 1 | 95 | GTRTFLR TYLSEIARRHPEFYAPELL *FAKR |
| 4997 | 10494 | A | 5308 | 1 | 338 | GTSLSA*GLNIDGQLGLGHTEDIPY YTPCRSLFG*PIQQVACGWHVTIML TEHGQALLCGCNSIVQLAGPHGHL RRVGT*TIELRRENA VHIGAALMPH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VALTTSRSIFQCR |
| 4998 | 10495 | A | 5309 | 3 | 472 | VTEFAKTCVADESAENCDKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDEL RD EGKASSAKQRLKCASLQKFGERAF KA\VARLSQRFP |
| 4999 | 10496 | A | 5310 | 12835 | 13995 | TIPIESDIFPSIFYLYLSSLAYADTYE ALSIFY*KKKLINLLLSLN*ATHFPK IMPVVQVELKAKFN*LFRKCF LPST NPLLCRWR*YDEWNIATS*LIPAKC SLFYLLC*TVSCLAENT*LLFFRLLV RYTKKVPQVSTPTLVEVSRNLGKVS SKCCKHPEAKRMPCAEDYVSL*KHI IN***KNFPFRYC*CYLS*AEGSNVC VCMFCACVCACTCVYV*YWQSRPR G**FFFF*DGVS LCCPGWSA VVPSR LTATSASQVQAILLPQPPK*LGLQV HATMPG*FFVFLVENFQLHLF*ISAL LPVL*LSVVLNQLCVLHEKTPVSDR VTKCCTESLVNRRPCFSALEVDETY VPKEFNAETTFHADICTLSEKERQI KKQT |
| 5000 | 10497 | A | 5311 | 1 | 349 | GTSKKLANKVVYNVGLCICLFDITK LEDAYVFPDGDGASHTKVHFRVCEC HPFLHEILTGKIKGCSPEGAHHPLR* HPDFPLFSRPPAFLSPSQYILSPREIL VHPSILKFRTRRPY |
| 5001 | 10498 | A | 5312 | 1 | 410 | IEHGIVTNWDDMEKIWHHTFYNEL RVAPEEHPVLLTEAPLNPKANREK MT/QGSVPLPAFPP*SLQIMFETFNTP AMYVAIQAVLSLYASGRITTGIVMD SGDGVTHTVPIYEGYALPHAILRMD LAGRDLTDYLMKIL |
| 5002 | 10499 | A | 5313 | 216 | 390 | GSADARAPPVLSPVIFCPS*FLTGRP LQGMVGMGQKDSYVGDEAQSKR GILTLKYPIEHGIVTNWDDMEKIWH HTFYNELRVAPEEHPVLLTEAPLN KANREKMTQVRLGRRPCSSRPFP SH FLPILISDGSSPAGRHHGGHGPEGLLR GRRGPEQAWHPDPEVPH |
| 5003 | 10500 | A | 5314 | 4 | 1254 | HAHAKLGTRAASSRTLFFRQLRRR VSLPVAMEEEIAALVIDNGSGMCK AGFAGGDA\ PRA\VFPSIVGRPRHQG VMVG\MGQK\DSYVGDEAQSKRGI LTLKYPIEHGIVTNWDDMEKIWHH TFYNELRVAPEEHPVLLTEAPLEP QGQTREKMTQ\IMFETFNTP\AMYR GPSRAVLSL*ASGR\TTGHCHGTLG DGVTHTVPIYGG LPHCSTPFLRLGP GLARDLTDYLMKILT*SEGYSFTTH GPSGKFVRD\KEKLCYVALDFEQE MATAASSSSLEKSYELPDGQVITIG NERFRCPEALFQPSFLGMESCGIHET TFNSIMKCDVDIRKDLYANTVLSGG TTMYPGIADRMQKEITALAPSTMKI KILAPPERKYSVWIGGSILASLSTFQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QMWISKQEYDESGPSIVHRKCF |
| 5004 | 10501 | A | 5315 | 279 | 418 | VEHSISNKENFLGQGTGCHACNLNT LGGRGGRITWRSGV*DQLDQH |
| 5005 | 10502 | C | 5316 | 274 | 530 | MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE XQIXKQTALV* |
| 5006 | 10503 | A | 5317 | 2 | 736 | RLAKTYETTLEKCCAAADPHECYA KVFDEFKPLVEEPQNLIKQNCLEFE QLGEYKFQNALLVRYTKKVP/SVVL LLRLAKTYETTLEKCCAAAHPEC YAKVFDEFKPLVEEPQNLIKQNCLE FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCKHPEA KRMPCAEDYLSVVLNQLCVLHEKT PVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLS |
| 5007 | 10504 | B | 5318 | 120 | 1070 | MPADLPSLAADFVESKDVCKNYAE AKDVFLGMFLYEYARRHPDYSVVL LLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNFHT ECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEV ENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDY SVVLLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQNC LEFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRKPRKSGQQML* |
| 5008 | 10505 | A | 5319 | 2 | 668 | |
| 5009 | 10506 | C | 5320 | 246 | 365 | MDDFAAFXXXCCXXDXKGDLLXR RKVKNLLLQVQLPLGF* |
| 5010 | 10507 | C | 5321 | 261 | 656 | MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE RQIKKQTALVELVKHKPKATKEQL KAVXDDFXAFVEKCKGDXKGELL XRRXVXNLL* |
| 5011 | 10508 | C | 5322 | 158 | 607 | MLCQSVGSKCKKHPEAKRMPCAED YLSVVLNQLCVLHEKTPVSDRVTK CCTESLVNRRPCFSALEVDETYVPK EFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVXDD FXAFVEKCKGDXKGELLXRRXVX NLL* |
| 5012 | 10509 | C | 5323 | 158 | 532 | MLCQSVPCAEDYLSVVLNQLCVLH EKTTPVSDRVTKCCTESLVNRRPCFS ALEVDETYVPKEFNAETFTFHADIC TLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCKKAD XKG* |
| 5013 | 10510 | A | 5324 | 2 | 740 | PADLPSLAADFVESKDVCKNYAEA KDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTLEKCCAAADPHECY AKVFDEFKPLVEEPQNLIKQNCLEF EQLGEYKFQNALLVRYTKKVPQVS TPTLVEVSRNLGK/VCCCTESLVNRR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PCFSALEVDETYVPKEFNAETFTFH ADICTLSEKERQIKKQTALVELVKH KPKATKEQLKAVMDDFAAFVEKCC KADDKETCFAEEG*KLGAASQAAL GLY |
| 5014 | 10511 | A | 5325 | 1 | 588 | |
| 5015 | 10512 | A | 5326 | 364 | 1356 | TGDHAFQLWKSMKHTFQVSTPTLV EVSRLGKVGSKCCKHPEAKRMPC AEDYLSVVLNQLCVLHEKTPVSDR VTKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQTALVELVKHKPKATKEQLKAV MDDFAAFVEKCCKADDEMPADLPS LAADFVESKDVCKNYAEAKDVFLG MFLYEYARRHPDYSVVLRLAKT YETTLKCCAAADPHECYAKVFDE FKPLVEEPQNLIKQNCLEQLGEY KFQNALLVRYTKKVPQVSTPTLVE VSRNLGKVGSKCCKHPEAKRMPCA EDYLSVVLNQLCVLHEKTPVSDRV TKCTESLVNRRPCFSALEVDETYV PSVNSNSCRGLKKPRKSGQQML*TS *SKKNAL\SEDYLSVVLNQLCVLHE KTPVSDRVTKCTESLVKGDHAFQ LWKSMKHTFPKSL/YAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLRLAKTYETTLKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCLEQLGEYKFQNALLVRYTKK VPQVSTPTLVE/VLKKPRKSGQQML* TS*SKKNALCRRLSIPWS*TSYVCC MRKRQ*VTESPIRNLGKVGSKCCK HPEAKRMPCAEDYLSVVLNQLCVL HEKTPVSDRVTKCTESLVNRRPCF SALEVDETYVPKEFNAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCCKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLRLAKTYETTLKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCLEQLGEYKFQNALLVRYTKK VPQVSTPTLVEVSRNLGKVGSKCCK HPEAKRMPCAEDYLSRGPEPVMCV A |
| 5016 | 10513 | A | 5327 | 1468 | 1946 | LHISWEGEPIDYSVVLRLAKTYE TTLEKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCLEQLGEYKF QNALLVRYTKKVPQVSTPTLVEVS RNLKVGSKCCKHPEAKRMPCAED YLSVVLNQLCVLHEKRQ*VTESPNA AQNPW*TGDAFQLWKSMKHTFP KSLMLKHSPSMQIYENQDSISSKLK ECCEKPLLEKSHCIAEVENDEMPAD LPSLAADFVESKDVCKNYAEAKDV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FLGMFLYEYARRHPDYSVLLRL AKTYETTLEKCCAAADPHECYAKV FDEFKPLVEEPQNLIKQNCLEFQ GEYKFQNALLVRYTKKVPQVSTPT LVEVSRN/LRKSQGLR*I*TSCGRAS EFNQTKL*AF*AAWRVQIPECAISS HQESTPSVNSNSCRGLKKPRKSGQH TKKVPQVSTPTLVEVSRNLGKVG KCKKHPEAKRMPCAEDYLSVVLNQ LCVLHEKTPVSDRVTCKCTESLGG TGRPCFSSSGKSMETYVPKGFNAE TFTFPGSFCT/LSWEGEPIDYSVLL LRLAKTYETTLEKCCAAADPHECY AKVFDEFKPLVEEPQNLIKQNCLEF EQLGEYKFQNALLVRYTKKVPQVS TPTLVEVSRNLGKVGSKCKHPEA KRMPCAEDYLSVVLNQLCVLHEKT PVSDRVTCKCTESLVNRRPVC |
| 5017 | 10514 | A | 5328 | 1 | 2063 | MKKVKERDSFIMEDLGAELKSSA YSRGVFRRDAHKSEVAHRFKDLGE ENFKALVLIAFAQYLQCPFEDHVK LVNEVTEFAKTCVADESAENCDS LHTLFGDKLCTVATLRETYGEMAD CCAKQEPERNECFQHKDDNPPLP RLVRPEVDVMCTAFHDNEETFLKK YLYEIARRHPYFYAPELLFFAKRYK AAFTECCQAADKAACLLPKLDEL DEGKASSAKQRLKASLQKFGERA FKAWAVARLSQRFPAEFAEVSKL VTDLTKVHTECCHGDLLECADDRA DLAKYICENQDSISSKLKECCEKPL EKSHCIAEVENDEMPADLPSLAADF VESKDVCKNYAEAKDVFLGMFLYE YARRHPDYSVLLRLAKTYETTLE KCCAAADPHECYAKVFDEFKPLVE EPQNLIKQNCLEF/EQLGKYKFQNA AISSVTPKKVPQVSTQLLTPTLVEVS K/NTLGKVGSKCKHPESKKKCPVA ENYLSVVLNQLCALLHEKTPVSDR VTKIAAQEPL/VNRRPCFSALEVR* NIPFPKEVNA/ET/TFHADICTLS ERQIRKQTALVELVETQAPRQKE QLKA/VLWDDFAAFVKKIAAKADD KETCFAEETISGNGAKKAIFLVNDE FILMSLTLIQNHRTYSSLPPCLYDSK KLLFHYLASIYPFVPPQDACKGVSE L |
| 5018 | 10515 | A | 5329 | 1 | 339 | RRRRKKNEKRKRQRKIKDEKSRKN SLRVEMRETWRQREKQKEEDREKR KGQKEKERRKREIEEKEST*CEQME IGKTKKVNIHCRWQTQLKLKFLHFS LFSIKMSLSSFSTRA |
| 5019 | 10516 | A | 5330 | 2 | 189 | ARGGDAGDAFDGFGGDDPSD*LS SCHIDVHRYLFSALCDCYTIFYFVHI RVFLLSMRLADTA |
| 5020 | 10517 | A | 5331 | 3 | 346 | HELETFP*CHNMPLLFYRDRLSASD MLQVRKVMHDHYESIITLNNESQST SSSNNEHPGGQERSLARA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5021 | 10518 | A | 5332 | 2 | 442 | VFMDADTLVLANIDDLFDREELSA APDPGWPCFNSGVFVYQPSVETY NQLLHLASEQGGDQGILNTFFSSWA TTDIRKHLPTIYNLSSISISYLP EDVSGAISHLVPLGGDSQAMAQAV LVFLGKEPGRGTEWGNKGPR |
| 5022 | 10519 | A | 5333 | 1 | 292 | VLANIDDLTREEMSAQTQGWPD C/FNSGVFVYQPSVET/YNQLLHLAS EQGSFDGGDQGILNTFFSSWATTDI RKHLPTIYNLSSISISYLPVLPE |
| 5023 | 10520 | A | 5334 | 81 | 1163 | VTNLRPRPPAHFVITMTDQAFVTL TTNDAYAKGALVLGSSLKQHRTR RLVVLATPQVSDSMRKVLETVFDE VIMVDVLDSGDSAHLTLMKRPELG VTLTKLHCWSLTQYSKCVFMDAD TL\VLANIDDLFDREELSAAPDPG G\PCFNSG\VFVYQPSVETYNQLL HLAS\EQGSFDGGDQGILNTFF*QL GQQQDIRKHLAFIYNLSNISIYSLP AFKVFGASAKVVHFLG\RVKPWNY TY\DPKTKSVK\SEAHDPNMTHPEFL ILWVGTSFTTNVLP LL\QQFGPWSK DT\CSYVN\VGRCLQGAISHLSLGEN PA\MAQPFVSSEERKERWEQQQAD YMGADSFNKRKLD TYLQ |
| 5024 | 10521 | A | 5335 | 1 | 241 | GTSNSEHALDDRSTAQCRVQM QVV QQL*LQLAKDKERLQAMMTHLHV KSTEPKAAPQPLNLVSSVTL SKSAL EAYALELT |
| 5025 | 10522 | A | 5336 | 13 | 229 | ACPRSPPPDPRLGCCFP PPPAVC*AP AGPHPDGTTSLECTPAPHPSCPEVS VQKPEPSALYGTGF PFG LQS |
| 5026 | 10523 | A | 5337 | 1 | 341 | GLSGTSSSSVKSSISP KRVARWSFS SRVCPVCPSSALSV*DSRSP*ASKSS SNASGSPFCRVKLLSCELQSKADS FSSSAVSRDRLSSSSMLSRGQL*Q ETSKEAQMPR |
| 5027 | 10524 | A | 5338 | 3 | 168 | |
| 5028 | 10525 | B | 5339 | 978 | 1502 | MSNLTLVCISTKHTPGISR AKEKKK GTSRLPTSLCQRRVGLTEEKSCSPEL QKFRSETITEELVGLMNKFVEDT KKG VHQKEGWPSAYGVTKIGVTV LSRIHARKLSEQRKGDKILLNACCP GWVRTDMAGPKATKSPEEGAETPV YLALLPPDAEGPHGQFVSEKRVEQ W* |
| 5029 | 10526 | A | 5340 | 3 | 239 | HEAKSSPNLVKAILQIQEATQIPRRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLESESMGT |
| 5030 | 10527 | A | 5341 | 3 | 322 | HEAKSSPNLVKAILQIQEATQIPRRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNL SSETMEAR KKWHNYQMIIEKNCQPTILHPAKLS FK |
| 5031 | 10528 | A | 5342 | 4 | 351 | VGRGRQSHLSHSPPTDPKGQQASP GWNPGVRMLPGLKWLPQPPAASLS *VPSSPTQQT SAGHLLSMSHEALTW |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VD RATGLAGNGEACVSGTQRHPGL SLAPPGCAPSPSSRAARA |
| 5032 | 10529 | A | 5343 | 3 | 163 | HEEQPEGLSPNLD RFLGDRHCNQFS SRD*PIFLARCSHEYSGRHPRLADSI LL |
| 5033 | 10530 | A | 5344 | 112 | 362 | EREQRFTGLNDVHYLPIMYIVVGCA IFIT*V*RGWSSPTKCRSTD TYCVNP STRLHAYMAPRHKLHSHCAERDPD QFTLLRHC |
| 5034 | 10531 | B | 5345 | 85 | 206 | XFSDPEVKKETRPALGSTVLLAPFL HEHEPPSAEVLPGSWRX* |
| 5035 | 10532 | A | 5346 | 142 | 653 | GFWHQRILGASDQAHLLLP HKQDG SADGARRVLACARGQGDLRLRLH LAAVPLQLPGGLRRRAVHVHGGGC QQDGGAESWS/PSPSSPRGPRTLHR VEKVPGAPVTPLPVAFSCNPDHGIE DPAFP*PAAGPR*LQEGPCGGSRAS RAP TPTSTRSCCTECLRN SLILIC |
| 5036 | 10533 | A | 5347 | 261 | 538 | GSR S RLLFSRGPRTYPAWK RSTGA PVTSP IAFSCNPDHGIEDPAFP*PAA GPR*LQEGPCGGSRASRAP TPTSTRS CCTKCLRN FLILIC |
| 5037 | 10534 | A | 5348 | 7 | 264 | FQKISALPQRS DYTHNTPH TDPARV SYKHAGANHTHIHTPMTNVSTTIYP PHAYLHTHTQKTPPHIYSTHAP*I*L FISTYAHTKN |
| 5038 | 10535 | A | 5349 | 208 | 713 | SVK MVRYS LDPENPTK SCKSRGSN LRVHFKN TRETAQA IKG MHIRKAT KYLKDVTLQKQCVFRRYNGGAGR CAQAKHWGWTQGR\WP*RVLNSL VIEHIQVNKAPKMRRRTYRAHGRIN PYMSSPCHIEMILTEKEQIVPKPEEE VAQKKKISQKKLKKQKLMARE |
| 5039 | 10536 | C | 5350 | 286 | 591 | MVRLFN LNPEKRQRKSWQIRGFQS SCFTLGT LVKLAQA IKG MHIRKATE VSERWSLYRNSVYHSDGNNGGVG RRAQAKQWGLGHKVGGPKKECLN FLLHML* |
| 5040 | 10537 | A | 5351 | 1 | 305 | GTSIYNVLYEVPLPPPGRSLKFSGVY GPIICQRPSTNELPLDFPVKEVFELL GVDNVYQLFTWALLQKYILLYVQR *CNVTKALELSNLLLFHICDIKLV |
| 5041 | 10538 | A | 5352 | 15 | 234 | LSCPDQVHPHSLVPYPEPRRATASV PETSGPPFPHRRPYATTPPALGHNP HA*LSSSFAGSRYKLGEMLHI |
| 5042 | 10539 | A | 5353 | 3 | 257 | HEVKYKNPAQ*QWHLGPDAHVPE EFRYHKQLIQSQLFLHYHLSQTFTL QESADLQNAFLNSGQCILNKPLKFA DLHSDFMKTI |
| 5043 | 10540 | A | 5354 | 3 | 334 | IIF IWNPKRA*IAEAILSKKNIAGGI TLPDFRLYNKAIVI*TAWYWHKNR HIDQWNRILNPEIKSHTYSQRIFDKI DKNIH*GKDTL FNKWCWERWIAIC RRIKLD SLV |
| 5044 | 10541 | A | 5355 | 1 | 119 | QKSRW*TPPNSYMKVNVPEKSRNG ETSLRTKIAVCQYYM |
| 5045 | 10542 | A | 5356 | 3 | 349 | HEPANADFAFRFY YLIASETPGKNIF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FSPPRFPAA YAMLSLGACSHSRSQIL EGLGFNLTESESDARRRCRQ*VGT LDLTGHGLQTRGGQGPWPRARPSR GGDAAAGSARLPPR |
| 5046 | 10543 | A | 5357 | 1 | 499 | |
| 5047 | 10544 | B | 5358 | 66 | 641 | MASKINTKALQSPKRPRSPGSNSKV PEIEVTVEGPNNNNNPQTSVRTPTQ TNGSNVPFKPRGREFSFEAWNAKIT DLKQKVENLNFNEKCGEALGLKQAV KVPFALFESFPEDFYVEGLPEGVPFR RPSTFGIPRLEKILRNKAKIKFIKKP EMFETAIKESTSSKSPPRKINSSPNV NTTASGVEDLNIIQ* |
| 5048 | 10545 | A | 5359 | 2 | 306 | ARGVCGGCRCLGFCGSVVGDLMY* NSFDCFKKVLRY*GFFGLYWGLIP* LIWFAPEQAIYLTDNVVRDKFT*R DGSDSLSAEVLAGGCALGSLVIVTN SL |
| 5049 | 10546 | A | 5360 | 3 | 120 | HEGKEPDIPLYETVQTVGPSHARTY TVASHSEGR*TIC |
| 5050 | 10547 | A | 5361 | 2 | 366 | SLPASDRPPISSPLATSGTIFSAISCF WDLPAFLWLAPSCQPTMSSQIRQN YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWKGTPDAMKAA MALEKKLNQALLDLHALGSART |
| 5051 | 10548 | A | 5362 | 1 | 108 | |
| 5052 | 10549 | A | 5363 | 2 | 536 | ARAARDWKNYSTDVEAAVNSLVN LYLQASYTYLSLGFYFDRDDVALE GVSHFFRELAEEKREGYERLLKMQ NQRGGRALFQDIKKPAEDEWKGTP DAMKAA MALEKKLNQALLDLHAL GSARTDPHL\CDFLEPHFIDEEVKLI KKMGDHLNLHRAGWPRRLGLGE YLFERLTLKHD |
| 5053 | 10550 | A | 5364 | 3 | 331 | HEQYPGSISISLTDLGCPDMPVIAR* TAAADESLVPTRLMLQLADYGPVI YSLVI*VCLTAAFTLAQQHSMKIY ADIIGSEDTTNEDYRSIALYFEREMR YLQAAKF |
| 5054 | 10551 | A | 5365 | 3 | 52 | HEQSWKAENEAF TLADLKQLPELN PPVLMPRGNVGTPLRVFLELIRACR LPPRIITQLHFQIPKIGYSLRYCNVPF EYEDSDTAVQE*LT |
| 5055 | 10552 | A | 5366 | 3 | 323 | STFFFFLRLQSLALVAQAGLRTQW RNLGSLQAPPPGFTPFSCSLPSSWD YRRPPRLA\NFFFFFFFVFLAETGFH CVLARMVVIS*PRDQPASASQSAGIT GVSD |
| 5056 | 10553 | A | 5367 | 3 | 337 | HERHEDTLTLKERNRGNGILDDID DHNIIYHLPDA*SEEYEFKEQTTL LRASIPFSVGGSNQLIEAIGKMVRGR LYPWSDVKVENPQHNDFMKLITML ITHMHDLQDV |
| 5057 | 10554 | A | 5368 | 16 | 313 | SHSVTQAGVQCWHLHAQLIFLYF LVETGFHRVSQDGLYLLTS*SARLG LPKCWDYRRDDHAWPVQFFKCS PRPQAILDFAFTSHELCLGSMRLLS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 5058 | 10555 | A | 5369 | 1665 | 1787 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5059 | 10556 | A | 5370 | 1431 | 1553 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5060 | 10557 | A | 5371 | 1740 | 1862 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5061 | 10558 | A | 5372 | 1173 | 1295 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5062 | 10559 | A | 5373 | 1027 | 1149 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5063 | 10560 | A | 5374 | 2250 | 2372 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5064 | 10561 | A | 5375 | 934 | 1092 | FFVFLVETGFHRVSQDGLDLLTS*S ARLSLPKCWDYRREPPCPPRIYILTR SR |
| 5065 | 10562 | A | 5376 | 2588 | 2824 | VAGTIGACHHAQLIFVFLVETGFHH VGQDGLDLLTS*STHLGLPKCWDS RREPLRPASPVVVFQRTSAPVMADLT PTVS |
| 5066 | 10563 | A | 5377 | 935 | 1138 | RRGFTMFHHVSQGGDLLTS*SARL GLPKCWDYRREPLCPAWKDY*CKL QDEVISQQGLKVSIVLIH |
| 5067 | 10564 | B | 5378 | 79 | 1551 | MSEVTKNSLEKILPQLKCHFTWNLF KEDSVSRDLEDRCNQNIEFLNTEFK ATMYNLLAYIKHLDGNNEAALECL RQAEELIQQEHAHQAEIRSLVTWGN YAWVYYHLGRLSDAQIYVDKVKQ TCKKFSNPYSIEYSELDCEEGWTQL KCGRNERAKVCFEKALEEKPNPE FSSGLAIAMYHLDNHPEKQFSTDVL KQAIELSPDNQYVKVLLGLKLQKM NKEAEGEQFVEEALKSPCQTDVLR SAAKFYRRKGDLDKAIELFQRVLES TPNNGYLYHQIGCCYKAKVRQMQ NTGESEASGNKEMIEALKQYAMDY SNKALEKGLNPLNAYSDLAEFLETE CYQTPFNKEVPDAEKQQSHQRYCN LQKYNKSEDVAHQHGLEGLSISK KSTDKEEIKDQPQNVSENLLPQNAP NYWYLQGLIHKQNGDLLQAAKCY EKELGRLLRDAPSGIGSIFLSASELE DGSEEMGQGA VSSSPRELLSNSEQL N* |
| 5068 | 10565 | A | 5379 | 925 | 1127 | FFVFLVETGFHRVSQDGLDLLTL*S THLGLPKCWDYRREPLRPATFSSYQ RNNPDILNDTIMPNK |
| 5069 | 10566 | A | 5380 | 438 | 815 | TRPSFSFNPLTLFFFLRRSLALSPRL ECGSAISAHCKLRLLGSSHSPTSASR VAGTTSARHHA WLMFFVFLVETG FHLVSQDSL DLLTS*SAPLGLPKCW DYRHEPPRPAHLHFLNFFLFSYT |
| 5070 | 10567 | A | 5381 | 7944 | 10115 | KQCNYGHNLKTC SNFFFFWRWSLA PSPRLECNGAISAHCKLRPPGFTFPS CLSLPSSWDYRRSPRAANFFVFLV ETGFHQVSQDGLDLLTL*SARLGLP KCWDYRREPPCPESALIF |
| 5071 | 10568 | A | 5382 | 1 | 211 | LKTSEKWRNRQDKSNKGSKKAER |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RATHADRNREAAIRRKTYTNERK HYEHHRTAGKDQDERATEDSRE* RE |
| 5072 | 10569 | A | 5383 | 2 | 373 | ARECHHLCKJNYMDLVKEFMTLNA SAPLRSSFSDTMIRLPALTYPLFPAL ATCAGYSDKA*SSISYVLHNSALWR ASGPTDHRDAPA*A*LESRRSTLRIC ELRTLYSLIKSTASNFDPIKLFS |
| 5073 | 10570 | A | 5384 | 112 | 913 | DFLSMPNRRGGVSLPPTPP*PPFSVT HTIFSVSFSFHWLKGSLRRQFSYCF YGMVLVPFSPHPPLSLSAPSKCLRIP PLPWGWVTAPRLRSHPSVTGRAVL ERKPSVRG*AGSLNTQARDTPPQLP ERPPEG*ALFPPFPYSMAPPSQLKPT LKITAVRS*ASGGATGLGGWSPLGL P*EQGLRPTATLTQTSGIALNPRSLT PAPQLRLSCPPHFALTTRA VPGGPQ PLAWGPEPGTPPAQPRPSPDSAQSH TVYRRESILFFIL |
| 5074 | 10571 | A | 5385 | 2 | 345 | SFWLLCGSSCSDLRSCQVLKCTRNI PYSLVPTASCEHLHGPCIYRPSVQS VLTCTAAQATNILSAQSLLSGPTTQ* WGLTYPCLLVGAADLTPTTPPPPT PAPPHLPSTPPP |
| 5075 | 10572 | B | 5386 | 36 | 340 | MFLDEYARRHPDYSVVLLRLAKT YETTLEKCCAAADPHECYAKVFDE FKPLVEEPQNLIKQNCLEFEQLGEY KFQNALLVRYTKKNALCRRLSIRGP EPVI* |
| 5076 | 10573 | A | 5387 | 3 | 182 | |
| 5077 | 10574 | C | 5388 | 602 | 877 | METTLRRKCCARLQILHGMAMPKV FRWNFKPLVGRSLRNLNPNKIVEAF WSQLGRSYKFGPMRYLVSFTPKE YPKCSNFPTLCRRVFKET* |
| 5078 | 10575 | A | 5389 | 1 | 404 | GTRNDKMEPGLEQGTIPRLDSVTSS ECFASSGFHEDRSLSDVEEQEDSDG FYKEPITMEDLISYSFQVAIGMESLS SRLCIHRDLEARNFHLSGNYCDTSL EF*IENYDIYL**FNIYSPTKLKPEDT RLKET |
| 5079 | 10576 | A | 5390 | 110 | 424 | LSLLQREREGHLNGSPSFMKCSGF YRLA*GVCV*VSFVL*Y*HILIYSML TVLILCIYFFNMLISGIYTDYAYFYIC YIYYCYIF*FILLCFYTLMTIFFGLI |
| 5080 | 10577 | A | 5391 | 2 | 361 | ARETVKRIQYPIPLEGRGLKPLIES LI*DGLLELCMSPYTTPILLVK*SDW *Y*LVEDLQAINQTVQTTHPVVPNP YTILSKIPYDHQWFTEIDLKDAFWA CPLAEDS*DIFTFEWARA |
| 5081 | 10578 | A | 5392 | 3 | 335 | QSQSWWRQKGVSRAGAGPIHPQGL LFGFS*GDLGPLGTLGEQGLIGQRG EPGLEGDSGPMGPDGLKGVRGDPG PDGEHGEKGQEGLMGEDGPPGPPG AAGVRGLHGKSGY |
| 5082 | 10579 | A | 5393 | 61 | 497 | |
| 5083 | 10580 | A | 5394 | 16 | 951 | RRPKIRDKFWGSV/KKLAHSEASPVI SGASKRAKKQINVYVGKGSS/QGK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / =possible nucleotide deletion; \ =possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MVVWVKLLDRDTVFALVNYIFFKG KWERPFEVKDTEEDFHVDQATT KVPMMLKRLGMFNIQHCKKLSSWV LLMKYLGNAATAIFFLPDEGKLQHLE NELTHDIVTKFLENEEDRRSASLHL PKLSITGTYDLK\TVLGQLGITKVFS NGADLSGVTEEAPLKLSKAVH*GC A*PSTEERGLKLAGGHVF*EGHYPC FIPPRGSSFNKPFVFLNGFEQN/SPSF PLFMGEKWVNPTPKITGLSLLNPSP PSLGPLPGMTLKKGLSWK |
| 5084 | 10581 | A | 5395 | 2 | 306 | GFDHVAQAGLEPLGSSDLPPSASQS AGITGMSHHTQPA YILKISFITLPFIIR SLS*VPFVFSIMYKSSFNFSPCGESVF STNLLNNEYLLIDWWLHFIIY |
| 5085 | 10582 | A | 5396 | 1 | 375 | |
| 5086 | 10583 | A | 5397 | 162 | 426 | |
| 5087 | 10584 | A | 5398 | 140 | 426 | |
| 5088 | 10585 | A | 5399 | 158 | 705 | PSEKNKNNLLGVVYVRHLPNLLD ETQIFSYSQFG\PVTRFRLSR\NKRT GN\SKGYAFLEFESEDVCQNSCLKQ WNNYLFGGKTLG/QCHFMPPEKVH KNSFKDWDFPFKQPSYPSVKRV*S ESDTNTKA/DGMEERFKKKERLLRK KLAKKGIDYDFPSLILQKTESISKTN RQTSTKGQVFT |
| 5089 | 10586 | A | 5400 | 2 | 388 | FLFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA |
| 5090 | 10587 | C | 5401 | 197 | 415 | MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF* |
| 5091 | 10588 | A | 5402 | 671 | 986 | KGVLLLLFFFKTESHSVAQAGVQW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA |
| 5092 | 10589 | A | 5403 | 65 | 921 | |
| 5093 | 10590 | A | 5404 | 213 | 442 | |
| 5094 | 10591 | A | 5405 | 1 | 1506 | |
| 5095 | 10592 | A | 5406 | 1 | 286 | DRLIYIPFPDEKSLVPILKANLGKSP VPKDLDFLDLVPWGCGRLLPRRG NQGCAHSLHSPAGHACYSLTLDR GFLQKSKPKAVKLPRFSFG |
| 5096 | 10593 | A | 5407 | 2 | 158 | |
| 5097 | 10594 | A | 5408 | 1 | 9064 | MLARAARGTGALLRGSLLASGRA PRRASSGLPRNTVVLFVPQQEAWV VERMGRFHRILEPGLNILIPVLDRI YVQSLKEIVINVPEQSAVTLDNVT QIDGVLRLIMDPYKASYGVEDPEY AVTQLAQTTMRSELGKLSLDKVFR ERESLNASIVDAINQAADCWGIRCL RYEIKDIHVPPRVKESMQMQVEAE RRKRATVLESEGTTRESAINVAEGKK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QAQILASEAEKAEQINQAAGEASAV LAKAKAKAEAIRILAAALTQHNGD AAASLTVAEQYVSAFSKLAKDSNTI LLPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGTAS LDEELDRVKMTWSPVPNFQLLNIPS NWGQPHAPGQTSTEV PADGDGATD GPLCLAHASLCCQVAGAAAAALPG AIAGGAVGWARIPRLRLSLSTGMQ KASVLLFLAWVCFLFYAGIALFTSG FLLTRLELTNHSSCQEPGPGSLPW GSQGKPGACWMA SRFSRVVLVID ALRFDFAQPQHSHVPREPPVSLPFL GKLSLQRIEIQPHHARLYRSQVDP PTTTMRQLKALTTGSLPTFIDAGSN FASHAIVEDNLIKQLTSAGRRVVM GDDTWKDLFPGA FSKAFFPSFNVR DLDTVDNGILEHLYPTMDSGEWDV LIAHFLGVDHCGHKHGPHPPEMAK KLSQMDQVIQGLVERLENDTLLVV AGDHGMMTTNGDHGGDSELEVSAA LFLYSPTAVFPSTPPEEPEVIPQVSLV PTLALLGLPIPGNIGEVMAELFSG GEDSQPHSSALAQASALHLNAQQV SRFLHTYSAATQDLQAKELHQLQN LFSKASADYQWLLQSPKGAEATLP TVIAELQQFLRGARAMCIESWARFS LVRMAGGTALLAASCFCILLASQW AISPGFPFCPLLLTPVAWGLVGAIAV AGLLGTIELKLDLVLLGAVAAVSSF LPFLWKAWAGWGSKRPLATLFP GPVLLLLLFR LAVFFSDSFVVAEAR ATPFLLGSFILLVVLHWEGQLLP PKLLTMPRLGTSATTNPPRHNGAY ALRLGIGLLCTRLAGLFHRCPEETP VCHSSPWLSPLASMVGGRKNLW YGACVAALVALLAAVRLWLRRYG NLKSPEPPMLFVRWGLPLMALGTA AYWALASGADEAPPRLRVLVSGAS MVLPRAVAGLAASGLALLLWKPVT VLVKAGAGAPRTRTVLTPFSGPPTS QADLDYVVPQIYRHMQEEFRGRLE RTKSQGPLTVAA YQLGSVYSAAMV TALTLAFPLLLLHAERISLVFLLLF LQSFLLLHLLAAGIPVTTPGKYLSSD SLKDNSDSQGLRKRQPPGNEADA RVRPEEEEEPLMEMRLRDA PQHFY AALLQLGLKYLFI LGIQLACALAAS ILRRHLMVWKVFAPKFIFEAVGFIV SSVGLLLGIALVMRVDGAVLLSSAS TERHCQQTTRGRKPTLVSVLVLDSE QRKDGRLRSALVSSYRFLETPSAGA ELFRPASATMSRQTTSVGSSCLDLW REKNDR LVRQAKVAQNSGLTLRRQ QLAQDALEGLRGLLHSLQGLPAAV PVLPLELTVTCNFILRASLAQGFE DQAQDIQSLERVLETQEQQGPRL QGLRELWDSVLRASCLLP ELLSALH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RLVGLQAALWLSADRLGDLALLLE TLNGSQSGASKDLLLLKLTWSPPAE ELDAPLTLQDAQGLKDVLLTAFAY RQGLQELITGNPDKALSSLHEAASG LCPRPVLVQVYTALGSCHRKMGNP QRALLYLVAALKEGSAWGPPLLEA SRLYQQLGDTTAELESLELLVEALN VPCSSKAPQFLIEVELLLPPDLASP LHCGTQSQTKHILASRCLQTGRAGD AAHYLDLLALLLDSSEPRVGPCMP EVFLEAAVALIQAGRAQDALTLCEE LLSRTSSLPKMSRLWEDARKGTKE LPYCPLWVSATHLLQGQAWVQLG AQKVAISEFSRCLELLFRATPEEKEQ GAAFNCEQGCKSDAALQQLRAAAL ISRGLEWVASGQDTKALQDFLLSV QMCPVSAKRLRPSFESSLPPLPLPL PPRGSGASVVRPTPRCRPRPARLAP LERTSGPGQVFRPTPPGRRPGALGR QSAVRPTTRRKPLVPGESRPREPEA PAGPEEDIKVQRLGNLPKITIKQWH NWNSDPMGLTIEFLLLTLLSKGDD LSTAILKQKNRPNRLIVDEAINEDNS VVSLSQPKMDELQLFRGDTVLLKG KKRREAVCIVLSDDTCSDEKIRMNR VVRNNLRVRLGDVISIQPCPDVKYG KRIHVLPIDDTVEGITGNLFEVYLKP YFLEAYRPIRKGDIFLVRGGMRAVE FKVVETDPSPYCIVAPDTVHCEGEP IKREDEEESLNEVGYDDIGGCRKQL AQIKEMVELPLRHPALFKAIGVKPP RGILLYGPPGTGKTLIARAVANETG AFFFLINGPEIMSKLAGESNLRKA FEEAEKNAPAIIFIDELDAIAPKREKT HGEVERRIVSOLLTLMDGLKQRAH VIVMAATNRPN SIDPALRRFGRFDR EVDIGIPDATGRLEILQIHTKNMKLA DDVDLEQVANETHGHVGADLAAL CSEAALQAIRKKMDLIDLEDETIDA EVMNSLAVTMDDFRVVRTTPVPQW ALSQSNPSALRETVVEVPQVTWEDI GGLEDVKRELQELVQYPVEHPDKF LKFGMTPSKGVLFYGPFGCGKTL AKAIANECQANFISIKGPELLTMWF GESEANVREIFDKARQAAPCVLFFD ELDSIAKARGGNIGDGGGAADRVIN QILTEM DGMSTKKNVFIIGATNRPDI IDPAILRPGRLDQLIYIPLPDEKSRVA ILKANLRKSPVAKAGARSWADVD LGVPGLKMTNGFSGS*P*QEILPACF AKLAIRESNREVKIKAKNREEGKT NPIKPMGRYE*WIDPVPAEIRRDSLL KEAQSFCAFLFSDNDIRKYEMFA QTLSQ/ESRGFGSFRFSGNQGGAGP SQGSGGGTGGSVYTEDNDDDLYG |
| 5098 | 10595 | A | 5409 | 96 | 299 | |
| 5099 | 10596 | A | 5410 | 174 | 324 | |
| 5100 | 10597 | A | 5411 | 74 | 242 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5101 | 10598 | A | 5412 | 129 | 899 | AAPGLGRGGGAAGGGAVCPGTE RPCAMAYAYLFKYIIIIGRTTGVG*N PCPNALQFTD/KRGFQPSAMTLTIGV EFGA\RMITIDGKQIKL\QIWDTAGQ ESFRS\TRSYYRGAAGALLVYDITR\ *DTFNHLTTWLEDARQHSNSNMV IMLIG\NKSD\LESRREVKKKE/EKGEA FA\REHGLIFMETSAGTGFQCRKEG ILFNTAKEILLKKFPRKGVFLTFN*W RANGH/IKLGPQPAAYPIATHAGQS G\GQQAGGGCC |
| 5102 | 10599 | A | 5413 | 1 | 408 | MQLKRANPGPRRAPVRETVMLLC WGVPPGRPYKVDTESALLYQGPHN TLFGYSVVLHSHGANR\WGAPTAN WLANASVINPGAIYRCRIGKNPGQT CEQLQLGSPNGEPCGKTCLEERDNQ WLGVTLSRQPGENG |
| 5103 | 10600 | C | 5414 | 1 | 1026 | MGLGIYLDQYTRQKGQDPVAELKQ LIPLVVSLSAPNLEMPLLKKKTNP TFLKSLSGGLNLFNFPFVETYTVEE VKVHPRNNTGGYNPEEEEDETASE NCFPWNVDGDLMEVASEVHIRRVQ KKEYVEENKIPRNPTYKGCEGPLQE NYKPLLNKIKEDTNKWKNIPCSWIG RTDTVKMAILPKHDRVAEQRVVGA LVKQRASQCPRCRGGRSGPPGTAT ASPSPGRRPFGAVIAPRFPshalssw YAGCNAEKSEVNAPGTQGMRFIS AASYKDWVQVLQOKDVSrnmgtk ARMmplgssggchtirtevtqdse GQLAAVTTTGYTVVgleppkvsd* |
| 5104 | 10601 | A | 5415 | 1 | 681 | |
| 5105 | 10602 | A | 5416 | 1 | 779 | MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEEK VPETTTRFWAPGVEAPGDDAERRR REASGPATRHSP\PTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSTVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCIIDQ SAWHVGRAEIRKLLPYCSTQGGLK YSDVTSGMVKDPPDVL\DRQKCLD ALAALRHAKWSSEIRF |
| 5106 | 10603 | A | 5417 | 1 | 1274 | MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGPPGPLGLLGV RPGMPPQPGPAPLRRPDSSDDRYV MTKHATIPTTEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLLSRIAE NLPKQLAFISPEKYDIKCAVSEAAII LNSCVEPKMQVTITLTSPiREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCVHIR ILRDLCQRVP\TWS\DFPSWAMELLV EKAISSASISPOSPGDAL\RRVFECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PD\QQR\EDITSSAQFALRLLAFA\ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RQIHKVLGMDPLPQMS\QRFN\IHNH QDR\RRDSDGVDGFEEAGKKDKKD YDNF |
| 5107 | 10604 | A | 5418 | 144 | 522 | VDLLRAAGRQWQGPLRPRPSGRR* SARRA/LGKTTYCTDPAKFISVLWT YLATMLHVELPHMNLSTMDLIEH YGKLAFNLDYYTEVLDLS*LLDHL AS/VPFLTAYRQVTEKLVQLIEDYIL RCFIHP |
| 5108 | 10605 | A | 5419 | 1 | 2437 | MAVPGEAEEEEATVYLVVSGIPSVLR SAHLRSYFSQFREERGGGFLCFHYR HRPERAPPQAAPNSALIPTDPAEAG QLLSQTSATDVRPLSTRDSTPIQTRT CCCVISVRGLAQAQRLIRMYSGRR WLD SHGTWLPGRCLIRRLRLPTEAS GLGSFPFKTRKELQSWKAENEAFTL ADLKQLPELNPPVLMPRGNVGTPL RVFLELIRACRLPPRIITQLQLQFPKT GSSRRYGNVPFEYEDSETVEQEELV YTAEGEEIPQGTYLADIPASPCGEPE EEVGKEEEEEESHSEDDDDRGEEWE RHEALHEDVTGQERTTEQLFEEEEIE LKWEKGGGSLVFYTD AQFWQEEE GDFDEQTADDWDVDM SVYYDRDG GDKDARDSVQMRLEQRLRDGQED GSVIERQVGTFERHTKGIGRKVMER QGWAEGQGLGCRCSGVPEALDS DG QHPRCKRGLGYHGEKLQPFQQLKR PRRNLGLISTIYDEPLPDQTESLL RRQPPTSMKFR TDMAFAVIGPPGSG KTTYCLGMSEFLRALGRRVAVVNL DPANEGLPYEC AVDVGELVGLGDV MDALRLGPNGGLLYCMEYLEANL DWLRAKLDPLRGHYFLDCPGQVE LCTHHGALRSIFSQMAQWDLRLTA VHLVD SHYCTDPAKFISVLCTSLAT MLHVELPHINLLSKMDLIEHYGKLA FNL\DYYTEVLDLSYLL*PPGLLTLS SATTRPASIEEA/MCKLIEDY\NLVSF IPLNIQDKESIQRVLQAVDKANGYC FGAQEQRSLEAMMSAAMGADFHS STLGIQEKYLAPSNQSVEQEAMQL |
| 5109 | 10606 | A | 5420 | 2 | 78 | |
| 5110 | 10607 | A | 5421 | 94 | 253 | |
| 5111 | 10608 | A | 5422 | 2 | 318 | |
| 5112 | 10609 | A | 5423 | 460 | 672 | |
| 5113 | 10610 | A | 5424 | 357 | 795 | |
| 5114 | 10611 | A | 5425 | 310 | 478 | |
| 5115 | 10612 | A | 5426 | 1 | 399 | |
| 5116 | 10613 | A | 5427 | 2 | 390 | |
| 5117 | 10614 | A | 5428 | 3 | 392 | GGKIIVGDATEKDASKKSDSNPLTE ILKCPTKVLLLRNMVGAGEVDEDL EVETKEECEK\YGKVGKCV\FEIPG APDDEAVRIFLEFERVE SAIKAVVD LNGRYFGGRVVKACFYNL DKFRVL DLAEQV |
| 5118 | 10615 | A | 5429 | 837 | 1005 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 5119 | 10616 | A | 5430 | 174 | 247 | |
| 5120 | 10617 | A | 5431 | 1 | 360 | |
| 5121 | 10618 | A | 5432 | 1 | 382 | |
| 5122 | 10619 | A | 5433 | 338 | 442 | |
| 5123 | 10620 | A | 5434 | 1 | 140 | |
| 5124 | 10621 | A | 5435 | 3 | 339 | PINFESVGPTYRGSSCLAVVPEFLG MSVAFVPDWLRGKAEVNQETIQRLL LE*NDQLIRCINLEYQNKARGNECVQ YQHVLRNLIYLA TIADAQSQPALS KAMGIIFQKQ |
| 5125 | 10622 | A | 5437 | 157 | 371 | |
| 5126 | 10623 | A | 5438 | 150 | 284 | |
| 5127 | 10624 | A | 5439 | 84 | 901 | ARKSVRMASSRMTRRDPLTNKVAL VTASTDGIGFAIARRLAQDRAHVVV SSRKQQNV DQAVATL\QGEGLSVT GTVCHVGKAEDRGAAWWPPAVKL HGGIDILVSNAAVNPFFGSIMDVTE EV\WDKTLD\NVKGP KP*MTKAVV PEMEKRGGGS\VVIVSSIAAFSPSPG FSPYNVSKTALLGLAQTLPIEL\APR NIRV\NCLAPG\LIKTSF\SRMLWMD KEKEESMKETLR\IRRLGEPEDCAGI VSFLCEDASYITGETV VVG\GGTPS RL |
| 5128 | 10625 | A | 5440 | 2 | 468 | |
| 5129 | 10626 | A | 5441 | 63 | 219 | |
| 5130 | 10627 | A | 5442 | 3 | 558 | |
| 5131 | 10628 | A | 5443 | 7 | 909 | DQCEVCRNSEVRPAACPGHSGSPA QGPPRPFRMKAAVLT LAVLFLTGSQ ARHFWQQDEPPQSPWDRVKDLAT VYVDVLKDSGRDYVSQFEGSALGK QLNLKLLDNWDSVTSTF\SKLREQ GPVTQEFWDNLEKETEGLRQEMSK DLEEVKAKVQPYL\DDFQKKW\QEE MELYRQKVEPLRAELQEGARQKLH ELQEKL SPLGEEMRDRARA\HVDAL RTHLAPYSGELRQRLGARLGALRE NGGARMGQYHA\QATEHLSTLSEK AKPALEDLRQGLLPVLESFKVSFLS ALEEYTKKLNTQ |
| 5132 | 10629 | A | 5444 | 3 | 195 | |
| 5133 | 10630 | A | 5445 | 189 | 263 | PPGSHLGHPANAPSH*GPYPGLHS |
| 5134 | 10631 | A | 5446 | 1905 | 2052 | |
| 5135 | 10632 | A | 5447 | 1903 | 2050 | |
| 5136 | 10633 | A | 5448 | 1 | 115 | |
| 5137 | 10634 | A | 5449 | 1 | 402 | GKTSKLEFSIYLAPHSTTAAIEPYN SILTTHTTLEHYD WAFMAYNGAIYDI CRRNLDIGRTTYTNLNTLIGQIESSIT ASLRFDGALNGDLT*FQTNLVPYPR IHFPLATYAPVISA EKAYHEQLSVA EITNAC |
| 5138 | 10635 | B | 5450 | 81 | 319 | XVVEPYN SILTTHTTLEHSDCAFMV DNEAIYDICRRNLDIERPTYTNLNLRL IGQIVSSITASLRFDGALNVDLTEFQ TNL* |
| 5139 | 10636 | A | 5451 | 1 | 422 | GKTSKLEFSIYPAPQVSTAVVEPYN SILTTHTTLEHSDCAFMVDNEAIYDI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: In USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | CRRNLDIERATYTNLNRJIGQIVSSIT ASLRFDGALNVDLTEFQTNLVPYPR MHLPLGTYAPVICA EK/AYHETAFV QKTTCLG*PSQQMW |
| 5140 | 10637 | A | 5452 | 771 | 1640 | ALQLHPHHPHPWSTLIVPFMVDN EAIYDICRRNLDIERPTYTNLNRVIR A/QMGPSITASLRFDGALNVDLTEF QTNPGAPTPIHLP/LWPTYAPVHLL AGGKPYHGTAFL*AGGFTNGLVLE ARPTQMGGNVDPWVHGVNYMGLL AWLYRGDVGFPKIDNGWPLPTIKN QAQHSFVDW/CGPTGLSRFGHSTY QPSTVVPGLTWAQV\QRAV\CMIA SNTTAIAEA*ARLDHKFDLMYAKR AFVHWYVGEGMKEGEFSEAREDM AALEKDYEEVGVDSVEGE GEEGE EY |
| 5141 | 10638 | A | 5453 | 89 | 435 | |
| 5142 | 10639 | A | 5454 | 2 | 287 | TNEIEPEEN*HTKARNFRFVTAINN TPRNIREG/GDHLHHWIALADCP TAHMYEDVALIKDHTLDNSLIRELQ TLQEFNITLETALVKGIDI |
| 5143 | 10640 | B | 5455 | 218 | 3940 | MSGGGGGGGSAPSRFADYFVICGL DTETGLEPDELSALCQYIQASKARD GASPFISSTTEGENFEQTPLRRTFKS KVLARYPENVEWNPFDQDAVGML CMPKGLAFKTQADPREPQFHAFIT REDGSRTFGFALTFYEEVTSKQICSA MQTLYHMHNAEYDVLHAPPADDR DQSSMEDGEDTPVTKLQRFNSYDIS RDTLYVSKCICLITPMSFMKACRSV LQQLHQA VTSPPPLPLESYIYNVL YEVPLPPPGRSLKFSGVYGPIICQRP STNELPLFDFPVKEVFELLGVENVF QLFTCALLEFQILLYSQHYQRLMTV AETITALMFPFQWQHVVYPILPASL LHFLDAPVPYLMGLHSNGLDDRSK LELPQEANLCFVDIDNHFIELPEDLP QFPNKLEFVQEVSEILMAFGIPPEGN LHCSESASKLKRLRASELVSDKRNG NIAGSPLHSYELLKENETIARLQALV KRTGVSLEKLEVREDPSSNKDLKV QCDEEELRIYQLNIQIREVFANRFTQ MFADYEVFVIQPSQDKESWFTNRE QMNFDKASFLSDQPEPYLPFLSRF LETQMFASFIDNKIMCHDDDDKDP VLRVFDSDRVDKIRLLNVRTPTLRTS MYQKCTTVDEAEKAIELRLAKIDHT AIHPHLLDMKIGQGKYEPGFFPKLQ SDVLSTGPASNKWTNRNAPAQWRR KDRQKQHTHLRLDNDQREKYIQE ARTMGSTIRQPKLSNLSPSVIAQTN WKFVEGLLKECRNKTKRMLVEKM GREAVELGHGEVNITGVEENTLIAS LCDLLERIWSHGLQVKQGSALWS HLLHYQDNRQRKLTSGSLSTSGILL DSERRKSDASSLMPPLRISLIQDMR HIQNIGEIKTDVGKARAWVRLSME |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KKLLSRHLKQLLSDHELTKKLYKR YAFLRCDDEKEQFLYHLLSFNAVD YFCFTNVFTTILIPYHILIVPSKKLGG SMFTANPWICISGELGETQIMQIPRN VLEMTFECQNLGKLTTVQIGHDNS GLYAKWLVEYVMVRNEITGHTYKF PCGRWLKGGMDDGSLERILVGELL TSQPEVDERPCRTPLQQSPSVIRRL VTISPNNKPKLNTGQIQESIGEA VNG IVKHFKPEKERGSLTLLLCGECGL VSALEQAFQHGFKSPRLFKNVFIWD FLEKAQTYETLEKNEVVPEENWH TRARNFCRFVTAINNTPRNIGQGWWQ VSDAGVLGEPEITSYTTGICPAG* |
| 5144 | 10641 | A | 5456 | 238 | 406 | |
| 5145 | 10642 | A | 5457 | 2 | 204 | |
| 5146 | 10643 | A | 5458 | 1 | 431 | |
| 5147 | 10644 | A | 5459 | 1 | 225 | |
| 5148 | 10645 | A | 5460 | 3 | 321 | |
| 5149 | 10646 | A | 5461 | 1 | 1257 | MSHRKFSAPRHGSLGFLPRKRSSRH RGKVKSFPKDDPSKPVHLTAFLGY KAGMTHIVREVDPRGSKVNKKEVV EAVTIVETPPMVVVGVGYVETPRG LRTFKTVFAEHISDECKRRFYKNWH KSKKKAFTKYCKKWQDEDGKKQL EKDFSSMKKYCQVIRVIAHTQMRL LPLRQKK\AHLMGDQVERGALWPE KADWAARER\LEQQVPVNQVFAGQD EMIDVIG\VTQGQKAYKGV\TSRWH TQESCPRKDPTEGLRK\ACIRAWH PARVAFSVARA\GQ\KGYHHRTEIN K\KIYKIGQGYLIKGG\KLIKNNAST\ DYDL\SLDKSINPSGWAFVHLW*K* PNDFVML\KG\CVVGTKK\RVLTLR KSFAGCRRKRRGFGEELTLSSIDTTS KFGHGRFQTMEEKKAFMG\PLKKD RIAKEEGA |
| 5150 | 10647 | A | 5462 | 114 | 456 | |
| 5151 | 10648 | A | 5463 | 3 | 76 | |
| 5152 | 10649 | A | 5464 | 2 | 951 | CWNSGEVRWPLPPPPPRFVARRKM ADLEEQLSDEEKVRIF\LKFFIHAPPG EINEGFNDVRLLLNNDNLLREGAA HAFAYNLDQFTPLKIEG\YEDQVLI TEHGRLGEMGKFL\DPKN\RICFKF* SL*GRRATDPKDPC\EV\ENAVESWR TSVETALRAYVKEHYPEWESGTVY GQKNRWDSQTIAC\ESHQFQAKNF WNGRWRSEWKFTITPSTTQVVGIL KIQVHYEDGNVQLVSHKDIQDSL TVSNEVQTAKEFIKIVEAAENEYQT AISENYQTMSDTTFKALRRQLPVTR TKIDWNKILSYKIGKEMQNA |
| 5153 | 10650 | A | 5465 | 3 | 553 | |
| 5154 | 10651 | B | 5466 | 26 | 384 | MHHEALSEALPGDNVGFNVKNVSV KDVRGRNVAGDSKNDPPMEAAAGF TAQVILNHPGQISAGYALYWIAIVD MVPKGKPMCVESFSDYPPLGRFAVR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DMRQTVAVGVKAVDKKAAGLAS* |
| 5155 | 10652 | A | 5467 | 1 | 1254 | |
| 5156 | 10653 | A | 5468 | 1 | 1386 | |
| 5157 | 10654 | A | 5469 | 33 | 1653 | KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKF EAAEMGKGSFKYAWVLDKLKAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVL\IVAA GVGEFEAGUSKNGQTREHALLAYT LGVKQLIVGVNKMMDSTEPYSQK RYEEIVKEVSTYIKKIGYY\PDTLAF EPISGWNGDDMLEPSANMPWFKG WKVTRKDG\NAS\GTTLLEAL\DCVL PPTRP\TDKPLR\LPLQ\DVYKIGGIG\ TVPVG\RVETGVLKPG\MGVTFAPS QRLQREVKICPKMHHEAFE*SSFLG DNVGF\NVKNVSCQGCSVRGNV*H GDSK\NDPPMEA/SLGFTAQVINLNH PGPNKAPG*CPWYWDCHTAHMAC KVCLSLKEKI*F/DRSW*KSLEDGP*I LGSLGDAGHWLIWVPGQAPCVFEK LLKTIPPLGRFA\VRDNEDRQLCGW VSIKSSWTKKAAGSWAKVTKSAQ KSSERLKWNIIPNTCHPTLYQVWEE RSQELFGSIGHLSLSSKRLVNDNNA S |
| 5158 | 10655 | A | 5470 | 2 | 4966 | |
| 5159 | 10656 | A | 5471 | 2 | 4821 | RWPRRARLLRRGRGGGGVESLPHF GAPVPRARLQLTARRGHAGLRARM REAAAALVPPPAFAVTPAAAMEEPP PPPPPPPPPEPETESEPECCLAARQE GTLGDSACKSPESDLEDFSDDETNT NLYGTSPSTPRQMKRMSTKHQRN NVGRPASRSNLKEKMNAPNQPPHK DTGKTVENVEEYSYKQEKKIRAAL RTTERDHKKNVQCSFMLDSVGGSL PKKSIPDVDLNPYLSLGCSNAKLP VSVPMPIARPARQTSRTDCPADRLK FFETLRLLKLTSVSKKKDREQRGQ ENTSGFWLNRNELIWLELQAWHA GRTINDQDFFLYTARQAIPDIINEILT FKVDYGSFAFVRDRAGFNGTSVEG QCKATPGTKIVGYSTHHEHLQRQR VSFEQVKRIMELLEYIEALYPSLQAL QKDYEKYAAKDFQDRVQALCLWL NITKDLNQKLRI MGTVLGIKNLSDI GWPVFEIPSPRPSKGNPEYEGDDT EGELKELESSTDESEEEQISDPRVPEI RQPIDNSFDIQSRDCISKLERLESE DDSLGWGAPDWSTEAGFSRHCLTSI YRPFVDKALKQMGLRKLILRLHKL MDGSLQRARIALVKNDRPVEFSEFP DPMWGS DYVQLSRTPPSSEEKCSA VSWEELKAMDLPSEFAPFLVLCRVL LNVIHECLKLRLEQRPAGEPSLLSIK QLVRECKEVLKGGLLMKQYYQFM LQEVLEDLEKPCDNIDAFEDLHKM LMVYFDYMRSWIQMLQQLPQASHS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LKNLLEEEWNFTKEITHYIRGGEAQ AGKLFCDIAGMLALKSTGSFLEFGLQ ESCAEFWTSADDSSASDEIIRSVEIS RALKELFHEARERASKALGFAKML RKDLEIAAEFRLSAPVRDLLDVLKS KQYVKVQIPGLENLQMFVPDTLAE EKSIIQLLNAAAGKDCSKDSDDVL IDAYLLLTKHGDRARDSSEDSWGTW EAQPVKVVPQVETVDTLRSMQVDN LLLVMMQSAHLTIQRKAFOQSIEGL MTLCQEQTSSQPVIKALQQLKND ALELCNRISNAIDRVDMFTSEFDA EVDESESVTLQQYYREAMIQGYNF GFEYHKEVVRLMSGEFRQKIGDKYI SFARKWMNYVLTKCESGRGTRPR WATQGFDFLQAIEPAFISALPEDDFL SLQALMNECIGHVIGKPHSPVTGLY LAIHRNSPRPMKVPRCHSDPPNPHLI IPTPEGFRGSSVPENDRLASIAAELQ FRSLSRHSSPTEERDEPAYPRGDSSG STRRSWELRTLISQSKDTASKLGPIE AIQKSVRLFEEKRYREMRRKNIIGQ VCDTPKSYDNVMHVGLRKVTFKW QRGNKIGEGQYGVYTCISVDTGEL MAMKEIRFQPNHKTIKETADELKI FEGIKHPNLVRYFGVELHREMYIF MEYCDEGTLEEVSRGLQEHVIRLY SKQITIAINVLEHGVHRDIKGANIF LTSSGLIKLGDGFCVSKLNNAQTM PGEVNSTLGTAAYMAPEVITRAKG EGHGRAADIWSLGCVVIMVTGKR PWHEYEHNFQIMYKVGGMGHKPPIP ERLSPEGKDFLSHCLESDPKMRWT ASQLLDHSFVKVCTDEE |
| 5160 | 10657 | A | 5472 | 3 | 425 | |
| 5161 | 10658 | A | 5473 | 1 | 234 | |
| 5162 | 10659 | A | 5474 | 3 | 260 | |
| 5163 | 10660 | A | 5475 | 3255 | 3467 | LNKNLGLIFFFFFFFFFFETASRSVTR LEYSGSILAHCELRLPGSRHSPVSA TWEAEAGELPEPRRQRLR |
| 5164 | 10661 | A | 5476 | 1 | 4497 | |
| 5165 | 10662 | A | 5477 | 2 | 891 | |
| 5166 | 10663 | A | 5478 | 1 | 9786 | |
| 5167 | 10664 | A | 5479 | 27 | 13959 | VPFSVAAAEPAQPARAARPRGRS PGAAPPQLAMDPPRPALLALLALPA LLLLLLAGARAEEMLENVSLVCPK DATRFKHLRKTYTYNYEAESSGVP GTADSRSATRINCKVELEVPQLCSFI LKTSQCILKEVYGFNPEGKALLKKT KNSEEFAAAMSRYELKLAIEGKQV FLYPEKDEPTYILNIRGHSALLVPP ETEEAKQVLFLDTVYGNCSTHFTV KTRKGNVATEISTERDLGQCDRFP IRTGISPLALIKGMTRPLSTLISSQS CQYTLDAKRKHVAEAIKCEQHLFL PFSYKNKYGMVAQVTQTLKLEDTP KINSRFFGEGTKKMGLAFESTKSTS PPKQAEAVLKTQVQLKLTISEQNI |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | QRANLFNKLVTCLRGLSDEAVTSLL PQLIEVSSPITLQALVQCGQPQCSTH ILQWLKRVHANPLLIDVVITYLVALI PEPSAQQRLREIFNMARDQRSRATLY ALSHAVNNYHKTNPTGTQELLDIA NYLMEQIQDDCTGDEDYTYLILRVI GNMGTMEQLTPELKSSILKCVQST KPSLMIQKAAIQALRKMEPKDKDQ EVLLQTFLLDDASPGDKRLAAYLML MRSPSQADINKIVQILPWEQNEQVK NFVASHIANILNSEELDIQDLKKLVK EVLKESQLPTVMDFRKFSRNYQLY KSVSIPSLDPASAKIEGNLIFDPNNY LPKESMLKTTLTAFGFASADLIEIGL EGKGFEPTEALFGKQGFFPDSVNK ALYWVNGQVPDGVSKVLVDHFGY TKDDKHEQDMVNGIMLSVEKLIKD LKSKEVPEARAYLRILGEELGFASL HDLQLLGKLLLMGARTLQGIPQMI GEVIRKGSKNDFFLHYIFMENAFEL PTGAGLQLQISSSGVIAPGAKAGVK LEVANMQAELVAKPSVSVEFVTNM GIIIPDFARSGVQMNTNFFHESGLEA HVALKPGKLFKIPSPKRPVKLLSGG NTLHLVSTTKTEVIPPLIENRQSWSV CKQVFPGLNYCTSGAYSNASSTDSA SYYPLTGDTRLELELRPTGEIEQYSV SATYELQREDRALVDTLKFTVQAE GAKQTEATMTFKYNRQSMTLSSSEV QIPDFDVLGTILRVNDESTEGKTS YRLTLDIQNKKITEVALMGHLSCDT KEERKIKGVISIPRLQAEARSEILAH WSPAKLLLQMDSSATAYGSTVSKR VAWHYDEEKIEFEWNTGTNVDTKK MTSNFPVDLSDYPKSLHMYANRLL DHRVPQTDMTFRHVGSKLIVAMSS WLQKASGSLPYTQTLQDHLNSLKE FNLQNMGLPDFHIPENLFLKSDGRV KYTLNKNLSLKIEIPLPFGGKSSRDLK MLETVRTPALHFKSVGFHLPSREFQ VPTFTIPKLYQLQVPLLGVLDLSTN VYSNLYNWSASYSGGNTSTDHFSL RARYHMKADSVVDLLSYNVQSGG ETTYDHKNFTLSCDGLRHKFLDS NIKFSHVEKLGNNPVSKGLLIFDASS SWGPQMSASVHLDSKKKQHLFVKE VKIDGQFRVSSFYAKGTYGLSCQRD PNTGRLNGESNLRFNSSYLQGTNQi TGRYEDGTLSLTSTSDLQSGIUKNTA SLKYENYELTLKSDTNGKYKNFAT SNKMDMTFSKQNALLRSEYQADYE SLRFFSLLSGSLNSHGLELNADILGT DKINSGAHKATLRIGQDGISTSATT NLKCSLLVLENELNAELGLSGASM KLTTNGRFREHNAKFSLDGKAALT ELSLGSAYQAMILGVDSKNIFNFKV SQEGLKLSNDMMGSYAEMKFDHT NSLNIAGLSLDFSSKLDNIYSSDKFY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KQTVNLQLQPYSLVTTLNSDLKYN ALDLTNNGKLRLEPLKLHVAGNLK GAYQNNEIKHIYAISSAALSASYKA DTVAKVQGVEFSHRLNTDIAGLAS AIDMSTNYNSDSLHFSNVFRSVMAP FTMTIDAHTNGNGKLALWGEHTGQ LYSKFLLKAEPLAFTFSHDYKGSTS HHLVSRKSISAALCHKVSALLTPAE QTGTWKLKTQFNNNEYSQDLDAY NTKDKIGVELTGRTLADLTLLDSPI KVPLLLSEPINIIDALEMRAVEKPKQ EFTIVAFVKYDKNQDVHSINLPFFET LQEYFERNRQTIIVLENVQRNLKH INIDQFVRKYRAALGKLPQQANDY LNSFNWERQVSHAKEKLTAITKKY RITENDIQIALDDAKINFNEKLSQLQ TYMIQFDQYIKDSYDLHDLKIAIANI IDEIIEKLSLDEHYHIRVNLVKTIH DLHLFIENIDFNKSGSSTASWIONVD TKYQIRIQIEKLQQLKRHIQNIDIQ HLAGKLKQHIEAIDVRVLLDQLGTT ISFERINDVLEHVKHVFVINLIGDFEV AEKINAFRAKVHELIEREVDQQIQ VLMDKLVELAHQYKLKETIQKLSN VLQQVKIKDYFEKLVGFIDDAVKK LNELSFKTFIEDVNFKFLDMLIKKLKS FDYHQFVDETNDKIREVTQRLNGEI QALELPQKAEALKLFLEETKATVA VYLESLODTKITLINWLQEALSSAS LAHMKAKFRETLEDTRDRMYQMDI QQELQRYLSLVGQVYSTLVITYISD WWTLAAKNLTDFAEQYSIQDWAK RMKALVEQGFTVPEIKTILGTMPAF EVSLQALQKATFQTPDFIVPLTDLRI PSVQINFKDLKNIKIPSRFSTPEFTIL NTFHIPSFTIDFVEMKVKIIRTIDQML NSELQWPVPDIYLRDLKVEDIPLARI TLPDFRLPEIAIPEFIPTLNLNDFQVP DLHIPEFQLPHISHTIEVPTFGKLYSI LKIQSPLFTLDANADIGNGTTSANE AGIAASITAKGESKLEVLNDFDQAN AQLSNPKINPLALKESVKFSSKYLR TEHGSEMLFFGNAIEGKSNTVASLH TEKNTLELSNGVIVKINNQLTLDN TKYFHKLNIPKLDFSSQADLRNEIKT LLKAGHIAWTSSGKGSKWKWACPRF SDEGTHESQISFTIEGPLTSFGLSNKI NSKHLRVNQNLVYESGSLNFSKLEI QSQVDSQHVGHSLVLTAKGMALFGE GKAEFTGRHDAHLNGKVIGTLKNS LFFSAQPFEITASTNNEGNLKVRFPL RLTGKIDFLNNYALFLSPSAQQASW QVSARFNQYKYNQNFSAAGNNENIM EAHVGINGEANLDFLNIPLTIPEMRL PYTIITTPPLKDFSLWEKTGLKEFLK TTKQSFDSLVAQYKKNKHRHSIT NPLAVLCEFISQSIKSFDRHFENRN NALDFVTKSYNETKIKFDKYKAEKS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HDELPRTFQIPGYTPVNVNVEVSPF TIEMSAFGYVFPKAVSMPSFSILGSD VRVPSYTLILPSLELPVLHVPRNLKL SLPDFKELCTISHIFIPAMGNITYDFS FKSSVITLNTNAELFNQSDIVAHLLS SSSSVIDALQYKLEGTTTLTRKRGL KLATALSLSNKFVEGSHNSTVSLTT KNMEVSVATTTKAQIPILRMNFKQE LNGNTKSKPTVSSSMFEKYDFNSSM LYSTAKGAVDHKLSLESLSYFSIES STKGDVKGSVLSREYSGTIASEANT YLNSKSTRSSVKLQGTSKIDDIWNL EVKENFAGEATLQRIYSLWEHSTKN HLQLEGLFFTNGEHTSKATLELSPW QMSALVQVHASQPSSFHDFPDLGQ EVALNANTKNQKIRWKNEVRIHSG SFQSQVELSNDQEKAHLDIAGSLEG HLRFLKNIILPVYDKSLWDFLKLDV TTSIGRRQHRLRVSTAFVYTKNPNGY SFSIPVKVLADKFIIPGLKLNDLNSV LVMPTFHVPFTDLQVPSCKLDREI QIYKKLRTSSFALNLPTLPEVKFPEV DVLTKYSQPEDSLIPFFEITVPESQLT VSQFTLPKSVSDGIAALDLNAVANK IADFELPTIIVPEQTIEIPSIKFSVPAGI AIPSFQALTARFEVDSPVYNATWSA SLKNKADYVETVLDSTCSSTVQFLE YELNVLGTHKIEDGTLASKTKGTFA HRDFSAEYEEDGKYEGLQEWEGKA HLNIKSPAFTDLHLRYQKDKKGIST SAASPAVGTVGMDMDEDDDFSKW NFYYSPQSSPDKKLTIFKTEL RVRES DEETQIKVNWEEEAASGLLTSKDN VPKATGVLYDYVNKYHWEHTGLT LREVSSKLRRNLQDHAEWVYQGAI REIDDIDERFQKGASGTTGTQYQEWK DKAQNLYQELLTQEGQASFQGLKD NVFDGLVRVTQEFHMKVKHLIDSLI DFLNFPRFQFPGKPGIYTREELCTMF IREVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISMREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFG\PSGVGWTVK YYEGEEKIVSLIKNLLVALKDFHSE YIVSASNFTSQLSSQVEQFLHRNIQ EYLSILTDPDGKGKEKIAELSATAQ EIIKSQAIAATKKIISDYHQFRYKLQ DFSDQLSDYYEK\FIAESKRLNDLSI QNYHTFLDYTSREFNWKKLAIQPQ SLNPYMKLAPGELYHYHPLIFLKEIFN LFFFSNLNFSHRHRKNCKLPILIKPY SEPALQ |
| 5168 | 10665 | A | 5480 | 2 | 316 | |
| 5169 | 10666 | A | 5481 | 2 | 401 | |
| 5170 | 10667 | A | 5482 | 126 | 415 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5171 | 10668 | A | 5483 | 3 | 499 | |
| 5172 | 10669 | A | 5484 | 1 | 241 | |
| 5173 | 10670 | A | 5485 | 12 | 308 | |
| 5174 | 10671 | B | 5486 | 394 | 565 | MSAEERLRSSGVLSQKVIAHSLGFD KHGNRLGRGKGYDAYLKRCLQH QEVKPYTLALAFKEQICLQVPVNEN DMK* |
| 5175 | 10672 | B | 5487 | 674 | 807 | MSAEERLRSSGVLSQKVIAHSEYQK SKRISIFLSMQDEIETEEIKDIFQRGK ICFLPSVRVPEQSHGYGLGFDKHGN RLGRGKGYDAYLKRCLQHQEVK PYTLALAFKEQICLQVPVNENDIK* |
| 5176 | 10673 | A | 5488 | 113 | 339 | |
| 5177 | 10674 | A | 5490 | 2 | 388 | FLFFFEMESRSVAQAGVQWCDLG SLQPPPPGLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA |
| 5178 | 10675 | C | 5491 | 197 | 415 | MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF* |
| 5179 | 10676 | A | 5492 | 768 | 1081 | KGVLFFFFKTESHSVAQAGVQW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA |
| 5180 | 10677 | A | 5494 | 305 | 477 | |
| 5181 | 10678 | A | 5495 | 1 | 903 | |
| 5182 | 10679 | A | 5496 | 111 | 295 | KPATSVPVIVCVCSSAKPELPLCPAT YTEHHAGQPHWWYHAAR/DLVSW K*QISQRGEINPH |
| 5183 | 10680 | A | 5497 | 1 | 505 | |
| 5184 | 10681 | A | 5498 | 3 | 345 | |
| 5185 | 10682 | A | 5499 | 1 | 1416 | |
| 5186 | 10683 | A | 5500 | 618 | 707 | |
| 5187 | 10684 | C | 5501 | 1729 | 2511 | MDIASTNTSNKSDTNMEQVPATND TIKRLESKLLKNQAKQQSESGRLSL GASRGSSVESLPPTSEGKRMSADMS EIEARIAATTGNGQPRRRSIQDLTVT GTEPGQVSSRSSSPSVRMITTSPTS EKPTRSHPWTPDDSTDNTNGSDNSIP MAYLTLDHQLQPLAPCPNSKESMA VFEQHCKMAQEYMKVQTEIALLLQ RKQELVAELDQDEKDQQNTSRLVQ EHKKLLDENKSLSTYYQQCKKQLE VIRSQQQKRQGT* |
| 5188 | 10685 | A | 5502 | 1 | 3489 | |
| 5189 | 10686 | A | 5503 | 1 | 246 | |
| 5190 | 10687 | A | 5504 | 40 | 124 | NVPQFTAKAPCKHEKCLNTNSPDLF EAC*DNIDQTAVSLTAPKTGKRK*R NKVQLS**PQFTAKAPCKHEKCLNT NSPDLFEAC |
| 5191 | 10688 | A | 5505 | 156 | 1001 | GIQQFGQYCLNMLQINQLLSKIKLA NPKEKTAMYLVLNELARFNRVQPQY KLLD*RGPAHSMFVSQSLGEQT WESEGSSIKKAQQA VGNKALTESTL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PKPI*KPPKSNVNNNPGCITPTVELN GLAMKRGRACHPQAIRSKAIPK**S *LQLSSHV*SEVS\FPIPKIFYVQLTV GNNEFFGEGKTRQAARHNAAMKA LQALQNEPI/LRKISSGMVNQERIW MMTK/HANKSEISLVFEIALKRNMP VSFEVIKESGPPHMKSFVTRVSVGE FSAEGEGNSKK |
| 5192 | 10689 | A | 5506 | 175 | 411 | |
| 5193 | 10690 | A | 5507 | 198 | 381 | |
| 5194 | 10691 | A | 5508 | 137 | 346 | |
| 5195 | 10692 | A | 5510 | 3 | 136 | |
| 5196 | 10693 | A | 5511 | 2 | 673 | |
| 5197 | 10694 | A | 5512 | 1 | 257 | |
| 5198 | 10695 | A | 5513 | 1 | 712 | PRKT/PPAPH\DGDRKELPRTKLLPP API\STD*SQHADRGTEP/GPIRPSIEP GPPVQFGTSDKSDLRVVGDSLIA EKELPASVTEAIPVSRDWQLLGSGA ASAEPQSKNLD SGHC VPEHSSSGQR LYPEVFYGSAGPSSSQISGGAMDFH LAFGSGQGRHLEKGPPDGQRSLGPE GTRSLGCPHPAEGVPLAPYPRGLYI DYKY/MKGERGGRGGVLGLGPHFP SSPFPWSPVPGAVC |
| 5199 | 10696 | A | 5514 | 2 | 322 | |
| 5200 | 10697 | A | 5515 | 1 | 6470 | MSDRSGPTAKGKDGGKYYSSLNLF TYKGKSLEIQKPA\VAPRHGLQSLG KVAIARR/MRPPANLPSLKAENKGN DPNVSLVPKDG TGWASKQE QSDPK SSDASTAQPPE SQPLPASQTPASNQP KRPPAAPENTPLVPSGVKSWAQAS VTHGAHGDGGRASSLLSRFSREEFP TLQAAGDQDKAAKERESAEQSSGP GPSLRPQNSTTW RDGGGRGPDELE GPD SKLHHGHDP RGG LQPSGPPQFP PYRGMMPPFMYPPYLPFPPPYGPQG PYRYPTPDGPSRFPRVAGPRGSGPP MRLVEPVGRPSILKEDNLKEFDQLD QENDDGWAGAHEEVDYTEKLKFS DEEDGRDSDEEGAEGHRDSQSASG EERPPEADGKKGN SPNSEPTPKTA WAETSRPPETEPGPPAPKPPLPPGDY PDRGGPPCKPPAPEDEDEA WRQRR KQSSSEISLAVERARRRREEEERRM QEERRAACAEKLR LDEKFGAPDK RLKAEP AAPPAAPSTPAPPPAVPKE LPAPPAPPPASAPTPETEPEEPAQAP PAQSTPTPGVAAAPTLVSGGGSTSS TSSGSFEASPVEPQLPSKEGPEPPEE VPPPTTPPVKVEPKGDGIGPTRQPP SQGLGYPKYQKSLPPRFQRQQEQ LLKQQQQHQWQQHQQGSAPPTVP PSPQPVT LGAVPAPQAPPPPKALY PGALGRPPPMPPMNFDP RWMMIPP YVDPRL LQGRPPLEFYPPGVHPSGL VPRERSDSLGLSSEPFDRHAPAMLR ERGTPVDPKLA WVG DVFTATPAE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PRPLTSPLRQAADEDDKGMRSETPP VPPPPPYLASYPGFPENGAPGPPISR FPLEEPGPRPLPWPPGSDEVAKIQTP PPKKEPPKEETAQLTGPEAGRKLPA SRSGAGPPPPRRESRTETRWGPRPG SSRGIPPEEPGAPPRRAGPIKKPPPP TKVEELPPKPLEQGDETPKPPKPDPL KITKGKLGPKETPPNGNLSAPRL RRDYSYERVGPTSCRGRGRGEYFA RGRGFRGTYGGRGRGG/RSEFRSYR EFRGDDGRGGGTGGPNHPPAPRGR HASETRSEGSEYEEIPKRCRQRGSET GSETHESDLAPSDKEAPTPKEGTLT Q/VPLAPPPPGAPPSPAPARFTC/RG GRRVFTPR/GVPSRRGRGGGR/PPPO VCPGWSPPAKSLAPKKPPTGPLPPS KEPLKEKLIPGLSPVARGGSNGGS NVGMEDGERPRRRRHGRAQQQDK PPRFRRLKQERENAARGSEGKPSLT LPASAPGPEEALTTVTVAPAPPRAA AKSPDLSNQNSDQANEEWETASESS DFTSERRGDKEAPPPVLLTPKAVGT PGGGGGGA VPGISAMSRGDL SQRA KDLSKRSFSSQRP GMERQNRRPGPG GKAGSSGSSSGGGGGGPGGRTGPG RGDKRSWSPK NRSRPPEERPPGLP LPPPPSSSA VFRLDQVIHSNPAGIQ QALACLSSRQGSVTAPGGHPRHKP GPPQAPQGSPRPTRYEPQRVNSG LSSDPHFEEPGPMVRGVGGTPRDSA GVSPFPKRRERPPRKPELLQEECLP PPHSSGFLGSKPEGPGPQAESRDTG TEALTPHIWNRLHTATSRKSYRPTS MEPWMEPLSPFEDVAGTEMSQSDS GVDLSGDSQVSSGPCSQRSSPDGGL KGAAEGPPKRPGGSSPLNAVCEGP PGSEPPRRPPPAPHDGRKELPREQP LPPGPIGTERSQRTDRGTEPGPIRPS HRP GPPVQFGTSDKDSLRLVVGDS LKAEKELTASVTEAIPVSRDWELLP SAAASAEPQSKNLD SGHCVPEPSSS GORLYPEVFYGSAGPSSSQISGGA MDSQLHPNSGG/FRPGTPSLHPYRS QPLYLPPGPAPPSALLSGVALKGQF LDFSTMQATELGKLPAGGVLYPPPS FLYSPAFCPSPLPDTSLQVRQDLPS PSDFYSTPLQPGGQSGFLPSGAPAQ QMLLPM\VDSQLPVVNFGSLPPAPP PAPPPLSLLPVGPALQPPSFVVRPQS SPSTGVL\/*LARPFPVYFGRTELHP VNIKPF RDFQKLSSNLGGPGSSRTP PTGRRPSSLRSFSGLNSRLQSRLS NLTSGVFRNQAASTFYQAGLPHPD ALRWIPKP WERTGRPPR\DGPSRR\ AEEP\GSRGDKEP\GLPPPR |
| 5201 | 10698 | A | 5516 | 2 | 119 | |
| 5202 | 10699 | A | 5517 | 1 | 325 | FFFFF*DRVSLLLPKLECNGTISAHC NLRLPGSSDSPASASSSFTIHVAPLP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QLRHY*IFYDGTRSLYAG*YSQNLLI YSAPRQPQYHFKDMNKILDSIQRSY TKI |
| 5203 | 10700 | A | 5518 | 228 | 481 | QFFRNTIFF*DRVSLLLPLECNSAIS AHHNLCLPGSSDSPASASRVAGITG TCHHTRLLAFVFLVETGFYHVSQSG LELLTSGD |
| 5204 | 10701 | A | 5519 | 175 | 431 | LIVKMPFLK*SWKIF*MSK**VMLIH *GFVFLFVCFF*DRVSLLLPRLECN GPISAHRLHLDPSSDSPASAYIKGF VRQLSHEE |
| 5205 | 10702 | A | 5520 | 257 | 453 | TKGGGYTORTAIQFILFIYLFY*DG VSLLLPRLE*NGAISAHCNHLPGSS DSQKKTCKNFCTQ |
| 5206 | 10703 | A | 5521 | 277 | 1230 | ISFHLSTFGAPSFFFFFEMEFSLLLPR LECNGAISAHRNLRLPGSSDSPASAS PVGWDYRHVHPRSANFVFFFSRDG VSPCWSGLVSNSRPQMIPPSRPPKV LDTGLATMPGLCLANFCGRNRVSL MCP8WSPELKQSTCLSLPKCWDYR RAAVPGLFILFFLRHRCPTLTQDEV QWCDHSSLQPTPEIKHPPASASQSS WDQRHAPLHLANFYFYF*FFETES\ HSVTRLECSGAILAHCNLCPLGSSY SPAPAS*VAGTTGAH/RRLANFFVFL VEMGFHHVRQVDARSLDLVICLPR PPKVLGLQDVSHHRPAYF |
| 5207 | 10704 | A | 5522 | 1 | 467 | FFFLF*EGVSLLLPRLECSGAISA/HC NLHLPSSDSPASASQEDGITGVRY HAWLIL/VFLVEIGFHHVGQADLKP *PQVIHPPLFFFFLRQSFALVAQAGV QWCDLSSLQTPPPRVQGILLAQPPE YLVAGFTGMRHHTRLFFFAFLVET GFHPC |
| 5208 | 10705 | A | 5523 | 293 | 681 | QGTILIGLCPFDITPAIVDILLAFWHV R\CPRPTVSCFCKKVLLV*NFFFFFF FFFETESVTRLECSGVILAHCNL RLPGSSDSHASASRVAETTGVRRHA WPIFVFLVETRFHHVGQAGLELLTS GD |
| 5209 | 10706 | A | 5524 | 274 | 321 | |
| 5210 | 10707 | A | 5525 | 2 | 733 | |
| 5211 | 10708 | A | 5527 | 1 | 3555 | MHYVLNSSSMETFVGEQNYEGSSR LCVCKRTREADDPSARDSVCEGVR ARFNICGINQIVLKCPIWGCENPAQ MGCPPVGKADRCGLLANSATCEKG MFCHADLVGITPTVFPSHPRCKTTA SAKLACQQDQVDLDRQSLSSIDKNPS ERGQSQLSNPTDDSWKGRPYANQK LFASLLIKCVVQLELIQTIDNIVFYPA TSKKEDAEHMVAAQQDTLDADIHI ETEDQGMKYMSSQHLFKLLDCLQ ESHFSKAFNSNYEQRTVLWRAGF KGKSKPNLLKQETSSLACCLRILFR MYVDENRRDSWEEIQORLLTVCS ALAYFITVNSESHREAWTSLLLLLL TKTLKINDEKFKAHASMYYPYLCEI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MQFDLPELRAVLRKFFLRIGVVYKI WIPEEPSQARCRAILPGFECEAERRQ ERVVPATVRGWGSLLRFCIPTSSYN KCLLNMYCVPDPIAMELSDANLQT LTEYLKKTLDPDPAIRRP AEKFLESV EGNQNYPLLLTLLEKSQDNVIKVC ASVTFKNYIKRNWRIVEDENKICE ADRVAIKANIVHMLSSPEQIQKQL SDAISIIGREDFPQKWPDLITEMVN RFQSGDFHVGVLRTAHSFLKRYR HEFKSNELWTEIKLVLDALPLTN LFKICDNAALYAQKYDEEFQRYLPR FVTAIWNLLVTTGQEVKYDLLVSN AIQFLASVCERPHYKNLFEDQNTLT SICEKVIVPNMEFRAADEEAFEDNS EEYIRRDLEGSDIDTRRRAACDLVR GLCKFFEGPVTGIFSGYVNSMLQEY AKNPSVNWKHKDAAIYLVTSLASK AQTQKHGITQANELVNLTEFFVNHI LPDLKSANAIMRSFSLQEAIIPIPT LITQLTQKLLAVSKNPSKPHFNHYM FEAICLSIRITCKANPAAVVNFEAL FLVFTEILQNDV/PSESDQYRKQIFI LLFQRLQNSKTTKFIKSK*NHLDVL QK**KKMFGMVLEKIIPEIQKVSG NVEKKICAVGITKLLTECPPMMDTE YTKLWTPLLQSLIGLFELPEDDTIPD EEHFIDIEDTPGYQTAFSQLAFAGK KEHDPVGQMVNNPKIHLAQLHLKL STACPGRSCGSSPVEDGVCIGAPRSP TASVCFPSLVGSINGPAPAPPPTVR TTSSGWHCGGACARKARRGPSGRS ALSRLDRSGPS |
| 5212 | 10709 | A | 5528 | 1 | 4611 | |
| 5213 | 10710 | A | 5529 | 58 | 3051 | CQLRSAAGVPSSVSVSPRDIAMEL SDANLQTLTEYLKKTLDPDPAIRRP AEKFLESVEGNQNYPLLLTLLEKS QDNVIKVCASVTFKNYIKRN\WRIV EDEPNKICEADRVAIKANIVHMLLS SPEQIQKQLSDAISNGREDFPQKW PDLALTEMVNRFQSGDFHVGVLRTA HSLFKRYRHEFKSNELWTEIK LVLDALPLTYLFKATIELCSTH ANDASALRILFSSLILISKLFYSLNFQ DLPEFFEDNMETWMNNFHTLLTLD NKLLQTDDEEEAGLLELLKSQICDN AALYAQKYDEEFQRYLPRFVTAIW NLLVTTGQEVKYDLLVSNAIQFLAS VCERPHYKNLFEDQNTLTSICEKVI VPNMEFRAADEEAFEDNSEEYIRRD LEGSDIDTRRRAACDLVRGLCKFFE GPVTGIFSGYVNSMLQEYAKNPSV NWKHKDAAIYLVTSLASKAQTQKH GITQANELVNLTEFFVNHIPLDLKSA NVNEFPVLKADGIKYIMIFRNQVPK EHLLVSIPLLINHLQAGSIVVHTYAA HALERLFTMRGPNNATLFTAAEIAP FVEILLTNLFKALTLPGSSENEYIMK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AIMRSFSLQEAIPYIPTLITQLTQK LLAVSKNPSKPHFNHYMFEAICLSIR ITCKANPAAVVNFEEALFLVFTEILQ NDVQEFIPYVFQVMSLLLETHKNDI PSSYMA LFPHLLQPVLWERTGNIPA LVRL LQAFLERGSNTIASAAADKIP GLLGVFQKLIASKANDHQGFYLLNS IIEHMPPE SVDQYRKQIFILLFQRLQ NSKTTKFIKSFLVFINLYCIKYGALA LQEIFDGIQPKMFGMVLEKIIPEIQK VSGNVEKKICAVGITNLLTECPPMM DTEYTKLWTPLLQSLIGLFELPEDD TIPDEEHFIDIEDTPGYQTAFSOLAF AGKKEHDPVGQMVNNPKIHLAQL HMLSTACPGRVPSMVSTSLNAEAL QYLQGYLQAASVTLL |
| 5214 | 10711 | A | 5530 | 1 | 396 | |
| 5215 | 10712 | A | 5531 | 1 | 1095 | |
| 5216 | 10713 | A | 5532 | 1 | 1077 | |
| 5217 | 10714 | A | 5533 | 1 | 986 | |
| 5218 | 10715 | B | 5534 | 214 | 975 | MEVKT KARELRDECTSLSSRFDQLE ERVLVMENQMNQMKQEEKFREKRI KRNEQSLQEIWDYVKRPNLRVIGVP ESDGENGTKLENTLQDIIQENFPNL ARKANIQIQETQRMPPQRYSSRRATP RHIIVRFTKVEMKETMLRAAREKG RVTHKGKPIRLTADLSAETLQAKRE WGPFI NILKEKNFQPRISYPAKLSFIS EGEIKSFTDKQMLRDFVTTTRPALKE LLKEALNMERNNQYQHCKNMPNC KDHPG* |
| 5219 | 10716 | A | 5535 | 3 | 1135 | |
| 5220 | 10717 | A | 5536 | 1 | 1023 | |
| 5221 | 10718 | A | 5537 | 2 | 2747 | LHLWGQGTDKQKDSSNLCRLKCPC LTALKRAVVLPARSWRSENGQTAS SKGKL TTRKDIYTENPSVHHHHQRP KVDKTTKMGGKQNRKTGNSKKQS ASPPPKERSASPPPKERSSSPATEQS WREN/DLDFDELRAEGFKRSNYSE LWEDIQTKGKEVENFEKNLEECITRI TNTEKCLKELMELKTKARELCEEC RSLRSRCDQLEERVSA MEDEVKMN EMNEMKREGKFREKRIKRNEQSLQ EIWDYVKRPNLRLTGVPESDGENG TKLENTLQDIIQENFPNLARQANVQI QEIQRTPPQRYSSRRATPRHIIVRFTK VEMKEKILRAAREKGRVTLKGKPIR LTADLSAETLQARREWGPFI NILKE KNFQPRISCPAKLSFISEGEIKYFTDK QMLRDFVTTKPALQELLKEALNME RNNRSPSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTKGKEVEN FEKNLEECITRITNTEKCLKELMELK TKARELREECRSLRSRCDQLEERVS AMEDEMNEMKREGKFREKRIKRNE QSLQEIWDYVKRPNLRLIGVPESDV ENGTKLENTLQDIIQENFPNLARQA NVQIQEIQRTPHRFSSRRATTRNLIV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RFTKVEMKEKMLRAAREKGRVTH KGKPIRLTADLLAETLQARREWGPI FNILKEKNFQPRISYPAKLSFISEGEI KYFTEKQMLRDFVTTSPAELLEKE ALNMERNNRRTTRQKVNKDIQELNS ALHQADLIDISRTLHPKSTEYTFESA PHHTYSKIDHIVGSKALLSKCKRTEI ITKCLSDHSAIKLELRKLTQNCCTT TWKLNNLLNDYWVQNMKAIEK MFFENNENKDTTYQNLWDTFKA VCRGKFIALNAHKRKQKRSKTDLT LSQLKELEKEEKHIQKLAEGKK |
| 5222 | 10719 | A | 5538 | 99 | 432 | |
| 5223 | 10720 | A | 5539 | 100 | 732 | |
| 5224 | 10721 | A | 5540 | 242 | 1300 | NPRRSGHSLEAKLRDSSYSELLRDIL QKHEAVHMEALDELYEALAETLM AKESTQGHRSYLLPSGGSVTLSEST AIISHGTTGLVTWDATLYLAEWAIE NPAAFTNRTVLELGSGAGLTGLAIC KDVPPPGIHLQRTCHSRVLEQLRGN VPSNGLSLEADITAKLDSRVTVAQ LDWDVATVHQLSAFQPDVIAADV LYCPEAIMSLVGVLRRLAACREDQ RAPEVYVAFTVRNPETCQLFTTELA PSTCEGVLSLSHLTDKDIRTHRGQA TLELLQTAARPPGSRASTIHPSLPMP RASAPAPPEHSPSWQPCAQMHPQQ PLPAHRDTDNPVPVHVGPVNYRA NKQAST |
| 5225 | 10722 | A | 5541 | 3 | 167 | |
| 5226 | 10723 | A | 5542 | 2 | 378 | |
| 5227 | 10724 | A | 5543 | 3 | 359 | |
| 5228 | 10725 | A | 5544 | 15 | 347 | |
| 5229 | 10726 | B | 5545 | 141 | 371 | DFGYFYGSSYVAAPDSSRTPGLSRS RDGLLVAKLDLNLCCQQVNDVWNF KMTGRYEMYARELAEAVKSNYSPT IVKE* |
| 5230 | 10727 | A | 5546 | 1 | 1154 | MAGAEWKSLEECLEKHLPLPDLQE VKRVLYGKELRKLDLPREAFEAAS REDFELQGYAFEAEEQLRRPRIVH VGLVQNRIPANAPVAEQVSALHR RIKAIVEVAAMCGVNIICFQEAWTM PFAFCTREKLPWTEFAESAEDGPTT RFCQKLAKNHDMVVVSPILERDSE HGDVLWNTAVVISNSGAVLGKTRK NHIPRVGDFNESTYYMEGNLGHVP FQTQFGRIAVNICYGRHHPLNWLM YSINGAEIIFNPSATIGALSESLWPIE ARNAAIANHCFTCAINRVGTEHFP NEFTSGDGKKAHQDFGYFYGSSYV AAPDSSRTPGLSRSRDGLLVAKLDL NLCCQQVNDVWKFKITGRYEMYAR ELAEAVKSNYSPTIVKE |
| 5231 | 10728 | A | 5547 | 424 | 604 | |
| 5232 | 10729 | A | 5548 | 52 | 318 | |
| 5233 | 10730 | A | 5549 | 3 | 148 | |
| 5234 | 10731 | A | 5550 | 258 | 458 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5235 | 10732 | A | 5551 | 1 | 217 | |
| 5236 | 10733 | A | 5552 | 246 | 361 | |
| 5237 | 10734 | C | 5553 | 69 | 254 | MDHLYNXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXEIQXXXXXERERNKN PFPAGDDIISRGVVGQ* |
| 5238 | 10735 | A | 5554 | 32 | 169 | NPVPPYPLCPALVFFLLLIYLLIY*PS PLLRMSAPAGKGFLFLSL |
| 5239 | 10736 | A | 5555 | 417 | 490 | |
| 5240 | 10737 | A | 5556 | 2 | 121 | |
| 5241 | 10738 | A | 5557 | 69 | 398 | |
| 5242 | 10739 | A | 5558 | 2 | 732 | GRVPSQCGWIRMRSRSCREDQKPG MDDQRDLISNNEQLSMLGRRPGAP ESKCSRGCPLHSAFSILVTLLLVVQA INAYFLYH*HGRLDKLTVPQNLQ LENLRMKLPKPPKPVSKMRMATP LL\MQALPMGALPQGPMQNATKYG NMTEDHVMHLLQNADPLKVYPPL KGSFPENLRHLKNTMETIDWKVFES WMHHWLLFEMSRHSLEQKPTDAPP KESLELEDPSGLGVTKQDLGPVPM |
| 5243 | 10740 | A | 5559 | 2 | 359 | |
| 5244 | 10741 | A | 5560 | 2444 | 2755 | DYYYFFEMESCSVAQAGVQWRDL GSLQPPPPSSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVGQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS |
| 5245 | 10742 | A | 5561 | 1724 | 1941 | AHLLYEWIFFFFFFFFEMESHVAQA GVLWRDLSSLQAPPPG\SQSDSPAS ASWVAGITGACHHARHEWNFKC |
| 5246 | 10743 | A | 5562 | 2 | 362 | |
| 5247 | 10744 | A | 5563 | 138 | 236 | |
| 5248 | 10745 | A | 5564 | 1 | 278 | |
| 5249 | 10746 | A | 5565 | 80 | 591 | RGCKREGLSMSSLIRRVISTAKAPG A\IGPPTVQAVLVDRTHLHFRDQIG HGPLPSWTS LCPGGVAGRSLNKL KNMGEIPESLPGCDF\TNVVKTTCS GLDINDLQLLFNEILQTVFSRSNFPA RAAYPSWLLLPQKGSRAEIEA\VAIQ GPLTTAFILSGDPCCVWDC |
| 5250 | 10747 | A | 5566 | 141 | 340 | |
| 5251 | 10748 | A | 5567 | 209 | 386 | |
| 5252 | 10749 | A | 5568 | 1 | 346 | |
| 5253 | 10750 | A | 5569 | 160 | 391 | |
| 5254 | 10751 | A | 5570 | 101 | 332 | |
| 5255 | 10752 | A | 5571 | 500 | 752 | |
| 5256 | 10753 | A | 5572 | 2 | 82 | |
| 5257 | 10754 | A | 5573 | 3 | 165 | |
| 5258 | 10755 | A | 5574 | 1 | 219 | |
| 5259 | 10756 | A | 5575 | 1 | 327 | |
| 5260 | 10757 | A | 5576 | 2 | 160 | |
| 5261 | 10758 | A | 5577 | 1 | 189 | QQLRHPDLHLQRRSQAQQHQGGQ DS*AQMLCRVPTVPSTTCGRTVSLP LPPKTQGHPHDLDP |
| 5262 | 10759 | A | 5578 | 2 | 224 | |
| 5263 | 10760 | A | 5579 | 1 | 1392 | |
| 5264 | 10761 | A | 5580 | 1 | 1272 | PGCGRPRAFSLNIADIEEKRGTSHF VRQTPSPSPNNL*YLIYRRYRQFHA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LQSKLEERFGPDSKSSALACTLPTLP GRRPLPSCCCRAAVRIPALNAYMK VPVGLATLARGRALPPWDPLQSG CLWSLSTQSQPSVSPDLCAWSLVR* PRQALGARVLDVRIFFYQSPYDSEQ VPQALRRLRPTRKV*VTSPWAST WPEPAAPRAEVTAPTLARLSHCNF KAGDVIFLLSRINKDWLEVSSEVRM EVRLKVFVKILKDFPEEDDPTNWLR CYYYEDTISTIKSVAWEGGACPAFL PSLRPLPLTSPSHGSLSHSKAPSGSQ MSHNAVTSHQRPGWPGQPHSPFFH PTLKDLELTR*GAGNGAGELDTLD AEGDLVRLSDEDVALMVRQARGL PSQKRLFPWKLHITQKDNRYRVYNT MP |
| 5265 | 10762 | A | 5581 | 437 | 728 | |
| 5266 | 10763 | A | 5582 | 570 | 1648 | TQPGTGWARLSTCSLGPSPMTMAVA QQLRAESDFEQLPDDVAISANIADIE EKRGFTSHFVFVIEVKTKGGSKYLI YRRYRQFHALQSKLEERFGPDSKSS ALACTLPTLPKVVYGVKQEIEM RIPALNAYMKSLSLPVWVLMDED VRIFFYQSPYDSEQVPQALRRLRPR TRKVKSVSPQGNSVDRMAAPRAEA LFDFTGNSKLELNFKAGDVIFLLSRI NKDWLEGTVRGATGIFPLSFVKILK DFPEEDDPTNWLR CYYYEDTISTIK DIAVEEDLSSTPLLKDLELTRREFQ REDIALNYRDAEGDLVRLSDEDV ALMVRQARGLPSQKRLFPWKLHIT QKDNRYRVYNTMP |
| 5267 | 10764 | A | 5583 | 1705 | 2233 | |
| 5268 | 10765 | A | 5584 | 1 | 354 | |
| 5269 | 10766 | A | 5585 | 270 | 390 | |
| 5270 | 10767 | A | 5586 | 3 | 132 | |
| 5271 | 10768 | A | 5587 | 234 | 362 | |
| 5272 | 10769 | A | 5588 | 1 | 402 | |
| 5273 | 10770 | A | 5589 | 2 | 509 | |
| 5274 | 10771 | A | 5590 | 3 | 1607 | SPRPGIPRCFHLVISTEHRRVMTEFG LSWVFLVAIFKGVQCEVQLVESGG DLVQPGGSLRLSCAASGFTFSSYAM HWVRQAPGKGLKYVSGISSNGRRT YYANSVKGRFTISRDN SKNTLYLQ MGS LRAEDMAVYYCARGGDHIVP AAVAPFHMDVWGQGT VTVSSASP TSPKVFPLSLCSTQPDGNVVIACLP G PGLLP GATQCDLERKRTGRDRQK LPTQPGCLRGPVHHEQPADPAGHT VPSRQVRDMPREALHESQPGCDCA LPSSLNSTYPISLNSTYPISLMLPPT VTAPTGPSKDLFLGSKATFTCTLP G LARDASGVTF TWDALKVGKSAVQG P*RRDLCG\CYSV\SSVLP GCAEAH GTHGEGPSLWHCWPYPESKDPA*PP TLFKIRGNTFPGPRFHLL\PPPSEGAG PWNELVTL\TCLGIGLSAPRMLLVC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | WVAGGHRSLREKYLTWA\SRQKP SQGTTTFAVTSILRVAAEDWKKGD TFSCMVGHEALPLAFTQKTIDRLAG KPTHVNVSVVMAEVDGTCY |
| 5275 | 10772 | A | 5592 | 2 | 315 | |
| 5276 | 10773 | A | 5593 | 245 | 455 | |
| 5277 | 10774 | A | 5594 | 1 | 2863 | MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEESNQTGTSRWDG VSKKAPRHLSVPCTRPREARQEAE DSTSRLSAESGETDQDAGDVGPDP PDSYYGLLGTLPCEALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTIQLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIK QAERVFPNSVICKTFHSMAYGHIGR KYQSKKKLNLFLKLPFMVNSVLAE GKGGFIRAKLVCKTLENFFASADEE LTIDHVPIWCKNSQGGQRMVEQSE KLNGVLEASRLWDNMRKLGECTEE AHQMTHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFSGFKRYVTAAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLPLPALRVEPFS\ EDEWNLLYVAVTRAKKRLIMTKS LENILTLAGEYFLQAELTSNVLKTG VVR\CCVGQCNNAIPVDTVLTMKK L\PIY*ATGK\ENKGGYLCHSCAEQ RIGPLAFLTASPEQVRAMERTVENI VLPRHEALLFLVF |
| 5278 | 10775 | A | 5595 | 3 | 613 | |
| 5279 | 10776 | A | 5596 | 2 | 1419 | PPHLLSSPFVAAPRARATAGFTLS ASAMQEIAHLQAGQCGNQIGAKFW EVISDEHGIDPTGTYHGDSDLQLERI NVYYNEATGAGNYVPRAVLVDLEP GTMDSVRSGPFGQIFRPDNFVFGQS GAGNNWAKGHYTEGAELVDAVLD VVRKEAESCDCLQGFQLTHSLGGG TGSGMGTLISKIREFPDRIMNTFS VVPSPKCQDTVVEPYNATLSVHQL VENTDETYCIDNEALYDICFRTLKL TTPTYGDLNHLVSAATMSGVTTCLRF PGQLNADLRKLAVNMVFPRLHFF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MPAFAPLTSRGSQQYRGLTVPELTQ QMFDANKMMAACDPRHGRYLTVA AVFRGRMSMKEVDEQMLSVQSKN SSYFVEWIPNNVKTAVCDIPPRGLK MAVTFIGNSTAIQELFKRISEQFTAM FRRKAFLHWYTGEDEMEFTEAE SNMNDLVSEYQQYQDATAEQGEFE EEAEEVA |
| 5280 | 10777 | A | 5603 | 1 | 384 | |
| 5281 | 10778 | A | 5604 | 185 | 700 | |
| 5282 | 10779 | A | 5605 | 1 | 414 | |
| 5283 | 10780 | A | 5606 | 3 | 138 | |
| 5284 | 10781 | A | 5607 | 1 | 433 | NNPDFKAGV/MALPTL/LQIQRHDD YLVMLKAIRILVQERLTQDAVAKA NQTKGLPVALDKHILGFDTGDAV LNEAAQILRLHIEELRELQTKINEA IVAVQAIHFWHVWWSKCHILGGGS PENWVCSRDLPLLLIAFFFNKV |
| 5285 | 10782 | A | 5608 | 1 | 459 | |
| 5286 | 10783 | A | 5609 | 118 | 375 | VAVVQIIFLPVFIAEKYKDLVPDnsk TADNATKNAEPLINLDVNNPDFKA GVMALANLLQIQRHDDYLVMLKA IRILVQERLTQD |
| 5287 | 10784 | A | 5610 | 344 | 513 | |
| 5288 | 10785 | A | 5611 | 3 | 116 | |
| 5289 | 10786 | A | 5612 | 3 | 869 | HEVFSRPRPGEPNREAGTMFRRRLT VLDYHNPAGFNCKDETEFRNFIVW LEDQKIRHYKIEDRGWLRNIHSSDW PK\FFEKYLRDVNCPFKIQDRQEI DWLLGFAVRPEYGDNAEKYKDLV PDNSK\TADNAPKNAEPWINLDVN NPDK\AGVMALG*PAFRFQRHDD\ FLVNA*RQFRIWVQERLTQDA\VA KAKSNKKRALPVALAQTHILGFD\T GDASSLMKLEILRIACTYEELRELT DQKSTKAIVAVQAIYC*SQRQDHRL GKSLEDEHFEDLQLSPLL |
| 5290 | 10787 | A | 5613 | 298 | 403 | |
| 5291 | 10788 | A | 5614 | 3 | 611 | |
| 5292 | 10789 | A | 5615 | 192 | 340 | |
| 5293 | 10790 | A | 5616 | 187 | 361 | |
| 5294 | 10791 | A | 5617 | 187 | 385 | |
| 5295 | 10792 | A | 5618 | 2 | 340 | |
| 5296 | 10793 | A | 5619 | 1 | 702 | EKYIQLVRQRALEGALGNTIYKSQ TAKGTPQETEGTSSGSKSNVRSGKR VPSGRMV/IHSHFPAEVT*E*TRVH WIWQS*COGESWKQVPFLCHSGS* RNALL\CLRHDVDALLWQPHSSKQ DDMWEHIATFNALGYVQASKRDK KFFACAPNYSYAALCECLRRVFIYR QPAPMSTVLYNKKGRQA\VGQVAK QQVASLETNDPNLGIQATNERLFV LTTKNLFLIKVNTEN |
| 5297 | 10794 | A | 5620 | 3 | 357 | |
| 5298 | 10795 | A | 5621 | 1 | 1926 | |
| 5299 | 10796 | A | 5622 | 1 | 362 | LQTSDEETGFSCLEFYVCAATSFVL VCIINWCKAD*DTRWTFRIKIGR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | T/SVVDLLYWRDINITGVVFGATLFL LLSLTVFSIVSVTAYIALALLSVTISF TIYKGVSHAIPKSDEGHPF |
| 5300 | 10797 | A | 5623 | 247 | 533 | KSFPGWQTYFSCGWVGCGLGRGS QNASPPASPLPQLPPG*RRSWPLRG TACRSWSALSGLWAAGLYHPPRMPP LMWEAGAGSPGELRGTRIRER |
| 5301 | 10798 | A | 5624 | 128 | 667 | |
| 5302 | 10799 | A | 5625 | 12 | 3756 | VPRLSRPSPSQSSPTPTTARGSETRP RRRRQQLQHHLHPPAMEDLDQSPL VSSSDSPRPQPAFKYQFVREPEDEE EEEEEEEEDEDEDELEEVLERKPA AGLSAAPVPTAPAAGAPLMDFGND FVPPAPRGPLPAAPPVAPERQPSWD PSPVSSTVPAPSPLSAAAVSPSKLPE DDEPPARPPPPPPASVSPQAEPVWTP PAPAPAAPSTPAAPKRRGSSGSVD ETLFALPAASEPVIRSSAENMDLKE QPGNTISAGQEDFPSVLLETAASLPS LSPLSAASFKEHEYLGNLSTVLPTE GTLQENVSEASKEVSEKAKTLLIDR DLTEFSELEYSEMGSFSVSPKAESA VIVANPREEIIVKNKDEEEKLVSNNI LHNQQELPTALTKLVKEDEVVSSEK AKDSFNEKRVAVEAPMREEYADFK PFERVWEVKDSKEDSDMLAAGGKI ESNLESKVDKKCFADSLEQTNHEK DSESSNDDTSFPSTPEGIKDRSGAYI TCAPFNPAATESIATNIFPLLGDPTSE NKTDEKKIEEKKAQIVTEKNTSTKT SNPFLVAAQDSETDYVTTDNLT KV TEEVVANMPEGLTPDLVQEACESEL NEVTGTKIAYETKMDLVQTSEVMQ ESLYPAAQLCPSFEESEATPSPVLPD IVMEAPLNSAVPSAGASVIQPSSSPL EASSVNYESIKHEPENPPPYEEAMS VSLKKVSGIKEEIKEPENINAALQET EAPYISIACDLIKETKLSAEPAPDFSD YSEMAKVEQPVPDHSELVEDSSPDS EPVDLFSDDSIPDVPQKQDETVM LV KESLTETSFESMIEYENKEKLSALPP EGGKPYLESFKLSLDNTKDTLLPDE VSTLSKKEKIPLQMEELSTAVYSND DLFISKEAQIRETETFSOSSPIEIDEF PTLISSKTDSFSKLAREYTDLEVSHK SEIANAPDGAGSLPCTELPHDLSLK NIQPKVEEKISFSDDFSKNGSATSKV LLPPDV SALATQAEIESIVKPKVLV KEAEKKLPSDTEKEDRSPSAIFS AEL SKTSVVDLLYWRDIKKTGVVFGA/ SAVFLLSLTVFSIVSVTAYIALAL LSVTISFRIYKGVIAIQKSDEGHP FRAISGNL/ESCLYLRELGSGRYSNS ALGSMWNCTVKGNFRAPSFSSWM DLVDSL/RSFAVLMWVFTYVGCLG LMVLDTTGFWALNF/ISSSGSWLIYE RHQAQUDH\YLGLANKNVKDAMA KIQAKIPGLKRKAE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5303 | 10800 | A | 5626 | 2 | 436 | RRQFEERQQEMEHVYELLENKMQQLQEESRLAKNEAARMAALVEAEKCNLELSEKLKGVTKNWEDVPGDQVKPDQ\YTEALAQRDK*VPSVLFLRLSFAHSQGIQQLSCSLSRT/RQ*ELHYF*DFMGPQPKTFFSGLNFQWYPL |
| 5304 | 10801 | A | 5627 | 3 | 309 | |
| 5305 | 10802 | B | 5628 | 454 | 645 | MTCKKENFSLKLLIYFLEERMQQKYEASREDIYKRNTTELKVEVESLKRELQDKKQPSGLKPWA* |
| 5306 | 10803 | A | 5629 | 1 | 294 | |
| 5307 | 10804 | A | 5630 | 14 | 228 | |
| 5308 | 10805 | A | 5631 | 201 | 350 | |
| 5309 | 10806 | A | 5632 | 262 | 626 | PSARPHCFGLEAMHARSLPCWNCSRRLLILAFS/WGSE/CCTRKPRIIDVYYNASNNELVRTKTLVKNCIVLIDSTPYR\QWYESH\YALPLGRKKGAKLTPEEEELNKKRSKKIQKKYDERKENAKISSLLEEQFQQGKLLACIASRPKQCGRADGYVLEGKELEFYLRK\IKARKRQINPCFVFTHGNGRVYCFVPTFMLPEYMTVFS\AIFPCPAKLIWGGGLQPLALTSASYCPETGSPHC |
| 5310 | 10807 | A | 5633 | 3 | 452 | |
| 5311 | 10808 | A | 5634 | 26 | 477 | NSTDSETRTHGARLLPDKTNVKAAWG\KVGAGAHAG\EYGAELERMFLSFPT\TKTYFPHFDL\SHG\SAQVKG/HTGKKVADALTNAVAN\DDMPNALSALSDLHAHKLRVDPVNFKLLSHCLAGGPWAAHLPRPSSTPGGATPSLEQSSWASC |
| 5312 | 10809 | A | 5635 | 1 | 147 | |
| 5313 | 10810 | A | 5636 | 1 | 503 | AAAARAARGTAGPWRSARLPALPASSLGAAAMAASAKRKQEEKHLKMLRDMTGLPHNRKCFDCDQRGPTYVNMTVGSFVCTSCSGSLRG*NPPHRVKSISMTTFTQQEIEFLQKHGNEVC\PEQAKVVASVHASISGSSASSTSS\TPEVRPLKSLLGDSAPTLHLN |
| 5314 | 10811 | A | 5637 | 272 | 360 | |
| 5315 | 10812 | A | 5638 | 1 | 1934 | WRRRRRLSRLCRLVWPVSPRTTAPGPRRAQYSQAAAAGSGAGGARRRRAAAAARAARGTAGPRRSAARLPALPASSLGAAAMAASAKRKQEEKHLKMLRDMTGLPHNRKCFDCDQRGPTYVNMTVGSFVCTSCSGSLRGLNPPHK/VGKSISMTTFTQQEIEFLQKHGNEVCKQIWLGLFDDRSAIPDFRDPQKVKEFLQEKYEKKRWYVPPEQAKVVASVHASISGSSASSTSS\TPEVKPLKSLLGDSAPTLHLNKGTPSQSPVVGSRQGGQKEKKQFDLLSDLGSDIFAAPAQSTATANFANFAHFNSHAAQNSANADFANFDAFGQSSGSSNFGGFPTASHSPFQPQTGGSAASVNANFAHFDNFPKSSSADFGTFNTSQSHQTASAVSKVSTNKAGLQTADKYAALANLDN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | IFSAGQGGDQSGFGTTGKAPVGSV VSVPSQSSASSDKYAALAE LDSVFS SAATSSNAYTSTSNASSNVFGTVPV VASAQTQPASSVPAPFG RTPSTNPF VAAAGPSVASSTNPFQTNARGATA ATFGTASMSMPTGFGTPAPYSLPTS FSGSFQQPAFPAQA AAFPQQTAFSQQ PNGAGFAAFGQTKPVVTPFGQVAA AGVSSNPFMTGAPTGQFPTGSSSTN PFL |
| 5316 | 10813 | A | 5639 | 1 | 307 | |
| 5317 | 10814 | A | 5640 | 957 | 3132 | GEEELWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR *PLGPWCRR\KKKGAE EEPKRRR QEKQAACPFYNHEQMGLLRDEALA EVKDMEQLLALGKEARACPY YGSR LAIPAAQLVLPYQMLLHAATRQA AGIRLQDQVVIIDEAHNLIDTITGMH SVEVSGSQLCQAHSQ LLYVERYG KRLKAKNLMYLKQILYLLEKFVAV LGGNIKQNPNTQSLSQTGTELKTIN DFLFQSQIDNINLFKVCVPSAPQMK HGHCR LNPKLVTQISNSDCPRVQRY CEKSMISRKLFGFTERYGAVFSSRE QPKLAGFQQFLQSLQPRTEALAAP ADESQASTLRPASPLMHIQGFLAAL TTANQDGRVILSRQGSLSQSTLKFL LLNPAVHFAQVVKECRAVVIAGGT MQPVSDFRQQLACAGVEAERVVE FSCGHVIPPDNILPLVICSGISNQPLE FTFQKREL PQMMDEVGRILCNLCG VVPGGVVCFFPSYEYLRQVHAHWE KGGLLGRLAARKKIFQEPKSAHQV EQVLLAYSRCIQACGQERGQVTGA LLSVVGGKMSEGINFSDNLGRCV VMVGMPFPNIRSAELQEKMAYLDQ TLPRAPGQAPPGKALVENLCMKAV NQSIGRAIRHQKDFASVLLDQRYA RPPVLAKLP AWIRARVEVKATFGPA IAAVQKFLQVYGTSLPLNHL SKLQD TFYPNTS NYAKGR |
| 5318 | 10815 | A | 5641 | 1 | 1668 | |
| 5319 | 10816 | A | 5642 | 947 | 2782 | GEEELWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR/ KKKGAE EEPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPY YGSR LAIPAAQLV VLPYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGSQL CQAHSQ LLYVERYGKRLKAKNL MYLKQILYLLEKFVAVLGGNIKQNP NTQSLSQTGTELKTINDFLFQSQIDN INLFKVQRYCEKSMISRKLFGFTER YGAVFSSREQPKLAGFQQFLQSLQP RTTEALAAPADESQASTLRPASPLM HIQGFLAALTTANQDGRVILSRQGS LSQSTLKFLLLNPAVHFAQVVKECR AVVIAGGT MQPVSDFRQQLACAG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VEAER\VVEF/SCGHVIPPDNILPLVICSGISNQPLEFTFQKRELPQMIFQEPKSAHQVEQVLLAYSRCIQACGQERGQVTGALLSVVGGKMSEGINFSDNLGRCVVMVGMPPFNIRSAELQEKMAYLDQTLPRAPGQAPPGKALVENLCMKAVNQSIGRAIRHQKDFASVVLDDQRYARPPVLAKLPWIRARVEVKATFGPAIAAVQKFHREKSASS |
| 5320 | 10817 | A | 5643 | 1143 | 3233 | GEEELWQGC SAGLPWLPAEPLCK* RREKPRFCAAYQRPLRGHAEKQAR\KKKGAEEEKPKRRRQEKQAACPFYNHEQMGLLRDEALAEVKDMEQLLALGKEARACPYRSRLAIPAAQLV VLSYQMLLHAATRQAAGIRLQDQVVIIDEAHNLIDTITGMHSVEVSGS\QLCQAHSQLLQYMERYGKRLKAKN LMYLKQILYLLEKFVAVLGGNIQK NPNTQSLSQGTGTELKTINDFLQSQINDINLFKVQRYCEKSMISRKLFGFT ERYGAVFSSREQPKLAGFQQFLQSLQPRTEALAAPADESQASVPQPASP LMHIEGFLAALTANQDGRVILSRQGSLSQSTLKFLLLNPAVHFAQVVKE CRAVVIAGGTMQPVSDFRQQLLACAGVEAERVVEFSCVFGPSLALTGH VIPPDNILPLVICSGISNQPLEFTFQKRELPQMMDEVGRILCNLCGVVPGGVVCFFPSYEYLRQVHAHWEKGGLL GRLAARKKIFQEPKSAHQVEQVLLAYSRCIQACGQERGQVTGALLSVVGGKMSEGINFSDNLGRCVVMVGMPPFNIRSAELQEKMAYLDQTLPRAPGQAPPGKALVENLCMKAVNQSIGRAIRHQKDFASIVLLDQRYARPPVLAKLPWIRARVEVKATFGPAIAAVQKVSPTFFFLRASPPRDHISHCLLSAQFHREKSASS |
| 5321 | 10818 | A | 5644 | 3 | 744 | |
| 5322 | 10819 | A | 5645 | 40 | 126 | |
| 5323 | 10820 | C | 5646 | 187 | 366 | MDERDSHCPYLLSSETTAKGTGLAESAGKEDPVELDSSLEARVRRRRPSTSMPLTSAPC* |
| 5324 | 10821 | A | 5647 | 1 | 382 | TADCAKPVPLAVVSLDSRYGQWESSIIHA\VTN*ASSSSSSSSSSSFVRVYPRFIEFIHFDIQSTGQ/RITSR*HPPR/DLRDALF*LNSLIPLVRTSSKSAARRP\GEAPRGTA VPGADPAGGTRPR |
| 5325 | 10822 | A | 5648 | 3 | 684 | QGPRAALGALFPCWAPGKYVHGVRAKHPRATARAPRGSP/LPPHRVSEKTIRVVVFHRRPAGPADPAPGPSRGHRGGAG/EPPTYSTPLMSLHRARLESSSTGSSFPADSAKPVPLAVVSLDSR*GQWESSIIHA\VTN*ASSSSSSSSSSSFVRVYPRFIEFLHFDIQSTGQ/RITSRQHPPR/DLRDALF*LNSRIPLVRTSSKSAARRR\GEAPRGTAAPGADPAGGP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5326 | 10823 | A | 5649 | 2 | 331 | |
| 5327 | 10824 | A | 5650 | 3 | 340 | |
| 5328 | 10825 | A | 5651 | 1 | 94 | |
| 5329 | 10826 | A | 5652 | 2 | 496 | ASMGCSPLLSLLSLLVGAWLKLGH*TAGHAGGAGKGDGALRPGGREPEAPLPASGMRLQPPAGEVALGAQGASPPCAFNFLLWNLSIQAQLRRVRGQGCSWRWLVLAQAIEELLGDPALVPTRRQPVGRAAPAPAASSLCCADPA GREVTQVVVVQVVVNSSS |
| 5330 | 10827 | A | 5653 | 3 | 997 | |
| 5331 | 10828 | A | 5654 | 3 | 131 | |
| 5332 | 10829 | A | 5655 | 112 | 289 | |
| 5333 | 10830 | A | 5656 | 35 | 5228 | LDPLGRMVMGIFANCIFCLKVKYLPQQQKKKLQTDIKENGKFSFSLNPQCTHIILDNADVLSQYQLNSIQKNHV HIANPDFIWKSIREKRLLDVKNYDPYKPLDITPPPDQKASSEVKTEGLCPDSATEEEDTVELTEFGMQNVEIPHL PQDFEVAKYNTLEKVGMEGGQEA VVVELQCSRDSRDCPFLISSHFLDD GMETRQFAIKKTSEDASEYFENYI EELKKQGFLREHFTPEATQLASEQ LQALLLEVMNSSTLSQEVSDLVE MIWAEALGHLEHMLLKPVNRISLN DVSKAEGILLVKAALKNGETAEQ LQKMMTEFYRLIPHKGTMPKEVNL GLLAKKADLCQLRDMVNV CETNL SKPNPPSLAKYRALRCKIEHVEQNT EEFLRVRKEVLQNHHSKSPVDVLQI FRVGRVNETTEFLSKLGNVRPLLHG SPVQNVGILCRGLLL PKVVEDRGV QRTDVGNLGSIGYFSDSLSTSIKYSH PGETDGTRLLLICDVALGKCMDLH EKDFSLTEAPPGYDSVHGVSQTASV TTD FEDDEFVYKTNQVKMKYIIF SMPGDQIKDFHPSDHTELEEYRPEF SNFSKVEDYQLPDAKTSSSTKAGLQ DASGNLVPLEDVHIKGRIDTVAQVI VFQTYTNKSHVPIEAKYIFPLDDKA AVCGFEAFINGKHIVGEIKEKEEAQ QEYLEAVTQGHGAYLMSQDAPDVF TVSVGNLPPKAKVLIKITYITELSILG TVGVFFMPATVAPWQQDKALNEN LQDTVEKICIKEIGTKQSFSLTMSIE MPYVIEFIFSDTHELKQKRTDCKAVI STMEGSSLDSSGFS LHGLSAAYLPR MWVEKHPEKESEACMLVFQPDLD VDLPDLANESEVIICLDCSSSMEGVT FLQAKEIALHALSLVGEKQKVNIQF GTGYKELFSYPKHITSNTAAAEFIM SATPTMGNTDFWKTLRYLSLLYPA RGSRNILLVSDGHLQDESLTLQLVK RSRPHTRL\FACGIGSTANRHVLRIL SQCGAGVFEYFNAKSKHSWRKQIE DQMTRLCSPSCHSVSVKWQQLNPD APEALQAPAQVPSLFRNDRLLVYGF IPHCTQATLCALIQEKEFCTMVSTTE |

WO 01/79449

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LQKTTGTMIHKLAARALIRDYEDGI LHENETSTEMKKQTLKSLIKLSKE NSLITQFTSFVAVEKRDENESFPDI PKVSELIKEDVDFLPYMSWQGE QEAVRNQSLLASSEWPELRLSKRK HRKIPFSKRKMELSQPEVSEDFEED ALGVLPAFTSNLERGRVEKLLDLS WTESCKPTATEPLFKKVSPWETSTS SFFPILAPAVGSYLTPTTRAHSPASL SFASYRQVASFGSAAPPRQFDASQF SQGPVPGTCADWIPQSASCPTGPPQ NPPSAPYCGIVFSGSSLSSAQAPLQ HPGGFTTRPSAGTFPELDSPLHFSL PTDPDPIRGFGSYHPSAYSPPHFQPS AASLTANLRLPMASALPEALCSQSR TTPVDLCLLEESVGSLEGSRCPVFAF QSSDTESEDELSEVLQDSCFLQIKCDT KDDSI PCFLEVKEEDEIVCTQHWQD AVPWTELLSLQTEGFWKLTPELG LILNLNTNGLHSFLKQKGIQSLGVK GRECLLDLIATMLVLQFIRTRLEKE GIVFKSLMKMDDPSISRNPWAFEAI KQASEWVRRTEGQYPSICPRLELGN DWDSATKQLLGLQPISTVSPLHRVL HYSQG |
| 5334 | 10831 | A | 5657 | 10 | 82 | |
| 5335 | 10832 | C | 5658 | 189 | 396 | MVHPAGPLASQXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXELWLHHLSSSS * |
| 5336 | 10833 | C | 5659 | 54 | 485 | MXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXRPEDFATYYCQ QNYISPLTFGGGKVEIXRTVAAPS VFIFPPSX* |
| 5337 | 10834 | A | 5660 | 5 | 417 | |
| 5338 | 10835 | A | 5661 | 3 | 398 | |
| 5339 | 10836 | C | 5662 | 12 | 451 | MXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXFSSYYCQ QSYSVPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQ* |
| 5340 | 10837 | A | 5663 | 3 | 679 | AWWNSETPAQLLFLLLWLPYTS EIVLTQAPGTLSPGERATLSCRAS QTIGSTYLAWYQQRPGQAPRFLIYG ASSRATGIPDSSSSSSSSSSSSSS SSSSSSSSSQYYTSPLTFGGGKTV EIRRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYSLSSST LTLSKADYEKHKVYAICEVTHQG |
| 5341 | 10838 | B | 5664 | 94 | 321 | XDRVITTCQATQDIGNYLNWYQHK PGKAPNLLIYDASNLETGVPSRFSG RSGTHFTFTISSLQPEDATYYCQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | YX* |
| 5342 | 10839 | A | 5665 | 3 | 764 | AWLESISPTMRVPAQLLGLLLWIP GSVADIMMTQTPLSLSVSPGQSASIS CKSSQSLLHSDGKTHVYWYLQKPG QSPQLLIYEVSSRFSGVPDRFSGSGS GTDFTLKITRVEAEDVGYYCQQY NSYLLFTFGPGTKVDIKRTVAA\PSV FIFPPASDEQLKSGTASVVCLL\NNFL F\RRRAKVQWEGGINALQSGNSQEC VTE\QDSKGSTYSL\SSTLTVSKADY EKHKVYACEVTHQGLSSPVTKSFN RGEC |
| 5343 | 10840 | A | 5666 | 1 | 534 | RRPRREPWKPQRSFSSSCYS/ELPDT TGEIVLTQSPGTLSPGERATLSCR ASQSVSNNYLA WYQQKPGQAPRLI IYDTSSRATGIPDRFSGSASGTDFTL TISRLEPEDFAVYYCQQYGSSPPMY TFGQGTKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKV QW |
| 5344 | 10841 | A | 5667 | 184 | 621 | LHECISVLFPISDTTGEIVLTQSPATL SLSPGERATLSCRASQSVNNNYLA WYQQKPGQPRLIYDASNRTGIP ARFSGSGSGTEFTFHSAACSLKDF CSLFTVQQLINWASDSPLGQGTRL GD/IKRTVAAPSVFIFPPSDE |
| 5345 | 10842 | A | 5668 | 156 | 364 | |
| 5346 | 10843 | A | 5669 | 2 | 2143 | SSDGSWWTGFQWREWRQAGRSVN SWDNPKEVRASSKDKSRGSIQEA MRMQSSAKLLCSAWTLAYSIAVRT LSSDSEGQPPLVIHRQTGSGEDLQQ TPTDLQLRVLTIIRKTNKQKGHPHQ NPISRRQEITKIRAEKKIETQKPFK KINESRSWFFEKINKIDRLARLIKK KIEKNQIDAIKNDKGNITTNPTIEQT TIREYYKHL YANKLEHLEEMDKFL DIYTLPRLNQEEVESVNRPTGSEIE AJINSLPTKKSPGPDRFTAELYQRYK EELVPFLLKLFQSIEKEGILPNSFYEA SIILISKPGRDTTKKENFRPISLMNID AKILNKILANQIQQHKKLIHHHQV GFIPGMQGWFNILKSINVIHHINRTK DKNHMIISIEAEKAFDKIQPFMLKT LNKLGIDGTLYLTKIIRAIYDKPTA NIILNGQKLEAFPFGTGRQGCPLSP LLFNIVLEALARAIQEKEIKGIQLG KEDVKLSLFADDMIVYLENPIVSAQ NLLKLISNFSEVSGYKINVOKSQAFI YTNNRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIVKMAIL PKTLNQKFSYWFRVNHYIHQRTP LKETEFTNTIATLYNGASP/RTAPKST GTNGHQASGLPRF*RIAFCSALVKS KRKLYQGYLPGQTDREEGVSWCP GGP |
| 5347 | 10844 | A | 5670 | 1 | 2781 | |
| 5348 | 10845 | A | 5671 | 1 | 2988 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 5349 | 10846 | A | 5672 | 1 | 3516 | |
| 5350 | 10847 | A | 5673 | 1 | 2850 | |
| 5351 | 10848 | A | 5674 | 1 | 2850 | |
| 5352 | 10849 | A | 5675 | 1 | 3087 | |
| 5353 | 10850 | A | 5676 | 1 | 3111 | |
| 5354 | 10851 | A | 5677 | 1 | 2742 | |
| 5355 | 10852 | A | 5678 | 1 | 3474 | |
| 5356 | 10853 | B | 5679 | 1 | 3264 | MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHIVGSKALLSKC KRTEITNCLSDHSAIKLELRIKNLTQ NRSTTWKLNQLLNDYWAHNEMK AEIKMFFETNENKDDTYQNLWDTF KAVCRGKFIALNAHKRKQERSKIDT LTSQLEKEKQEQTTHSKASRRQEIT KIRAELEKETQKILQKINESRSWFF ERINKIDRPLARLIKKKREKNQIDAI KNDKGDITTDPTIEQNTIREYYKHL YTNKLENLEEMDKFLDTYTLPRLN QEEVESLNRPTGPEIVAINSLPTKK SPGPDGFTAKFYQRYKEELVPFLK LFQSIEKEGILPNSFYEASILPKPGR DTTKKENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGMQGW FNIHKSINVIQHINRPKDKNHMISID AEKAFDKIQPFMLKTLNKLIGIDGT YFKIISAIYDKPTANIILNGQKVEAFP LKTGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNIPCS WVGRJIVKMAILPKVIYRFNAIPIK LPMFTFFTELEKTTLKFIWNALITKSI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRDIDQWNRTEPSEIT PHIYNLIFDKPEKNKQWGKDSLNN KWCWENWLAICRKLKLDPLTPYT KINSRWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKQTTIRVNRQ PTKWEKIFATYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKKHMKKCSSSLAIREMQIK TTMRYHLTPVRMAIHKSGNNRTW EYNILCSLVPLLCSSLWLHLTDHHL KEDRTKHLTASDNLEKTELSRWKE RALLYEHRVLRPAIDSQHSCAPRRJ QGHLVCGSDLTGFMDDVAVILIDVS PF* |
| 5357 | 10854 | A | 5680 | 1 | 3780 | |
| 5358 | 10855 | A | 5681 | 1 | 3290 | MGELITPLSTLDRSTRQKVNKDTQE LNSALHQGDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHILGSKALLSKCKR TEITNYLSHSAIKLELRIKNLTQN RSTTWKLNLLNDYWIHNEMKAE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | IKMFFETNENKDDTTYQNLWDAFKA VCRGKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDTIKND KGDIA TNPTIEIQT TIREYYKHL YAN KLENLEEMDKFLDTYTLPRLNQEE VESLNR PITGAEIVAIINSLPTKKSPG PDGFTAESYQRYKEELVPFLLKLFQ SIEKEGILPNSFYEASILIPKPGRDTT KKENFRLISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQGWFN RKSINVIQHINRAKDKNHMISIDAE KAFDKIQPFMLKTLNKL GIDGTYF KIIRAIYDKPTANIHLNGQKLEAFPLK TGTRQGCPLSPLL FNIVLEVLARAIR QEKEIKGIQSGKEEVKLSLFADDMI VYLENPIVSDQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNIPCSW VGRISIVKMAILPKVIYRFSAIPIKLP MTFFTELEKTTLKFIWNQKRARIAK AILSQKNKAGGITLPDFKLYYKATV TKTARYWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRKLKLD PFLTPY TKINSRWIKDLNIRPKTIKTLEENLG STIQDIGMGKDFMSKTPKAMATKD KIDIWDLIKLSFCTAKETTIRVNGQ PTKWEKIFATYSSDKGLISRICNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYA AAKKHMKKCSSSLAIRQM QIK TTMRYHLTP/VKFRSTSHQSP*REAR GPGPLANAGSPGLRQIPETCHLKH PLGM LLLSHHSALSATHNPTPCKLQS SVMFTTSAAMLSDPWGLRKGLGRE MFSCKTTEGNQLEAGAAEQSLYAL PKPSDLQT |
| 5359 | 10856 | A | 5682 | 1 | 3780 | |
| 5360 | 10857 | A | 5683 | 1 | 2877 | |
| 5361 | 10858 | A | 5684 | 1 | 3126 | |
| 5362 | 10859 | A | 5685 | 3 | 3244 | |
| 5363 | 10860 | A | 5686 | 1540 | 3288 | SSGLHPWDARLVQYTQINKCNPAY KQSQRQKPHYYYQLEAFPLKTGTRQ QPFMLKT/LYSIVLEVLARAIRQKKE IKGIQLGKEEVKLSLFADDMIVYLE NPIVSAQNLLKLISNFSKVSGYKINV QKSQAFLYTKNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNIPCSWVGRIN IVKMAILPKVIYRFNAIPIKLPMTFFT ELEKTTLKFIWNQKRARIAKSILSQK NKVGGITLPDFKLYYKATVTKTAW YWYQNRVIDQWNRKEPSEITPHTY NYLIFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLD PFLTPYTKINS RWIKDLNVRPKTIKTLEENLGITI QD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | IGMGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRQPTT WEKIFTTYSSDKGLISRIYNELKQIY KKKTNNPIKKWVKDMNRHFSKEDI YAAKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIHKSGNNRCWRG CGEIGTLLHCWWDCCLVQPLWKS VWRFLRDLELEIPFDPAIPLLG IYPND YKSCCYKDTCT |
| 5364 | 10861 | A | 5687 | 1182 | 3406 | YQSLAETQPKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQVGFIP GMQGWFNIRKSINVTQHINRAKDK NHMIISIDAEKAFDKIQQPFMLKTLN KLGIDGTYFKIIRAIYDNPTANIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFADNMIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYTNNR QTESQIMSQLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDTNK WKNIPCSGVEGRNIVKMAILP/KELE KTTLKFIWNQKRAHIAKSILNQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEITQHIYSYLI FDKPEKNKQWGKDSL FNKWCWEN WLAICRKLKLDPFLTPYTKINSRWI KDLNVRPKTIKTLEENLGITIQDIGM GKDFMSKTPKAMATKDKIDKWDL VKLKSFCTAKETTIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDMNRHFSKEDIYAA KKHMKKCSSSLAIREMQIKTTMRY HLTPVRMAIHKSGNNRCWRGCGE TGTLHCWWDCCLAQPLWKS VWR FLRDLELEIPFDPAIPLLG IYPNDYKS CCYKDTCTRMFIAALFTIAKTWNQP KCPTIIDWIKKMWHIYTMEYYAAIK NDEFVSFVGTWMKLEIILSKLSQEQ KTTHRIFSLIGGN |
| 5365 | 10862 | A | 5688 | 1 | 7578 | |
| 5366 | 10863 | A | 5689 | 16775 | 19999 | KMIKGISPPIPQKYKTTIREYYKHLY ANKLENLEEMDKFLDTYTLPRLNQ EEVESLNRSTGSEIEAII NSLPTKKSP GPDGFTAIFYQRYKEELVPFLKL FQSIEKEGILPNSFYESSILIPKGRDT TKKENFRPISPLMNI DAKILNKILA KRIQQHIKKLMHHDQVGFIPGMQ GWFNIRKSINVIQHINRAKDKNHMIIS IDAEKAFDKIQQPFMLKTLNKL GIDGTYFKIIRAIYDKPTANIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFA DDMIVYVENPIVSAQNLLK LISNFSKVSGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIKYL GIQLTRDVKDLFKENYKPLLKEIKED TNKWK NIPCSWVGRINTVKMAILPK VIYRFNAIPIKLPMPPFTELEKTTLK FIWNQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KRARIAKSILRQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNLYIFHKPEKNKQ WGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNVRPKTI KMLEENLGITIQDIGMGKDFMSKTP KAMATKDKIDKWDLIKLKSFCTAK ETTITVNRQPTKWEKIFATYSSDKG LISRIYNELKQIYK\KKTNNPIKKWA RDMNRHFSKEDIYAAKKHMKKCSS SLAIREMOIKTTMRYHLTPVRMAII KKSGNNRSWYFEKINKIDRLLARLI KKKREKNQIDAIKNDKGDITTDPTTEI QTTTREYYKHL YANKLENLEEMDK FLDTYNLPRLKQEEVESLNRPIRGSE IVAIINSLPTKKSPGPDGFTAIFYHR YKEELVPLLLKLFQSIEKEVILPNSF YEASIIIPKPDRDTAKKENFRPISLM NIDAKILNKILANRIQQHIKKLIHHD QVGFIPGMQGWFNIRKSVNVIQHIN RTKDKNHMUISIDAEKSFDKIQQHF MLKTLNKL GIDGSYLKIRATYDKP TANIILNGQKLEAFPLKTGTRHGCP LSPLLFNIVLEV LARAIRQEKEIKGIQ LGKEEVKLSLFIDDMIVYLENPIISA QNLLKLISNFSSLRIQNQCTKITSILV HQ |
| 5367 | 10864 | A | 5690 | 78 | 308 | |
| 5368 | 10865 | A | 5691 | 1 | 611 | GASLGGFLAQKFAEYTHKSPRVHSL ILCNSFSDTSIFNQTWTANSFWLMP AFMLKKIVLGNFSSGPVDPMMADA IDFMVDRLES LGQSELASRLTLNCQ NSYVEPHKIRDIPVTIMDVFDQSAL STEAKEEMVQA\YPNARRAHLKTG GNFPYLCRSAEGNLMVQIHL LQFH GTKYAAIDPSMVSAEELEVQKGS L GISQEEQ |
| 5369 | 10866 | A | 5692 | 3 | 301 | |
| 5370 | 10867 | A | 5693 | 75 | 361 | |
| 5371 | 10868 | A | 5694 | 3 | 356 | |
| 5372 | 10869 | A | 5695 | 1 | 583 | SPLAAKSPPSLHLL E/AFKNITSSSPE RHIFGEDRVVSEQPQVGTLEERN DV VEALTGSAASRLRGGTSSRRLSSTP LPKAKRSLESEMYLEGLGRSHIASP SPCPDRMPLPSPTESRHSSSIPPVSSP PEQKVGLYRRQTELQDKSEFSDVD KLAFKDNEEFESSFECVDQKQIEEQ KEEEKIREQQVKERRQR |
| 5373 | 10870 | A | 5696 | 306 | 4412 | RLMMAQSNMFTVADVLSQDEL RK KLYQTFKDRGILDTLKTQLRNQLIH ELMHPVLSGELQPR SISVEGSSLLIG ASNSLVADHLQRCGYEYSLSVFFPE SGLAKEKVFTMQDLLQLIKINPTSSL YKSLVSGSDKENQKGFLMHFLKEL AEYHQAKESCNMETQTSSTFN RDS LAEKLQLIDDQFADAYPQRIKFESL EIKLNEYKREIEEQ LRAEMCQKLKF FKDTEIAKIKMEAKKKYEKELTMF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QNDFEKACQAKSEALVLREKSTLE RIHKHQEIETKEIYAQRQLLLKDMD LLRGREAELKQRVEAFELNQKLQE EKHKSITEALRRQEQNIKSFEETYDR KLKNELLNFHRLHGVCLALGILI*L WQVLEFGGSSPQECFYFLLLEPKGQL VTAGKGK*NCENVPFGLANPDIMLL AVGSQDCA*SLSTKVLTLVGGGQM VQVDWK*PSDYHLGLSLLCAV*I*F TPLLFVSVETN*KVIAFSK*PYDNTT LHFV*LSFGTQFIGSRKGFTGHFMFR GYIPGFSIEDFEVYKLSCLAPSGAPV P*ISSCTDNSLSRKMPEELIFSHSDS\ RYQLELKDDYIIRTNRLIEDERKNK EKAHLQEELIAINSKKEELNQSVN RVKELELELESVKAQSLAITKQNHM LNEKVKEMSDYSLLKEEKLELLAQ NKLLKQQLLESRNENLRLNRLAQ APELAVFQKELRKA EKAI VVEHEEF ESCRQALHKQLQDEIEHSAQLKAQI LGYKASVKSLTTQVADLKLQLKQT QTALENEVYCNPQKQSVIDRSVNGLI NGNVVPCNGEISGDFLNNPFKQENV LARMVASRITNYPTAWVEGSSPDS DLEFVANTKARVKELQQEAERLEK AFRSYHRRVIKNSAKSPLAAKSPPS LHLLEAFKNITSSSPERHIFGEDRVV SEQPQVGTLKEERNDVVEALTGSE ASRLRGGTSSRRLSSTPLPKAKRSL ECEMYLEGLGRSHIASPSPCPDRMP LPSPTESRHSLSIPPVSSPPEQKVGLY RRQTELQDKSEFSDVDKLA FKDNE EFESSFEFNSFNENTLTSKYVAKW LCWELHRILLGKGAPSYFGFSSRAP VSCPHTALPFFVLVLLLRTHGTIVPH AAAGNMPRQLEMGGLS PAGDMSH VDAAAA AVPLSYQHPSVDQKQIEE QKEEEKIREQQVKERRQREERRQSN LQEVLERERRELEKLYQERKMIEES LKIKIKKELEMENELEMSNQEIKDK SAHSENPLEKYMKIQQEQDOESAD KVPVPWAGQSVGGGHPGLPWLNFL GRESVFSIEDKKSSKMMVQEGSLVD TLQSSDKVERHCIDPLWRTQQQGTI LEAETGPSPDIEPASAFLDLRLPSL |
| 5374 | 10871 | A | 5697 | 3 | 721 | |
| 5375 | 10872 | A | 5698 | 3 | 265 | |
| 5376 | 10873 | A | 5699 | 2 | 216 | |
| 5377 | 10874 | A | 5700 | 3 | 268 | |
| 5378 | 10875 | A | 5701 | 2 | 465 | |
| 5379 | 10876 | A | 5702 | 1 | 196 | |
| 5380 | 10877 | A | 5703 | 2 | 213 | |
| 5381 | 10878 | A | 5704 | 1 | 438 | LQTWGPKQVC/SFFRRGGFEERVLL KNIRENGITGALLPCLDESRFENLGV SSLGERKKLLSYIQRLVQIHVDTMK\ VGYLAGCLVHALGEKQPELQISERD VLCVQIAGLCHDLGHGPF SHMFDG RFIPLARPEVKWTVCIHTVNSQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5382 | 10879 | A | 5705 | 2 | 1925 | |
| 5383 | 10880 | A | 5706 | 330 | 590 | |
| 5384 | 10881 | A | 5707 | 3 | 139 | |
| 5385 | 10882 | A | 5708 | 2 | 126 | |
| 5386 | 10883 | A | 5709 | 1 | 157 | |
| 5387 | 10884 | A | 5710 | 85 | 489 | EKPLRWDSHLSCMLCWQAGFEAEQ KVS GSSRKLAISHALLEMLTPPPAG AMIPPPPSLPGPPRPGMMPVAPHMG GPPMMPMMGPPPPGMMMPVGPAPG MRPPMGGHMPMMPGPPVTRPPARP MMVPTRPGMTRPDR |
| 5388 | 10885 | A | 5711 | 235 | 874 | VVRRSGFLFCLFVFLSSMNSASVD GHLSGCRLFLFLSPLFRFYCDYCDT/ YLSPHDSPSVRQTHCSGK\KHIENV KDYYQK\WMEK\QSQSL\DKTTAA FQQGKIPPTPFSAPPPAGA\MIPPPK /SFPGPPSPLV*MPKHPHMGGPFPW MPMMGPSFLLGDGWPVG\PASGEL RP\PMG\GHYCQLIAWGPPMDVGPS CPFH*WCPLGPGMTRPDR |
| 5389 | 10886 | A | 5712 | 2 | 406 | FRSPADPPVHCDKE*VLEVQREDED YHDSAKEKDEEDDSITRLLEFELEA YSLSHNDYDGIKKLLQQLFLKAPVN TAE\TNFLIQNHIGSVIKHTDVS*D SIDDMDDEDEAFGFISLLNLPDRKGT QCGEQIQE |
| 5390 | 10887 | A | 5713 | 3 | 379 | AVERGVPHPFDSPVQRDEEEKEVD TEDDDDDSDQEKDDEDNALDEEV NIEF\EAYSLSYNDYDGIKKLLPQLFI AAPVNTAKLPDLLIQNHIGSAIKQ TDVSEDSNDDMDEEEASYSIDRLYN |
| 5391 | 10888 | B | 5714 | 65 | 188 | MWGFRIPADALIQRDEEEKEVLNE DEDDDDSDKEKDEEDRX* |
| 5392 | 10889 | A | 5715 | 3 | 365 | |
| 5393 | 10890 | A | 5716 | 3 | 356 | |
| 5394 | 10891 | A | 5717 | 1 | 168 | |
| 5395 | 10892 | A | 5718 | 281 | 422 | |
| 5396 | 10893 | A | 5719 | 1 | 107 | |
| 5397 | 10894 | A | 5720 | 3 | 291 | |
| 5398 | 10895 | A | 5721 | 1 | 1260 | WRTAAFWAFTVFLGDIILLTDVVIH EDQWIGETVLQSTFSSQLNLGSYS SIQPEEYSSVCEVVLQDLLAYVSS KHSYLRDLPPRQPQRVNSIDFV\EL EHLQPDVLVHGSTKELLDFITL\TEG S/VYSYRGQKQ\KKVMLTV\DQAQG QHYALVLWGSWGQPGYPQLQRKK GYIWEFKYLFVQCNYTLENLELHTT PWSSCECLFDDDIRAITFKAKFQKS APSFVKISDLATHLEDKCSGVVLIK AQISELAFPITASQKIALNAHSSLKSI FSSLPNIVYTGCAKCGLELETDENRI YKQCFSCLPFTMKKIYYR\PALMTAI DGRHDVCIRVESK\IEKILLNISADC LNRVIVPSSEITYGMVVADLFHSL AVSAEPCVLKIQSLFVLDENSYPLQ QDFSLLDFYPDIVKHGANARL |
| 5399 | 10896 | A | 5722 | 122 | 390 | TFCVRSGLLDFAFPEPWGWGEKWK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NWPESLEVWVLVLA VPLTHCDLGI LCCEDISQVLHVSQQI*PTRPGKR*L LGCAEVVLSSSASPG |
| 5400 | 10897 | A | 5723 | 605 | 902 | |
| 5401 | 10898 | A | 5724 | 116 | 470 | |
| 5402 | 10899 | A | 5725 | 1 | 9786 | |
| 5403 | 10900 | A | 5726 | 10996 | 13825 | MLTLRTRRS DGKMKSGFILGLSRAR SSFPM TTKRATPGHCRDPLEGLRF LKNILPVYDKSLWDFLKL DVTTSIG RRQH LRVSTAFVYTKNPNGYSFSIP VKVLADKFITPGLKLNDLNSVLVM PTFHVPFTDLQVPSCKLD FREIQIYK KLRTSSFALN LPTLPEVKFPEVDVLT KYSQPEDSLIPFFEITVPESQLTVSQF TLPKSVSDGIAALDLNAVANKIADF ELPTIIVPEQTIEIPSIKFSVPAGIVIPS FQALTARFEVDSPVYNATWSASLK NKADYVETSLDSTCSSTVQFLEYEL NVLGTHKIEDGTLASKTKGTLAHR DFSAEYEEDGKFEGLOEWEGKAHL NIKSPAFTDLHLRYQKDKKGISTSA ASPAVGTVGMDMDEDDDFSKWNF YYSPQSSPDKKLTIFKTEL RVRESDE ETQIKVNWEEEAASGLLTSLKDNVP KATGVLYDYVNKYHWEHTGLTLR EVSSKLRRNLQNNAEWVYQGAIRQ IDDIDVRFQKAASGTTGT YQEWKD KAQNLYQELLTQEGQASFQGLKDN VFDGLVRVTQKFHMKVKHLIDSLID FLNFRFQFPGKPGIYTREELCTMFI REVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISMYREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFDPSIVGWT VKY YELEEKIVSLIKNLLVALKDFHSEYI VSASNFTSQLSSQVEQFLHRNIQEY LSILTDPDGKGKEKIAELSATAQEII KSQAIA TKKIISDYHQQFRYKLQDF SDQLSDYYEKFIAESKRLIDLSIQNY HTFLIYITELLKKLQSTTVMNPYMK LAPGELTIL |
| 5404 | 10901 | A | 5727 | 3 | 182 | |
| 5405 | 10902 | A | 5728 | 2 | 221 | |
| 5406 | 10903 | A | 5729 | 577 | 722 | |
| 5407 | 10904 | A | 5730 | 3 | 176 | |
| 5408 | 10905 | A | 5731 | 1 | 496 | LLGVAPSRAFQEEILR/DRASFHE/RP NLFALKHPTSKAECTAEKCYRVTK GRGIFPSGSPFKSVTLEDGKTFIPGQ GNNA YVFPGVALGVIAGGIRHIPDEI FLLTAEQIAQEVFEQHL SQGRLYPP LSTIRDVSLRIA IKVLDYAYKHNLDS YTWPK EAMNVQTV |
| 5409 | 10906 | A | 5732 | 228 | 448 | |
| 5410 | 10907 | A | 5733 | 3 | 1877 | EGEDRGLPRTMGAALGTGTRLAPW |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PGRACGALPRWTPPTAPAQGCHSKP GPARPVPLKKRGYDVTRNPHLNKG MAFTLEERLQLGIHGLIPPCFLSQDV QLLRIMRYYERQQSDLDKYIILMTL QDRNEKLFYRVLTSDVEKFMPIVYT PTVGLACQHYGLTFRPRGLFITIHD KGHLATMLNSWPEDNIKAVVVTDG ERILGLDGLGCYGMGIPVGKLALYT ACGGVNPQQCLPVLLDVGTNNEEL LRDPLYIGLKHQRVHGKAYDDLLD EFMQAVTDKFGINCLIQFEDFANAN AFRLLNKYRNKYCMFNDDIQGTAS VAVAGILAAALRITNNKLSNHVVFQ GAGEAAMGIAHLLVMALEKEGVPK AEATRKIWMVDSKGLIVKGRSHLN HEKEMFAQDHPESNSLDEVVRLVK PTAIIGVAALAEA\FTEQILRNMAF\ RRAPIIFALSNNPPRKAECTA\EKCYR VTEGPRGFFASG\SPF*GVLIWEMGK TFIPGGRGNNA\YVFPG\IATG\IA\ GGIRHIP\DEIFLLDSRAKLPQEVSEQ HLSQGRLYPPLSTIRD\SLRIAIVL DYAYKHNLVSYYPEPKDKEAFCKI PGSYTPDYDSFYT/VDSYIWAQGKA MNVQTV |
| 5411 | 10908 | A | 5734 | 14 | 304 | |
| 5412 | 10909 | A | 5735 | 3 | 413 | |
| 5413 | 10910 | A | 5736 | 2 | 328 | |
| 5414 | 10911 | A | 5737 | 3 | 472 | VTEFAKTCVADESAENCCKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLOHKDDNPNLPRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKCASLQKFGERAF KA\VARLSQRF |
| 5415 | 10912 | A | 5738 | 1 | 2975 | MKWVTFISLLFLFSSAYSRGVFRRT PLGPASSLPQSFLKCLEQVRKIQGD GAALQEKLCA TYKLCHPEELVLLG HSLGIPWAPLSSCPSQALQLAGCLS QLHSGFLYQGLLQALEGISPELGPT LDTLQLDVADFATTIWQQMEELGM APALQPTQGAMP AFASAFQRRAGG VLVASHLQSFLEVSYRVLRLAQP GGGDAHKSEVAHRFKDLGEENFKA LVLIAFAQYLQQCPFEDHVKLVNEV TEFAKTCVADESA*/ENCCKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLOHKDDNPNLPRLVRP EVDVMCTAFHDNEETFLKKYLYEI AR\RHPTCIAPELLFFAKRYKAAFT\ ECCQAADKAACL\LPKLDEL\RDEG KASSAKQRLKCASLQKFGRKSFSK HGA VARLSQEVFPKLEFCQEVSVQ *WTGL*PKFPHGNC\CHGRSCFECC WMDR/RRDLWPKYILWKIQDFDLP S*TRDCC\EKPLVWGKIPTCICRK WEN*WRLPGLDFAFH*ACLIFVWK VKGCFGQNYCLRAKDVFPGACFLY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | \DYARRAS*FTLFVPAEDLPRTYET TLEECCAAADPHECYAKVFDEFKPL VEEPQNLIKQNCLEFEQLGEYKFQN ALLVRYT\KKVPQVSTPTLVEVSRN LGKVGSKCCKHPEAKRMPCAEDYL SVVLNHLCLVHEKTPVSDTVTKCC TESFVNTPPCFSALEVDETYVPKHF NAETFTFHAHISTLSQKERQIKKQT ALVDLVKHKPKATKEQLKAVMDD FAAFVEKCKKADDKETCFAEEGKK LVAASQAALGLTPLGPASSLPQSFL LKCLEQVRKIQGDGAALQEKLCAT YKLCHPEELVLLGHSLGIPWAPLSS CPSQALQLAGCLSQLHSGFLYQGL LQALEGISPELGPTLDTLQLDVADF ATTWQQMEELGMAPALOPTQGA MPAFASAFQRRAGGVLVASHLQSF LEVSYRVLRHLAQP |
| 5416 | 10913 | A | 5739 | 132 | 918 | |
| 5417 | 10914 | A | 5740 | 59 | 335 | |
| 5418 | 10915 | A | 5741 | 219 | 642 | KGWFLGAFHKLKTMKHLLLLTMG C/VF*VKSQGVNDNMEEGFFSARGHR PLDKKREEAPSLRPAPPISGRWAI RASSQPKQLATSKGK*ERKSPWIAG KVVFSRLDPDLG\VVCCSLQGCSVC QGGFFLTTRGKGPFQELVV |
| 5419 | 10916 | A | 5742 | 1 | 359 | |
| 5420 | 10917 | A | 5743 | 1 | 322 | |
| 5421 | 10918 | A | 5744 | 2 | 862 | FVDGKLHGRGSTDDKGPVAGWINA LEAYQKTGQEIPVNVRFCLGEMEE SGSEGLDELIFARKDTFFKDVDYVC ISDNYWLGGKKPCITYGLRGICYFFI EVECSNKDLHSGVYGGSVHEAMTD LILLMEEHKL YDDIDFDIEEFAKDV GAQILLHSHKSHLHLDLLPVVVRLL GQALFHTAHFPDNIPSSSKDILMHR WRYPSSLHGIEGAFSGSGAKTVIP RKVVGKFSIRLVNMTPEVVGEQA CGAGTRESMSSLGYPSRAEDDSGLS ALPSQPQPFILYAT |
| 5422 | 10919 | A | 5745 | 455 | 601 | SLAICGSCPFLKTFTITGVFLSSL*YD PSKPALTGRMILSQFVLLNKK |
| 5423 | 10920 | A | 5746 | 25 | 458 | |
| 5424 | 10921 | A | 5747 | 3 | 396 | |
| 5425 | 10922 | A | 5748 | 2 | 797 | AGPAALGGAGLCRAADAGLCSAGC GFVKVVKNA YFKRYQVKFRRR\R KGKT\DY YARKRLVIQDKNKYNT KYRMIV\RV TNRDII CQIAYARIEGD MIVCAA*CTPNLPKYGV\KVGLTNY AAA\CT\GLLL\ARRL\LNRFG\MDN \YEGQV\EVTG\DEYNVESIDWSAQ GAF\TCY\LDAGLAR\TT\TG\NKVFG\ ALKGMLWMGGLSIPHSSKRFLGLSI PHSTK*ILGYDSENKEFNAEVRKHI MGQKFADDLHCLIEEDENASKK |
| 5426 | 10923 | A | 5749 | 172 | 333 | |
| 5427 | 10924 | A | 5750 | 2 | 282 | SLSREVQRQMHLVFFSKNKLKAGY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *-Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LMSVESSE/CFLEEVG/SQALVAGSY MPPSTVLQQIDS/VANADIINAAKKF VS/GQKSMAAGGNLGHHTPLVDEL |
| 5428 | 10925 | A | 5751 | 813 | 998 | |
| 5429 | 10926 | A | 5752 | 1 | 1418 | MKLLTRAGSFSRFYSLKVAPKVKA TAAPAGAPPQPQDLEFTKLPNGLVI ASLENYSPVSRIGLFIKAGSRYEDFS NLGTTHLLRLTSSLTTKGASSFKITR GIEAVGGKLSVTATRENMAYTVEC LRGDVDILMEFLNVTTAPEFRRWE VADLQPQLKIDKAVAFQNPQTHVIE NLHAAA YQNALANPLYCPDYRIGK VTSEELHYFVQNHFTSARMALIGLG VSHPVLKQVAEQFLNMRGGLGLSG AKANYRGGEIREQNGDSL VHAAFV AESAVAGSAEANAFSVLQHGPRLV GHHVKSGQQQPPAHLHQ\AVAKA\T QQPFDVSAFNASYSDS\GLFG\YTIS QGHQLAGDCIK\AA\YNQVKTIA\QG NLSNTDV\QAAQEPS*KAGIP*WSV ESSE\CFLEEVVRVPRALVAGSYMPP VHSSFQQI/DSPKRGWGGAKMPDII NGGKRSSFVSGPEVQWAASLENLGT LHLFV |
| 5430 | 10927 | A | 5753 | 150 | 355 | |
| 5431 | 10928 | A | 5754 | 2 | 388 | FLFFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVVGQAGLELLAPS DPPA |
| 5432 | 10929 | C | 5755 | 197 | 415 | MLYVVGLEPHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF* |
| 5433 | 10930 | A | 5756 | 764 | 1079 | KGVLFFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA |
| 5434 | 10931 | A | 5757 | 213 | 383 | |
| 5435 | 10932 | A | 5758 | 1 | 981 | |
| 5436 | 10933 | A | 5759 | 124 | 354 | |
| 5437 | 10934 | A | 5760 | 2 | 646 | CGGIHGNHTFKMALNQFSDMSFAEI KHKYLWSEPQNCSATKSNYLRTG PYPPSVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALESAIAIATGKMLS LAEQQLVDCAQDFNNHGCQGGPLS QAFEYILYNKGIMGEDTYPY\QGKD GYCK\FQP\GKAIGFVKDVANITYD EEAMVEAVALYNPVSFAFEVTQDF MMYRTGIYSSTSCHKTPDK |
| 5438 | 10935 | A | 5761 | 1 | 218 | |
| 5439 | 10936 | A | 5762 | 272 | 364 | |
| 5440 | 10937 | A | 5763 | 1 | 1956 | |
| 5441 | 10938 | A | 5764 | 105 | 533 | |
| 5442 | 10939 | A | 5765 | 292 | 568 | |
| 5443 | 10940 | A | 5766 | 1 | 279 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 5444 | 10941 | A | 5767 | 3 | 352 | |
| 5445 | 10942 | A | 5768 | 375 | 485 | TPGLK*FSHLDLLNCWDYRCETVH LAEIAQVSEKQI |
| 5446 | 10943 | A | 5769 | 3 | 221 | |
| 5447 | 10944 | A | 5770 | 793 | 1039 | SFSFTFKMLSGRRETFFFGRFFWF VV\VFFFLAGRGSFALVAQAGVQ WRDLRSLQPPPRGFRFFCLSLPGA CGPRYLGG |
| 5448 | 10945 | C | 5771 | 33 | 334 | MSDSGKSSPVAHSILWTWGRDSDA YRDKQHILWPKRADCTESYPRVPA GGELPTYFLPPENKGLRIHELNSDD YSTEEEAQTPDCSITDFTRRHTLSYL V* |
| 5449 | 10946 | A | 5772 | 194 | 593 | |
| 5450 | 10947 | A | 5773 | 1 | 877 | |
| 5451 | 10948 | A | 5774 | 2 | 352 | |
| 5452 | 10949 | A | 5775 | 3 | 726 | EQEVVDYDPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKKHPEA KRMPCAEDYLSVVLNQLCVLH/EK TPVSDRVTKCCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKKHPEA KRMPCAEDYLSRGPEPVMCVA |
| 5453 | 10950 | A | 5776 | 4274 | 5255 | HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLQHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVDFTT KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIIDFVLV SNIILPKFNHLCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*LÆSLEF GGSGENVVDYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFTTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSLWDLGT LSV |
| 5454 | 10951 | A | 5777 | 15 | 218 | |
| 5455 | 10952 | A | 5778 | 141 | 318 | |
| 5456 | 10953 | A | 5779 | 1 | 290 | TMSLNRLQEFGTSLVTLDAPHILPE GDELLEENQEGCFS*SFLFATNATL GPRLWSPWLASGLSLPEACASPKH AAQGPHPPQPPRLQPPQHSVCQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5457 | 10954 | A | 5780 | 2 | 643 | GTRLFEQLGEYKFQNALLIRYTKKV PQVSTPTLVEVSRNLGKVGSKCCK HPESKKECPVQEDYLSRGSWNQLL CVCIEKTPVKLTESPKC\CTESLG*T GRPLLFSALGKFDWKHYGFPKRSF NCLKTFHLSMAGFMAHFEEGRRT NSRKTNWHLFELVETQGPRQQKRQ LKA\VMGGFAAFVEKCKKADDKET CFAEEGKKLVAASQAALGL |
| 5458 | 10955 | A | 5781 | 1 | 135 | |
| 5459 | 10956 | A | 5782 | 1 | 330 | |
| 5460 | 10957 | A | 5783 | 247 | 434 | |
| 5461 | 10958 | A | 5784 | 140 | 2569 | SGSPVLDPSEPQPLAAMHVIKRDGR QERVMFDKITSRIQKLCYGLNMDF VDPAQITMKVIQGLYSGVTTVELDT LAAETAATLTTKHPDYAILAARIA\V SNLHKETKKVFSVDMEDLYNYINP HNGKHSPMVAKSTL\DIVLANKDRL NSAIIYDRDFSYNFYGFKTLERSYLL KINGKVAERPQHMLMRVSVGIHKE DIDAAIETYNLLSERWFTHASPTLFN AGTNRPOLSSCFLLSMKDDSIIEGY DTLKQCALISKSAAGGIGVAVSCIRA TGSYIAGTNGNSNGLVPMLRVYNN TARYVDQGGNKRPGAFIYLEPWH LDIFEFLDLKKNTGKEEQRRDLFF ALWIPDLFMKRVETNQDWSLMCPN ECPGLDEVWGEEFEKLYASYEKQG RVRKVVKAAQQLWYAIIESQTETGTP YMLYKDSCNRKSNQQNLGTIKCSN LCTEIVEYTSKDEVAVCNLASLALN MYVTSEHTYDFKKLAEVTKVVVRN LNKIIDINYYPVPEACLSNKRHRPIGI GVQGLADAFILMRYPFESAEQAQLLN KQIFETIYYGALEASCDLAKEQGPY ETYEGSPVSKGILQYDMWNVTPTD LWDWKVLKEKIAKYGIRNSLLIAP MPTASTAQILGNNESEIPTYTSNIYTR RVLSGEFQIVNPHLLKDLTERGLWH EEMKNQIIACNGSIQSIPEIPDDLKQL YKTVWEISQKTVLKMAAERGAFID QSQSLNIHIAEPNYGKLTSMHFGYGW KQGLKTGMYYLRTRPAANPIQFTL NKEKLDKEKVSKEEEKERNTAA MVCLENRDECLMCGS |
| 5462 | 10959 | A | 5785 | 1 | 161 | |
| 5463 | 10960 | A | 5786 | 2 | 170 | |
| 5464 | 10961 | C | 5787 | 219 | 398 | MSQESVILFYSGMSLFLFLFRVVT NFTFFPLAVICIRASHLLACPLPSLS LPHQPTH* |
| 5465 | 10962 | A | 5788 | 2 | 472 | |
| 5466 | 10963 | A | 5789 | 3720 | 5308 | PLLPLSPPHLTEVEGQGRMVGTEE TWSNCSGAFKPKCSPQPQICLV LAP TRELAQQVQQVADDYGKCSRLKST CIYGGAPKGPQIRDLERGVEICISTP GRLIDFLESGKTNLSRCTYLVLDET DKMLDMGSEPQIL*IGDPIRPDRQTL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MWSATWPKEVRQLAEDFLRDYTOI NVGNLELSANHNILQIVDVCMESEK DHKLIQLMEEIMAEKENKTIFVETK RRCDDLTRMRDGPAMCIHGD KSQPERDWVLNEFRSGKAPILIATD VASRGLDVEDVKFVINYDYPNSSD YVHRIGRTARSTNKGTAFTFTPGN LKQARELIKVLEENQAINPKLMQL VDHRGGGGGGGGKGGRSRYRTTSSA NNPNLMYQDECDRLRGVKDGGGR RDSASYRDRSETDRAGYANGSGYG SPNSAFGAQAGQYTYGQGTGAAA YGTSSYTAQEYGAGTYGASSTTSTG RSSQSSSQFSGIGRSGQQPQPLMS QQFAQPPGATNMIGYMGQTAYQYP PPPPPPPSRK |
| 5467 | 10964 | A | 5790 | 1 | 307 | |
| 5468 | 10965 | A | 5791 | 2821 | 5781 | |
| 5469 | 10966 | A | 5792 | 1 | 981 | |
| 5470 | 10967 | A | 5793 | 99 | 1023 | NHKDGEKTEQKNGKL*KSECLSKN KAGGITLPDFKLYKATVTKTAWY WYQNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGNDLNFKNWC WENWLAICRKLKLDPLTPYTKINS RWIQDLNIRPKNIKTLEEILGNTIQDI GMGKDFKSKTPKAMAIAKIDKW DLIKLSFCTEKETTIRVNRQPTWE KIFAIYSSEKGLISRIYNELQQIYKKK TNNPIQKRVKDMNRHFSKEDIYAA K\KT*KNAHHHMKKCSSSPAIREIQI KTTMRYHLIPRMVIIKKSGNKGCV RGCGEIGTVLH |
| 5471 | 10968 | A | 5794 | 3 | 1218 | |
| 5472 | 10969 | B | 5795 | 1 | 1098 | MIDKGDITDPSEIQTIREYYNYLY TNKLENLEEMDKFLDTYTLPRLNQ EEVESLNRPTTGSEIEAIMNSLPTKK VQDQMDSQPNSTRVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADDMIV YLENPIVSARNLLKLIGNFSKVSGY KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLKRDVKDLFK ENYKPLLKEIKEDTNKWKSIKSWV GRINIMKMAILPKVIYRFNAIPNKL MPFFTELEKTTLKFIWNQKRAHIAK SILSQKNKAGGITLPDFKLYKATV TKTAWYWYQNRDIDQWNRTEPSEI MPHIYNHLIFDKPDKNKKWGKDSL FNKWCWENWQPYVES* |
| 5473 | 10970 | A | 5796 | 1 | 1245 | |
| 5474 | 10971 | A | 5797 | 1 | 969 | MIVYLENPIVSAQNLLKLIGNFSRVS GYKINVQKSQAFLYTNNRQTENQII SELPFTIASKRIKYLGIQLTRDVKDL FKENYKTLLKEIKEDTKKWKNIKCS WVGRINIVKIAILPKVIYRFSAIPIKL PMTFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGIMLPDFKLYKATV TKTAWYWYQNRDIDQWNRTEPS EIMLHIYKHLIFDKPDKNKQWGKDS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /-possible nucleotide deletion; \-possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LFNKWCWENWLAICRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKMLEEN LGNTIQDIGTGKDFMSKTPKAMAT KAKIDKWDL/LRFCTAK*TTIRV |
| 5475 | 10972 | B | 5798 | 1 | 1383 | MGDFNTPLSTLDRSKRQKVKKDIQ ELNSALHQVDLIDYRTPYPKSTEYT FFSAQHHTYSKTDHIVGSKELLSKC KRTEITNCLSDHSAIKLELRJKKLTQ NRSTTWKLNLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLRTLK AVCRGKFVALNAHQKQKISKIDTL TSQLELEKQEQTHSKASRRQEI TKI RAELKEIETQKTLQKINDSRSWAIR QEKEIKGIQLGKEEVQLSLFADDMI VHLENPIVSAQNLLKLIGNFSKVSG YKINVKKSQAFLYTNNRQTESQIMS EFPFTIASKRIKYLGIQLTRDVKDLF KENYKTLLEIKEDTNKWKNI PCS WVGRINIVKMAILPKVIYRFNAISIK LPMFTFTEL GKPTLKL VWNQKRVRI AKSILSQKNKAGGIMLPDFKLYYKA TVTKTAWYQNRDIDQWNRTEP SEIMPHITTI* |
| 5476 | 10973 | A | 5799 | 1 | 1272 | MIISMDAEKAFDKIQQCFMLKTLNK LGIDGTYLKKIRAIYDKPTVNIILNG QKLEALPLKTGTRQGCPLSPLLFNIV LQALARAIRQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVKAQNLLKL ISNFSKVSGYKISMQKSQAFLYTNN RQIESQIMSELPFTIASKRIKYLGIQL TRDVKDLFKENYKPLLNEIKEDKN KWKNIPCSWVGRINIVKMAILPKFI WRQKRAHIAKSILSQKNKAGGIKLP DFKLYYKATVTKTAWYQNRDI DQWNRTEPSEIMLHIHNYLIFDKPD KNKKWRKDSL FNKWCWENWLAK CRKLKLHPFLT PYTKINSRWIKDLH VRPKTIKMLEENLGITIQDKGMGKD FMSKTPEALATKANIDKSDLIKLS SCKVETTIRVNRQPTWEKIFAIYSS |
| 5477 | 10974 | A | 5800 | 1 | 1398 | |
| 5478 | 10975 | A | 5801 | 564 | 2444 | LTNQKKSRTRWIHSRILPEVQGGAV LEVLAIRAIRQEKVEVKGIQLGKEEV KLSLFADDMIVYLENPIISAQNLLKL IGNFSKVSGYKINVQKSQAFLYTNN RETESQIMSELPFTTASRIKYLGIQ LTRDVKELFKETYNPLLNEIKEDTT KWKNIPCSWVGRINIVKIALPKVICI FNAIPIKLPMTFFTELEKTTLKFI RNQ KRARIAKSILSQKNKAGDVTLPDFK LYYKATVTKTVWYQNRDIDQW NRTEPSEIILHIYNHLIFDTPDKNKK WGKDSL FNKLCWENWLAICRKLKL DPFFTPYTKINSRWIKDLHVRPKTIK MLEENLGNTIQDIGIGKDFMTKTQK AMATNAEIIHKWDLIKLKH FCTAKE TTIRVNRQPTKWENIFAIYSSDKRLI SRIYKELKHIYKRKTNNPINKWAKD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPVRMAIHK SGNNRCWRGCGENHSQQTTITRTKIQ TLHVLNHRWELNNENTWTQEGEH HTLGPVVGWGRGEGQQCISPYSMG KASIPHAVLWVFFGLCQNAPNLDW SLVSLWWCLLGFTNFFCKEPDCKY VRLFRPLGIVFATPPLPPPPSSSTS S |
| 5479 | 10976 | A | 5802 | 1 | 2430 | |
| 5480 | 10977 | A | 5803 | 2022 | 4573 | |
| 5481 | 10978 | A | 5804 | 1169 | 3077 | VHCRFWILALCOMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQNLLIL QLISNFSKVSGYKINVQKSQAFLYT NNRQTESQMRSELPFTVATKRIKYL GIQLTRDVKDLFKENYKLLNEIKE DTNKWKNIPRSWVGGRINLVKMAI LPKVITYRFNAIPIKLPMFTFFTELEKTT LKFIWNQKRALIAKSSLSQKNKTGG ITLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNLIFDK PDKNKKIWGKDSL FNK WFWENCL AICRKLKLDPFLVTNYTKINSRWIKD LNFRPKTIKTLEDNLGNTIQDIGMG KDFMSLP/KTPEAMATKAKIDKWD LIKLSFCTAKETTIRVNRQPTKWE KIFAIYSSDKGLISRIYNELKQIYKK KITNNPIKKWAKDTNRHFSKEDIYA ANRHMRCSSSLVIREMQIKTTMR YHLTPVRTAIHKSGDNRCWRGCGE IGTLLHCWWDCCLVQPLWKS VWR FLRDLELEIPFDPAIPLLG IY PKDYKS CCYKDTCTCMFIAALFTIAKTWNQP KCPTMIDWIKKMWHIYTMEYYAAI KNDEFVSFVGTWMKLEIILSKLSQE QKTKHCIFSLIGGN |
| 5482 | 10979 | A | 5806 | 133 | 358 | |
| 5483 | 10980 | A | 5807 | 3 | 164 | |
| 5484 | 10981 | A | 5808 | 1573 | 1720 | |
| 5485 | 10982 | A | 5809 | 1573 | 1720 | |
| 5486 | 10983 | A | 5810 | 1 | 4860 | |
| 5487 | 10984 | A | 5811 | 2 | 2887 | VRVIKSEDDVLVVCPTILTEDGMQA QHLGATLALYRLVKGQSVHQLLPP TYRDVWLEWSDAEKKREELNKME TNKPRDLFIKLLNKLKQQQQQQQ QHSENKRENSDPEESWENLVSDE DFSALSLESANVEDLEPVRNLFRKL QSTPKYQKLLKERQQLPVFKHRDSI VETLKRHRV V V VAGETGSGKSTQV PHFLLEDLLLNEWEASKCNIVCTQP RRISAVSLANRVCDELGCENGPGG RNSLCGYQIRMESRACESTRLLYCT TGVFA*GKLQEDGLSK*CVSMFIVD EV\HER\SVQSDFLIILKEILQKRSD LHLILMSATVDSEKFSTYFTHCPILR ISGRSYPVEVFHLEDIIEETGFVLEK |

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| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; / = possible nucleotide deletion; \ = possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DSEYCQKFLEEEEEEVTINVTSKAGGI KKYQEYIPVQTGAHADLNPFIYQKY SSRTQHAILYMNPHKINLDLILELLA YLDKSPQFRNIEGAVLIFLPGLAHIQ QLYDLLSNDRRFYSEYKVIALLHSI LSTQDQAAAFITLPPPGVRKIVLATNI AETGITIPDVVFVIDTGRTKENKYHE SSQMSSLVETVFSKASALQRQGRA GRVRDGFCEFRMYTRERFEGFMDYS VPEILRVPLEELCLHIMKCNLGSPED FLSKALDPPQLQVISNAMNLLRKIG ACELNEPKLTPLGQHLAALPVNVKI GKMLIFGAIFGCLDPVATLAAVMTE KSPFTTPIGRKDEADLAKSALAMAD SDHLTIYNAYLGWKKARQEGGYRS EITYCRRNFLNRTSLTLEDVKQELI KLVKAAGFSSSTTSTWEGNRASQT LSFQEIALLKAVLVAGLYDNVKGII YTKSVDVTEKLACIVETAQGKAQV HPSSVNRDLQTHGWLLYQEKIRYA RVYLRETTLITPPVLLFGGDIEVQH RERLLSIDGWYFQAPVKIAVIFKQL RVLIDSVLRKKLENPKMSLENDKIL QITELIKTENN |
| 5488 | 10985 | A | 5812 | 1 | 132 | |
| 5489 | 10986 | A | 5813 | 383 | 667 | |
| 5490 | 10987 | A | 5814 | 2444 | 2755 | DYYYFFEMESCSVAQAGVQWRDL GSLQPPPPSSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVGQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS |
| 5491 | 10988 | A | 5815 | 1724 | 1941 | AHLLYEWIFFFFFFFFFEMESHVAQA GVLWRDLSSLQAPPPGQSQSDSPAS ASWVAGITGACHHARHEWNFKC |
| 5492 | 10989 | A | 5817 | 37 | 2496 | |
| 5493 | 10990 | A | 5818 | 2 | 1814 | |
| 5494 | 10991 | A | 5819 | 1 | 394 | |
| 5495 | 10992 | A | 5820 | 2 | 1785 | QLFACVPKTSPPATVISSVTSTCSSL PSVSSAPITSGQAPTIFLPASTSQAQ LSSQKMESFSAVPPTKEKVSTQDQP MANLCTPSSTANSCSSASNTPGAP ETHPSSSPTPTSSNTQEEAQSSVSD LSPMSMPFASNSEAPLTLTSPRMV AADNQDTSNLPQLAVPAPRVSHRM QPRGSFYSMVPNATHQDPQSIFVT NPVTLTPPQGPPAAVQLSSAVNIMN GSQMHNIPANKSLPPTFGPATLFNH FSSLFDSSQVPANQGWGDGPLSSRV ATDASFTVQSAFLGNSVLGHLENM HPDNSKAPGFRPPSQRIVSTSPVGLP SIDPSG\SSPSSSAPLASFSGIPGNQ GFFLQGP\APVGGLLSFNRQHF/SFP HPW\TSASNSCDSPIPSVSSGSSSPLS ATSVAPPTLG\QPKGSQCQSRIRKGY LPPIGTERLARILQGGSAQAPAGVT SFVAPVGHSGUWSFGVNAVSEGLS GWSQSVMG\NHPMAFNNSGPKAH FSQHQPMERDDSGMVAPSNIFHQP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MASGFVDFSKGLPISMYGGTIIPSHP QLADVPGGPLFNGLHNPDPAWNPM IKVIQNSTECTDAQQVKA |
| 5496 | 10993 | A | 5821 | 3 | 125 | |
| 5497 | 10994 | A | 5822 | 3448 | 3831 | KNRFCSGVSSNSKSNNSCVYVYIDR DIDTHTYIHIHTNICIHLFFFFFETES HALSPRLECNGVISAHCNLHPPG\SS DSPASAARVAG\ITGTCHHAQLIFFF FVFLVETGFHHAAQAGSQTPDLR*S TPLGFPKC*DYRR/AAIVPGIFLLH*I R*KVPTLLTDMRNASEYDCDFSTN KIDKEETFS*NASLNLCLLST*PYEM VTHFKGY*ILPLFFFFFLRQSL/SSVT QAGVQWHNLGSLQPLPPGFKQFSC LSLPSSWDYRYQLPRLA/NF/FVFLV ETGFHHAAQAGSQTPDLR |